

```
Method
                  BLASTX
NCBI GI
                   q4406780
BLAST score
                   509
E value
                   2.0e-51
                   128
Match length
% identity
                   75
                   (AC006532) putative multispanning membrane protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   11539
                   21655 1.R1040
Contig ID
5'-most EST
                  LIB3051-035-Q1-K1-C4
Method
                   BLASTX
NCBI GI
                   g2739386
BLAST score
                   475
E value
                   1.0e-47
Match length
                   168
% identity
                   59
                  (AC002505) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   11540
Contig ID
                   21656 1.R1040
5'-most EST
                  LIB3051-037-Q1-K1-C4
Method
                  BLASTX
NCBI GI
                   g2224901
BLAST score
                  263
E value
                   7.0e-23
Match length
                   136
% identity
                   49
                  (U67134) PcMYB1 protein [Petroselinum crispum]
NCBI Description
Seq. No.
                   11541
Contig ID
                   21656 2.R1040
5'-most EST
                   LIB3087-004-Q1-K1-G4
Method
                   BLASTX
NCBI GI
                   g2224899
BLAST score
                   377
E value
                   5.0e-36
Match length
                   203
% identity
                   47
NCBI Description
                  (U67133) DNA-binding protein PcMYB1 [Petroselinum crispum]
                   11542
Seq. No.
Contig ID
                   21657 1.R1040
5'-most EST
                   dpv701103216.h1
Method
                   BLASTX
NCBI GI
                   q1786134
BLAST score
                   207
                   1.0e-16
E value
                   97
Match length
% identity
                   51
NCBI Description
                  (AB000451) PEThy; ZPT2-5 [Petunia x hybrida]
```

Seq. No. 11543

Contig ID 21658 1.R1040 5'-most EST zsg701129482.h1

Method BLASTX

```
NCBI GI
                   q4519417
BLAST score
                   382
                   2.0e-36
E value
Match length
                   109
% identity
                   62
NCBI Description
                  (AB024327) WD-40 repeat protein [Homo sapiens]
Seq. No.
                   11544
Contig ID
                   21661_1.R1040
5'-most EST
                   fua701041663.h1
Method
                   BLASTX
NCBI GI
                   q3935138
BLAST score
                   969
                   1.0e-105
E value
Match length
                   358
% identity
                   54
NCBI Description
                  (AC005106) T25N20.2 [Arabidopsis thaliana]
Seq. No.
                   11545
Contig ID
                   21662_1.R1040
5'-most EST
                   LIB3051-039-Q1-K1-B10
Method
                   BLASTX
NCBI GI
                   g2642450
BLAST score
                   669
E value
                   2.0e-70
Match length
                   168
% identity
                   77
                   (AC002391) putative metal ion transporter (Nramp)
NCBI Description
                   [Arabidopsis thaliana] >gi 3169188 (AC004401) putative
                   metal ion transporter (Nramp) [Arabidopsis thaliana]
Seq. No.
                   11546
Contig ID
                   21665 1.R1040
5'-most EST
                   jC-gmst02400031f11a1
Method
                   BLASTX
NCBI GI
                   q4521322
BLAST score
                   402
E value
                   8.0e-39
Match length
                  156
% identity
                   53
NCBI Description
                   (U11790) mitotic centromere-associated kinesin [Cricetulus
                  griseus]
Seq. No.
                  11547
Contig ID
                  21665 3.R1040
5'-most EST
                  LIB3170-049-Q1-K2-E3
Method
                  BLASTX
NCBI GI
                  q2497528
BLAST score
                  467
E value
                  1.0e-46
Match length
                  199
% identity
                  50
```

Seq. No. 11548

laevis]

NCBI Description

KINESIN-LIKE PROTEIN KIF2 (KINESIN-RELATED PROTEIN XKIF2)

>gi\_1171151 (U36486) kinesin-related protein XKIF2 [Xenopus

```
Contig ID
                  21665 4.R1040
5'-most EST
                  uC-gmflminsoy016g07b1
Method
                  BLASTN
NCBI GI
                  q4159706
BLAST score
                  43
E value
                  5.0e-15
Match length
                  207
% identity
                  80
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MGL6, complete sequence [Arabidopsis thaliana]
Seq. No.
                  11549
Contig ID
                  21666 1.R1040
5'-most EST
                  hyd700728575.h1
Method
                  BLASTX
NCBI GI
                  q2864624
BLAST score
                  558
E value
                  1.0e-90
Match length
                  437
% identity
                  25
NCBI Description
                 (AL021811) putative protein [Arabidopsis thaliana]
Seq. No.
                  11550
Contig ID
                  21672 1.R1040
5'-most EST
                  LIB3051-111-Q1-K1-E2
Seq. No.
                  11551
Contig ID
                  21674 1.R1040
5'-most EST
                  uC-gmrominsoy069a01b1
Method
                  BLASTX
NCBI GI
                  g1717871
BLAST score
                  577
E value
                  2.0e-59
Match length
                  259
% identity
                  45
NCBI Description
                  UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 15 (UBIQUITIN
                  THIOLESTERASE 15) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE
                  15) (DEUBIQUITINATING ENZYME 15) >gi_1078006_pir__S53974
                  hypothetical protein YMR304w - yeast (Saccharomyces
                  cerevisiae) >gi_798946_emb_CAA89137 (Z49212) unknown
                  [Saccharomyces cerevisiae]
Seq. No.
                  11552
Contig ID
                  21675 1.R1040
5'-most EST
                  LIB3170-011-Q1-K1-B10
Method
                  BLASTX
NCBI GI
                  g2244993
BLAST score
                  316
E value
                  6.0e-29
                  91
Match length
% identity
                  66
NCBI Description
                  (Z97341) similarity to AMP-activated protein kinase beta
```

NCBI Description

(29/341) similarity to AMP-activated protein kinase beta [Arabidopsis thaliana]

Seq. No. 11553

Contig ID 21677\_1.R1040 5'-most EST jex700905308.h1



Method BLASTX g2498512 NCBI GI BLAST score 310 E value 4.0e-28 Match length 229 33 % identity NCBI Description LDLC PROTEIN >gi 1082264 pir A53542 brefeldin A-sensitive Golgi protein LDLC - human >gi\_575654\_emb\_CAA84427\_ (Z34975) ldlCp [Homo sapiens] 11554 Seq. No. Contig ID 21687 1.R1040 5'-most EST LIB3051-112-Q1-K1-E6 BLASTX q3776559

Method BLASTX
NCBI GI g3776559
BLAST score 440
E value 4.0e-43
Match length 165
% identity 57

NCBI Description (AC005388) Strong similarity to gene F14J9.26 gi 3482933

cdc2 protein kinase homolog from A. thaliana BAC

gb\_AC003970. ESTs gb\_Z35332 and gb\_F19907 come from this

gene. [Arabidopsis thaliana]

Seq. No. 11555

Contig ID 21688 1.R1040

5'-most EST LIB $30\overline{5}1-114-Q1-K1-E10$ 

Method BLASTN
NCBI GI g2760167
BLAST score 43
E value 7.0e-15
Match length 179
% identity 81

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MCO15, complete sequence [Arabidopsis thaliana]

Seq. No. 11556

Contig ID 21689 1.R1040 5'-most EST asn701134480.h1 Method BLASTX

Method BLASTX
NCBI GI g3776559
BLAST score 639
E value 1.0e-66
Match length 160
% identity 73

NCBI Description (AC005388) Strong similarity to gene F14J9.26 gi\_3482933

cdc2 protein kinase homolog from A. thaliana BAC

gb\_AC003970. ESTs gb\_Z35332 and gb\_F19907 come from this

gene. [Arabidopsis thaliana]

Seq. No. 11557

Contig ID 21691\_1.R1040

5'-most EST LIB3109-021-Q1-K2-F8

Method BLASTX
NCBI GI g2632106
BLAST score 1493
E value 1.0e-166

2000



391 Match length % identity 71 (Z98760) arginyl-tRNA synthetase [Arabidopsis thaliana] NCBI Description Seq. No. 11558 21692 1.R1040 Contig ID  $6HA - 0\overline{2} - Q1 - B1 - C9$ 5'-most EST 11559 Seq. No. Contig ID 21693 1.R1040 5'-most EST zzp700833775.h1 BLASTX Method g2498883 NCBI GI BLAST score 984 E value 1.0e-107 Match length 344 49 % identity SPLICEOSOME ASSOCIATED PROTEIN 145 (SAP 145) (SF3B150) NCBI Description >gi 1173905 (U41371) spliceosome associated protein [Homo sapiens] 11560 Seq. No. 21694 1.R1040 Contig ID zsg701119058.h1 5'-most EST BLASTX Method q4325345 NCBI GI BLAST score 1719 E value 0.0e+00Match length 490 68 % identity (AF128393) similar to thioredoxin-like proteins (Pfam: NCBI Description PF00085, Score=42.9, E=1.4e-11, N=1); contains similarity to dihydroorotases (Pfam: PF00744, Score=154.9, E=1.4e-42, N=1) [Arabidopsis thaliana] Seq. No. 11561 21695\_1.R1040 Contig ID 5'-most EST jsh701066575.h1 Method BLASTX NCBI GI g1869901 BLAST score 287 E value 2.0e-25 Match length 140 36 % identity (X99699) XIAP associated factor-1 (ZAP-1) [Homo sapiens] NCBI Description 11562 Seq. No. 21695 2.R1040 Contig ID 5'-most EST g5058490 Method BLASTX

NCBI GI q1869901 BLAST score 268 4.0e-23 E value Match length 132 % identity

NCBI Description (X99699) XIAP associated factor-1 (ZAP-1) [Homo sapiens]

```
11563
Seq. No.
                  21697 1.R1040
Contig ID
5'-most EST
                  jC-gmst02400018g03a1
Method
                  BLASTX
NCBI GI
                  g3935152
BLAST score
                  483
                  1.0e-48
E value
Match length
                  111
                  75
% identity
NCBI Description (AC005106) T25N20.16 [Arabidopsis thaliana]
                  11564
Seq. No.
                  21697 2.R1040
Contig ID
                   jC-gmf102220069f09a1
5'-most EST
Method
                  BLASTX
NCBI GI
                   q3935152
BLAST score
                   439
E value
                   1.0e-43
                   97
Match length
                   76
% identity
                   11565
Seq. No.
Contig ID
                   21698 1.R1040
```

NCBI Description (AC005106) T25N20.16 [Arabidopsis thaliana]

5'-most EST leu701156073.h1 BLASTX Method NCBI GI g3273101 BLAST score 312

E value 2.0e-28 194 Match length % identity 40

(Y17613) N7 protein [Medicago truncatula] NCBI Description

11566 Seq. No.

21700 1.R1040 Contig ID

5'-most EST jC-gmle01810080h05a1

Method BLASTX g1737492 NCBI GI BLAST score 378 4.0e-36 E value 133 Match length % identity 23

(U81318) poly(A)-binding protein [Triticum aestivum] NCBI Description

11567 Seq. No.

21701 1.R1040 Contig ID

uC-gmflminsoy047e07b1 5'-most EST

BLASTN Method g1403521 NCBI GI BLAST score 134 E value 4.0e-69 Match length 359 89 % identity

NCBI Description P.vulgaris mRNA for chitinase

11568 Seq. No.

21704 1.R1040 Contig ID

2002



```
iex700903486.hl
5'-most EST
                  BLASTX
Method
                  g2702281
NCBI GI
                  367
BLAST score
                  8.0e-35
E value
                  94
Match length
                  71
% identity
                  (AC003033) putative protein disulfide isomerase precursor
NCBI Description
                   [Arabidopsis thaliana]
                  11569
Seq. No.
                  21705 1.R1040
Contig ID
                  LIB3051-067-Q1-K1-B6
5'-most EST
                  BLASTX
Method
                  g2351378
NCBI GI
                  824
BLAST score
                   5.0e-88
E value
                   295
Match length
                   55
% identity
                  (U54558) translation initiation factor eIF3 p66 subunit
NCBI Description
                   [Homo sapiens] >gi_4200328_emb_CAA18440_ (AL022313)
                   EIF3-P66 [Homo sapiens]
                   >gi_4503523_ref_NP_003744.1_pEIF3S7_ UNKNOWN
                   11570
Seq. No.
                   21707 1.R1040
Contig ID
                   LIB3109-027-Q1-K1-G5
5'-most EST
                   BLASTX
Method
                   q729332
NCBI GI
                   308
BLAST score
E value
                   2.0e-28
                   111
Match length
                   52
% identity
                   DHP1 PROTEIN >gi_629894_pir__S43891 dhp1 protein - fission
NCBI Description
                   yeast (Schizosaccharomyces pombe) >gi_496393_dbj_BAA04601_
                   (D17752) Dhp1 protein [Schizosaccharomyces pombe]
                   >gi_1177359_emb_CAA93235_ (Z69240) dna exoribonuclease
                   [Schizosaccharomyces pombe]
                   11571
Seq. No.
                   21708 1.R1040
Contig ID
                   LIB3107-047-Q1-K1-C1
5'-most EST
Method
                   BLASTX
                   g2160164
NCBI GI
                   209
BLAST score
                   2.0e-16
E value
                   69
Match length
                   55
 % identity
                   (AC000132) No definition line found [Arabidopsis thaliana]
NCBI Description
                   11572
 Seq. No.
                   21709 1.R1040
 Contig ID
                   LIB3051-081-Q1-K1-B6
 5'-most EST
                   BLASTX
 Method
                   q4559381
 NCBI GI
```

463

3.0e-46

BLAST score

E value



Match length 114 % identity 74

NCBI Description (AC006526) hypothetical protein [Arabidopsis thaliana]

Seq. No. 11573

Contig ID 21710\_1.R1040 5'-most EST smc700748782.h1

Method BLASTX
NCBI GI 94455260
BLAST score 441
E value 2.0e-51
Match length 169
% identity 61

NCBI Description (AL035353) protein kinase-like protein [Arabidopsis

thaliana]

Seq. No. 11574

Contig ID 21711 1.R1040

5'-most EST jC-gmf102220086g04d1

Method BLASTX
NCBI GI g3176726
BLAST score 449
E value 2.0e-44
Match length 140
% identity 64

NCBI Description (AC002392) putative serine proteinase [Arabidopsis

thaliana)

Seq. No. 11575

Contig ID 21713\_1.R1040 5'-most EST asn701135209.h1

Method BLASTX
NCBI GI 94220479
BLAST score 1560
E value 0.0e+00
Match length 402
% identity 84

NCBI Description (AC006069) unknown protein [Arabidopsis thaliana]

Seq. No. 11576

Contig ID 21714 1.R1040

5'-most EST uC-gmrominsoy173c02b1

Method BLASTX
NCBI GI g3033391
BLAST score 373
E value 9.0e-36
Match length 121
% identity 57

NCBI Description (AC004238) putative amino acid transporter [Arabidopsis

thaliana]

Seq. No. 11577

Contig ID 21715 1.R1040

5'-most EST LIB3170-061-Q1-K2-B4

Method BLASTX
NCBI GI g4468984
BLAST score 643

```
E value
                  4.0e-67
Match length
                  213
                   60
% identity
NCBI Description
                  (AL035605) putative protein [Arabidopsis thaliana]
                  11578
Seq. No.
Contig ID
                  21716 1.R1040
5'-most EST
                  sat701004561.h1
Method
                  BLASTX
NCBI GI
                  q818849
BLAST score
                  417
E value
                  9.0e-41
Match length
                  113
                  65
% identity
                  (U25430) nucleotide pyrophosphatase precursor [Oryza
NCBI Description
                  sativa]
Seq. No.
                  11579
                  21723 1.R1040
Contig ID
                  zhf700960253.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q2275211
BLAST score
                  603
E value
                  1.0e-62
Match length
                  171
% identity
                  70
                  (AC002337) RNA helicase isolog [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  11580
                  21724 1.R1040
Contig ID
5'-most EST
                  kl1701206422.h1
                  BLASTX
Method
                  g2245024
NCBI GI
BLAST score
                   301
                   2.0e-27
E value
Match length
                   124
% identity
NCBI Description
                  (Z97341) cyanohydrin lyase homolog [Arabidopsis thaliana]
                   11581
Seq. No.
                   21725 1.R1040
Contig ID
                   jC-gmro02800032h12a1
5'-most EST
Method
                  BLASTX
                  g3355617
NCBI GI
BLAST score
                   491
E value
                   7.0e-49
Match length
                  110
% identity
                   81
                  (AJ000229) unnamed protein product [Hordeum vulgare]
NCBI Description
Seq. No.
                  11582
```

Contig ID 21727\_1.R1040

5'-most EST LIB3170-051-Q1-K1-A2

Method BLASTX
NCBI GI g2347188
BLAST score 335
E value 3.0e-31

Match length 102 % identity 53 (AC002338) laccase isolog [Arabidopsis thaliana] NCBI Description >gi 3150401 (AC004165) putative laccase [Arabidopsis thaliana] 11583 Seq. No. 21728 1.R1040 Contig ID 5'-most EST uC-gmflminsoy100h04b1 Method BLASTX a117188 370

NCBI GI BLAST score 4.0e-35 E value Match length 179 % identity 41

NCBI Description CYTOCHROME P450 71A1 (CYPLXXIA1) (ARP-2)

>gi 81423 pir A35867 cytochrome P450 71A1 - avocado

Seq. No. 11584

Contig ID 21729 1.R1040

LIB3170-052-Q1-K1-E7 5'-most EST

BLASTX Method NCBI GI q416639 295 BLAST score E value 1.0e-26 Match length 97 % identity 66

NCBI Description INDOLE-3-ACETIC ACID INDUCED PROTEIN ARG2

>gi 287564\_dbj\_BAA03307\_ (D14411) ORF [Vigna radiata]

11585 Seq. No.

21732 1.R1040 Contig ID

5'-most EST LIB3093-051-Q1-K1-A7

Method BLASTX g2633727 NCBI GI BLAST score 361 E value 4.0e-34 Match length 196 % identity 38

NCBI Description (299111) ykrT [Bacillus subtilis]

Seq. No. 11586

21733\_1.R1040 Contig ID

5'-most EST jC-gmle01810062h08a1

Method BLASTX NCBI GI q2909781 BLAST score 748 2.0e-79 E value Match length 213 % identity 73

NCBI Description (AF020288) MgATP-energized glutathione S-conjugate pump

[Arabidopsis thaliana]

Seq. No. 11587

Contig ID 21741 1.R1040 vzy700752756.hl 5'-most EST

Method BLASTX



```
NCBI GI
                  q4006881
BLAST score
                   717
E value
                   1.0e-75
Match length
                  177
% identity
                  79
                  (Z99707) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  11588
                  21752 1.R1040
Contig ID
                  txt700733990.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q4539330
BLAST score
                  1094
E value
                  1.0e-119
                  341
Match length
% identity
                   65
NCBI Description
                  (AL035679) putative receptor-like protein kinase (fragment)
                   [Arabidopsis thaliana]
                   11589
Seq. No.
Contig ID
                   21759 1.R1040
5'-most EST
                   fua701042337.h1
Method
                  BLASTX
NCBI GI
                   g2583128
BLAST score
                   1022
E value
                   1.0e-111
Match length
                   246
% identity
                   83
                  (AC002387) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   11590
Seq. No.
                   21759 2.R1040
Contig ID
5'-most EST
                   asn701134884.h2
Method
                   BLASTX
NCBI GI
                   q2583128
BLAST score
                   451
                   6.0e-45
E value
                   106
Match length
% identity
                   82
                  (AC002387) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   11591
                   21760 1.R1040
Contig ID
5'-most EST
                  LIB3109-029-Q1-K1-A5
Seq. No.
                   11592
Contig ID
                   21762 1.R1040
                   LIB3051-037-Q1-K1-D4
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2459440
BLAST score
                   388
                   3.0e-37
E value
Match length
                   149
                   50
```

11593 Seq. No.

% identity

NCBI Description

(AC002332) putative receptor kinase [Arabidopsis thaliana]



Contig ID 21763\_1.R1040 5'-most EST trc700561979.h1

Method BLASTX
NCBI GI g2435518
BLAST score 442
E value 1.0e-43
Match length 150
% identity 69

NCBI Description (AF024504) contains similarity to C3HC4-type zinc fingers

[Arabidopsis thaliana]

Seq. No. 11594

Contig ID 21764 1.R1040

5'-most EST LIB31 $\overline{3}$ 9-023-P1-N1-H5

Method BLASTX
NCBI GI g3367568
BLAST score 927
E value 1.0e-100
Match length 234
% identity 76

NCBI Description (AL031135) protein kinase - like protein [Arabidopsis

thaliana]

Seq. No. 11595

Contig ID 21764\_2.R1040 5'-most EST g5126628

Seq. No. 11596

Contig ID 21764\_3.R1040

5'-most EST LIB3093-025-Q1-K1-E8

Method BLASTX
NCBI GI g3367568
BLAST score 302
E value 2.0e-27
Match length 74
% identity 76

NCBI Description (AL031135) protein kinase - like protein [Arabidopsis

thaliana]

Seq. No. 11597

Contig ID 21766 1.R1040

5'-most EST LIB30 $\overline{5}$ 1-084-Q1-K1-F6

Method BLASTX
NCBI GI g3142291
BLAST score 442
E value 6.0e-44
Match length 130
% identity 63

NCBI Description (AC002411) Contains similarity to adenylate cyclase

gb\_AF012921 from Magnaporthe grisae. EST gb\_Z24512 comes

from this gene. [Arabidopsis thaliana]

Seq. No. 11598

Contig ID 21770\_1.R1040

5'-most EST LIB3051-114-Q1-K1-F6

Method BLASTX NCBI GI g2911059



```
BLAST score 514
E value 4.0e-52
Match length 132
% identity 73
NCBI Description (AL021961) putative protein [Arabidopsis thaliana]
Seq. No. 11599
```

Contig ID 21771\_1.R1040 5'-most EST LIB3087-011-Q1-K1-B9

Method BLASTX
NCBI GI g1172555
BLAST score 766
E value 3.0e-81
Match length 276
% identity 54

NCBI Description 34 KD OUTER MITOCHONDRIAL MEMBRANE PROTEIN PORIN

(VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN) (VDAC)

(POM 34) >gi\_629720\_pir\_\_S46936 34K porin - potato >gi\_1076682\_pir\_\_A55364 porin (clone pPOM-34) - potato mitochondrion >gi\_516166\_emb\_CAA56599\_ (X80386) 34 kDA

porin [Solanum tuberosum]

Seq. No. 11600

Contig ID 21789 1.R1040

5'-most EST jC-gmle01810068d10a1

Method BLASTX
NCBI GI g3135263
BLAST score 878
E value 1.0e-94
Match length 231
% identity 74

NCBI Description (AC003058) hypothetical protein [Arabidopsis thaliana]

Seq. No. 11601

Contig ID 21791\_1.R1040 5'-most EST epx701108317.h1

Method BLASTX
NCBI GI g2689720
BLAST score 494
E value 9.0e-50
Match length 144
% identity 67

NCBI Description (AF037168) DnaJ homologue [Arabidopsis thaliana]

Seq. No. 11602

Contig ID 21791\_2.R1040 5'-most EST fde700872837.h1

Method BLASTX
NCBI GI g2689720
BLAST score 187
E value 4.0e-14
Match length 65
% identity 58

NCBI Description (AF037168) DnaJ homologue [Arabidopsis thaliana]

Seq. No. 11603

Contig ID 21793\_1.R1040

2009



```
5'-most EST
                  k11701206965.hl
Method
                  BLASTX
NCBI GI
                  q418507
BLAST score
                  327
E value
                  6.0e-30
Match length
                  161
% identity
                  40
                  S-ADENOSYLMETHIONINE: 2-DEMETHYLMENAQUINONE
NCBI Description
                  METHYLTRANSFERASE >gi 541097 pir S40872 hypothetical
Seq. No.
                  11604
```

protein f161 - Escherichia coli >gi\_305032 (L19201) ORF\_f161 [Escherichia coli] >gi\_1336002 (U56082) S-adenosylmethionine: 2-demethylmenaquinone methyltransferase [Escherichia coli] >gi\_1790364 (AE000467) menaquinone biosynthesis, unknown [Escherichia coli]

Contig ID 21794 1.R1040 rlr700895453.hl 5'-most EST Method BLASTX NCBI GI q542200 BLAST score 505 E value 9.0e-51 248 Match length % identity 41

NCBI Description hypothetical protein - garden asparagus

>gi 452714 emb CAA54526 (X77320) unknown [Asparagus

officinalis]

Seq. No. 11605 21794 2.R1040 Contig ID 5'-most EST fde700876502.hl

Seg. No. 11606

Contig ID 21795 1.R1040 5'-most EST zhf700961481.h1

BLASTX Method NCBI GI q2088651 BLAST score 318 E value 3.0e-29 169 Match length % identity 41

(AF002109) hypersensitivity-related gene 201 isolog NCBI Description

[Arabidopsis thaliana]

Seq. No. 11607

Contig ID 21797 1.R1040

5'-most EST LIB3051-081-Q1-K1-F4

Method BLASTN NCBI GI g563624 BLAST score 73 E value 9.0e-33 Match length 101 94 % identity

NCBI Description S.tuberosum (PU141) mRNA for U14 small nucleolar RNA

Seq. No. 11608

21798 1.R1040 Contig ID

2010



LIB3092-022-Q1-K1-F11 5'-most EST Method BLASTX NCBI GI q4455155 BLAST score 615 9.0e-64 E value 153 Match length 76 % identity (ALO22023) EF-1 alpha - like protein (fragment) NCBI Description [Arabidopsis thaliana] Seq. No. 11609 Contig ID 21808 1.R1040 kmv700737708.h1 5'-most EST Method BLASTX NCBI GI g2809246 BLAST score 525 E value 2.0e-53 Match length 180 % identity 53 NCBI Description (AC002560) F2401.15 [Arabidopsis thaliana] Seq. No. 11610 Contig ID 21813 1.R1040 5'-most EST LIB3051-047-Q1-K1-G11 BLASTX Method NCBI GI g3367574 BLAST score 391 E value 9.0e-38 Match length 156 % identity 55 (AL031135) hypothetical protein [Arabidopsis thaliana] NCBI Description Seq. No. 11611 21815\_1.R1040 Contig ID 5'-most EST LIB3170-037-Q1-K1-G12 Method BLASTX NCBI GI q3600038 BLAST score 488 E value 4.0e-49 Match length 195 % identity 61 NCBI Description (AF080119) similar to Saccharomyces cerevisiae transcription regulator SPO8 (SW:P41833) [Arabidopsis thaliana] Seq. No. 11612 21816 1.R1040 Contig ID 5'-most EST LIB3051-053-Q1-K2-G2 Method BLASTX NCBI GI q2979544

BLAST score 408 E value 6.0e-40Match length 135 % identity 58

(AC003680) putative cytochrome P-450 [Arabidopsis thaliana] NCBI Description

Seq. No. 11613

```
21829 1.R1040
Contig ID
5'-most EST
                  jC-gmle01810053g12a1
                  BLASTX
Method
NCBI GI
                  q1652892
BLAST score
                  1274
E value
                  1.0e-140
Match length
                  534
                  48
% identity
NCBI Description (D90909) ABC transporter [Synechocystis sp.]
                  11614
Seq. No.
                  21829 4.R1040
Contig ID
5'-most EST
                  LIB3138-037-Q1-N1-B5
```

 Seq. No.
 11615

 Contig ID
 21831\_1.R1040

 5'-most EST
 uC-gmrominsoy101c12b1

 Method
 BLASTX

 NCBI GI
 q4510376

Method BLASTX
NCBI GI g4510376
BLAST score 423
E value 3.0e-41
Match length 184
% identity 48

NCBI Description (AC007017) unknown protein [Arabidopsis thaliana]

 Seq. No.
 11616

 Contig ID
 21850\_1.R1040

 5'-most EST
 LIB3051-019-Q1-E1-B8

 Method
 BLASTX

 NCBI GI
 g4206196

 BLAST score
 177

 E value
 8.0e-25

E value 8.0e-25
Match length 267
% identity 31

NCBI Description (AF071527) hypothetical protein [Arabidopsis thaliana]

 Seq. No.
 11617

 Contig ID
 21850\_2.R1040

 5'-most EST
 sat701009092.h1

Method BLASTX
NCBI GI g4206196
BLAST score 170
E value 6.0e-20
Match length 129
% identity 49

NCBI Description (AF071527) hypothetical protein [Arabidopsis thaliana]

Seq. No. 11618

Contig ID 21856 1.R1040 5'-most EST uaw700664314.h1

Seq. No. 11619

Contig ID 21856\_2.R1040 5'-most EST awf700839331.h1

Method BLASTX
NCBI GI g3643598
BLAST score 279



8.0e-27 E value 86 Match length (AC005395) putative poly(A) polymerase [Arabidopsis 70 % identity NCBI Description thaliana] 11620

Seq. No.

21857 1.R1040 Contig ID LIB3051-112-Q1-K1-G10 5'-most EST

BLASTX Method g2244797 NCBI GI 308 BLAST score 6.0e-28 E value 197 Match length

NCBI Description (Z97336) hypothetical protein [Arabidopsis thaliana]

11621 Seq. No.

21859 1.R1040 Contig ID

LIB3051-117-Q1-K1-G10 5'-most EST

BLASTX Method q2894596 NCBI GI 231 BLAST score 3.0e-19 E value 68 Match length

NCBI Description (AL021889) putative protein [Arabidopsis thaliana]

11622 Seq. No.

21860 1.R1040 Contig ID nsy700645635.hl 5'-most EST

BLASTX Method g2653879 NCBI GI 535 BLAST score 2.0e-54 E value 164 Match length 62

(AF026389) adenyl cyclase [Nicotiana tabacum] % identity NCBI Description

11623 Seq. No.

21912 1.R1040 Contig ID rlr700895763.hl 5'-most EST

BLASTX Method q3341679 NCBI GI 279 BLAST score 1.0e-24 E value 137 Match length

(AC003672) dynamin-like protein phragmoplastin 12 % identity NCBI Description

[Arabidopsis thaliana]

11624 Seq. No.

21913\_1.R1040 Contig ID uC-gmropic111c08b1 5'-most EST

BLASTX Method g2827631 NCBI GI 819 BLAST score



1.0e-87 E value Match length 236 65 % identity

NCBI Description (AL021636) putative protein [Arabidopsis thaliana]

Seq. No.

11625

Contig ID

21914 1.R1040

5'-most EST

LIB3092-039-Q1-K1-F2

BLASTX Method NCBI GI g1723260 BLAST score 300 E value 3.0e-50 289 Match length 40 % identity

HYPOTHETICAL GTP-BINDING PROTEIN C3F10.16C IN CHROMOSOME I NCBI Description

>gi\_1182063\_emb\_CAA93314\_ (Z69369) unknown

[Schizosaccharomyces pombe]

Seq. No.

11626

Contig ID

21937 1.R1040

5'-most EST

LIB3051-015-Q1-E1-D10

Method BLASTX NCBI GI q129320 BLAST score 1043 E value 1.0e-114 Match length 202 % identity 92

NCBI Description P21 PROTEIN >gi 99943 pir A33176 P21 protein - soybean

Seq. No.

11627

Contig ID 5'-most EST 21937 2.R1040

xpa700797216.hl

Method BLASTX NCBI GI g129320 BLAST score 268 E value 1.0e-23 Match length 62

79 % identity

NCBI Description P21 PROTEIN >gi 99943 pir A33176 P21 protein - soybean

Seq. No.

11628

Contig ID 5'-most EST 21946 1.R1040

Method

zsg701120292.hl BLASTN

NCBI GI

g3046851

BLAST score E value

37 3.0e-11

Match length % identity

125

82

NCBI Description

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MIJ24, complete sequence [Arabidopsis thaliana]

Seq. No.

11629

Contig ID 5'-most EST 21947 1.R1040 uxk700669883.hl

Method NCBI GI BLASTX g4106395

E value Match length

% identity

NCBI Description

154

75



```
BLAST score
                  1482
                  1.0e-165
E value
                  362
Match length
                  74
% identity
                  (AF073744) raffinose synthase [Cucumis sativus]
NCBI Description
                  11630
Seq. No.
                  21948 1.R1040
Contig ID
5'-most EST
                  LIB3051-015-Q1-E1-B11
Seq. No.
                  11631
                  21950 1.R1040
Contig ID
                  jC-qmf102220054c05a1
5'-most EST
Method
                  BLASTX
                  g2827713
NCBI GI
                  798
BLAST score
E value
                  3.0e-85
Match length
                  191
% identity
                  77
                  (AL021684) pyridoxal-phosphate-dependent aminotransferase -
NCBI Description
                  like protein [Arabidopsis thaliana]
                  11632
Seq. No.
Contig ID
                  21953 1.R1040
5'-most EST
                  LIB3170-065-Q1-K1-E2
Method
                  BLASTX
                  g4204270
NCBI GI
                  1159
BLAST score
                  1.0e-127
E value
Match length
                  232
                  91
% identity
                  (AC005223) branched-chain alpha-keto acid decarboxylase E1
NCBI Description
                  beta subunit [Arabidopsis thaliana]
                   11633
Seq. No.
                  21957 1.R1040
Contig ID
5'-most EST
                  leu701156115.h1
                  BLASTX
Method
                  g2230757
NCBI GI
BLAST score
                  1262
E value
                  1.0e-141
                   360
Match length
% identity
                  (Y11969) dnaJ-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  11634
Contig ID
                  21960 1.R1040
                  LIB3051-027-Q1-K1-H6
5'-most EST
Method
                  BLASTX
NCBI GI
                  g1168470
                   620
BLAST score
                   1.0e-64
```

2015

PROTEIN KINASE APK1A >gi 282877 pir S28615 protein kinase,

tyrosine/serine/threonine-specific (EC 2.7.1.-) - Arabidopsis thaliana >gi\_217829\_dbj\_BAA02092\_ (D12522)



protein tyrosine-serine-threonine kinase [Arabidopsis
thaliana]

Seq. No. 11635 Contin ID 21960

Contig ID 21960 2.R1040

5'-most EST LIB3107-020-Q1-K1-D12

Method BLASTX
NCBI GI g3461835
BLAST score 504
E value 4.0e-51
Match length 129
% identity 79

NCBI Description (AC005315) putative protein kinase [Arabidopsis thaliana]

>gi\_3927840 (AC005727) putative protein kinase [Arabidopsis

thaliana]

Seq. No. 11636

Contig ID 21961\_1.R1040

5'-most EST LIB3051-035-Q1-K1-H6

Method BLASTX
NCBI GI g4056482
BLAST score 470
E value 4.0e-47
Match length 144
% identity 38

NCBI Description (AC005896) putative ABC transporter [Arabidopsis thaliana]

Seq. No. 11637

Contig ID 21962 1.R1040

5'-most EST LIB3051-040-Q1-K1-H6

Method BLASTX
NCBI GI g2444176
BLAST score 341
E value 4.0e-32
Match length 145
% identity 50

NCBI Description (U94782) unconventional myosin [Helianthus annuus]

Seq. No. 11638

Contig ID 21979 1.R1040

5'-most EST LIB3051-042-Q1-K1-H10

Method BLASTX
NCBI GI g3287695
BLAST score 561
E value 7.0e-58
Match length 145
% identity 80

NCBI Description (AC003979) Similar to hypothetical protein C34B7.2

gb\_1729503 from C. elegans cosmid gb\_Z83220. [Arabidopsis

thaliana]

Seq. No. 11639

Contig ID 21981 1.R1040

5'-most EST LIB3093-045-Q1-K1-H11

Method BLASTN NCBI GI g575671 BLAST score 479



E value 0.0e+00 Match length 870 % identity 89

NCBI Description M. varia mRNA for pplMs protein

Seq. No. 11640

Contig ID 21981 2.R1040 5'-most EST zhf700962152.h1

Seq. No. 11641

Contig ID 21984 1.R1040

5'-most EST LIB3065-025-Q1-N1-B7

Method BLASTX
NCBI GI g3212863
BLAST score 713
E value 2.0e-75
Match length 181
% identity 75

NCBI Description (AC004005) putative translation initiation factor

[Arabidopsis thaliana]

Seq. No. 11642

Contig ID 21995 1.R1040

5'-most EST LIB3051-085-Q1-K1-B1

Method BLASTX
NCBI GI g4432821
BLAST score 648
E value 7.0e-68
Match length 176
% identity 71

NCBI Description (AC006593) putative transmembrane protein [Arabidopsis

thaliana]

Seq. No. 11643

Contig ID 21996 1.R1040

5'-most EST uC-gmrominsoy302g09b1

Method BLASTX
NCBI GI g3355471
BLAST score 564
E value 5.0e-58
Match length 138
% identity 70

NCBI Description (AC004218) putative lysophospholipase [Arabidopsis

thaliana

Seq. No. 11644

Contig ID 21997\_1.R1040 5'-most EST pmv700891165.h1

Method BLASTX
NCBI GI g3080524
BLAST score 292
E value 3.0e-26
Match length 124
% identity 48

NCBI Description (AL022599) hypothetical protein [Schizosaccharomyces pombe]

Seq. No. 11645

2017

Seq. No.

Contig ID

11650

22002 1.R1040



```
21998 1.R1040
Contig ID
5'-most EST
                  LIB3109-010-Q1-K1-G7
                  BLASTX
Method
NCBI GI
                  q3395431
BLAST score
                  339
E value
                  4.0e-31
Match length
                  294
% identity
                  35
NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]
Seq. No.
                  11646
                  21998_2.R1040
Contig ID
5'-most EST
                  uC-gmropic068a06b1
Method
                  BLASTX
NCBI GI
                  q3395431
BLAST score
                  203
E value
                  1.0e-15
Match length
                  102
% identity
                  43
NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]
                  11647
Seq. No.
                  21999 1.R1040
Contig ID
5'-most EST
                  uC-gmropic009a10b1
                  BLASTX
Method
NCBI GI
                  g4510418
BLAST score
                  717
E value
                  9.0e-76
                  246
Match length
                  55
% identity
NCBI Description (AC006929) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  11648
                  22000 1.R1040
Contig ID
5'-most EST
                  gsv701048485.h1
Method
                  BLASTN
NCBI GI
                  g2760165
                  39
BLAST score
E value
                  2.0e-12
                  143
Match length
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MAC9, complete sequence [Arabidopsis thaliana]
Seg. No.
                  11649
                  22001 1.R1040
Contig ID
5'-most EST
                  zhf700953446.h1
Method
                  BLASTX
NCBI GI
                  g2707336
BLAST score
                  329
E value
                   3.0e-30
Match length
                  91
% identity
NCBI Description (AF037442) histone acetyltransferase [Arabidopsis thaliana]
```



5'-most EST hrw701058211.hl Method BLASTX NCBI GI g3080402 BLAST score 768 E value 8.0e-82 Match length 193 % identity NCBI Description (AL022603) putative NADPH quinone oxidoreductase [Arabidopsis thaliana] >gi 4455266 emb CAB36802.1 (AL035527) putative NADPH quinone oxidoreductase [Arabidopsis thaliana]

Method BLASTX
NCBI GI g392783
BLAST score 1683
E value 0.0e+00
Match length 510
% identity 70

NCBI Description (AC005727) hypothetical protein [Arabidopsis thaliana]

Seq. No. 11652 Contig ID 22009

Contig ID 22009 1.R1040 5'-most EST wrg700786127.h2

Method BLASTX
NCBI GI g2618691
BLAST score 1653
E value 0.0e+00
Match length 441
% identity 73

NCBI Description (AC002510) putative chloroplast envelope Ca2+-ATPase

[Arabidopsis thaliana]

Seq. No. 11653

Contig ID 22009 2.R1040

5'-most EST jC-gmle01810062e03d1

Method BLASTX
NCBI GI g2618691
BLAST score 268
E value 2.0e-23
Match length 90
% identity 57

NCBI Description (AC002510) putative chloroplast envelope Ca2+-ATPase

[Arabidopsis thaliana]

Seq. No. 11654

Contig ID 22009 3.R1040 5'-most EST 6HA-02-Q1-E1-B3

Method BLASTX
NCBI GI g2618691
BLAST score 248
E value 6.0e-21
Match length 75
% identity 60

NCBI Description (AC002510) putative chloroplast envelope Ca2+-ATPase



## [Arabidopsis thaliana]

Seq. No. 11655 22010 1.R1040 Contig ID 5'-most EST LIB3051-046-Q1-K1-F10 Method BLASTN g2344870 NCBI GI BLAST score 82 E value 4.0e-38 Match length 138 % identity 90 NCBI Description Phaseolus vulgaris mRNA for purple acid phosphatase 11656 Seq. No. 22010 2.R1040 Contig ID 5'-most EST LIB3051-116-Q1-K1-A7 Method BLASTX q4160280 NCBI GI BLAST score 1452 0.0e + 00E value Match length 419 79 % identity (AJ006224) purple acid phosphatase [Ipomoea batatas] NCBI Description Seq. No. 11657 22015 1.R1040 Contig ID kl1701204762.h1 5'-most EST Method BLASTN NCBI GI q2358139 BLAST score 34 2.0e-09 E value Match length 143 % identity 87 NCBI Description Arabidopsis thaliana chromosome 1 YAC yUP8H12 complete sequence [Arabidopsis thaliana] Seq. No. 11658 22017 1.R1040 Contig ID LIB3051-014-Q1-E1-B6 5'-most EST BLASTX Method q4049632 NCBI GI BLAST score 1009 E value 1.0e-110 Match length 246 % identity 78 (AF039406) pyruvate dehydrogenase kinase [Arabidopsis NCBI Description thaliana]

Seq. No. 11659

Contig ID 22017\_2.R1040

5'-most EST jC-gmf102220125c01a1

Method BLASTX
NCBI GI g3641834
BLAST score 290
E value 7.0e-26
Match length 75



% identity

(AJ007312) pyruvate dehydrogenase kinase [Arabidopsis NCBI Description

thaliana]

Seq. No.

11660

Contig ID

22017 3.R1040

5'-most EST

LIB3107-018-Q1-K1-B5

Seq. No.

11661

Contig ID 5'-most EST 22022 1.R1040

LIB3139-085-P4-N4-B3

Method NCBI GI BLAST score E value Match length

171 4.0e-91 415

BLASTN

q473216

% identity

NCBI Description P.sativum (little marvel) HSC71.0 mRNA

Seq. No.

11662

85

Contig ID

22022 2.R1040

5'-most EST

uC-qmflminsoy081b11b1

Method BLASTN NCBI GI g2642647 BLAST score 106 E value 1.0e-52 274 Match length % identity 85

NCBI Description

Spinacia oleracea cytosolic heat shock 70 protein (HSC70)

mRNA, complete cds

Seq. No.

11663

Contig ID 5'-most EST 22023 1.R1040 pcp700993427.hl

Method NCBI GI BLASTX g1169128

BLAST score E value

% identity

606

Match length

5.0e-63148 78

NCBI Description

SERINE/THREONINE-PROTEIN KINASE CTR1 >gi 166680 (L08789) protein kinase [Arabidopsis thaliana] >gi 166682 (L08790)

protein kinase [Arabidopsis thaliana]

Seq. No.

11664

Contig ID 5'-most EST 22023 2.R1040 sat701010696.hl

Method NCBI GI BLASTX g1169128

BLAST score E value

246 3.0e-21

Match length % identity

60 80

NCBI Description

SERINE/THREONINE-PROTEIN KINASE CTR1 >gi 166680 (L08789)

protein kinase [Arabidopsis thaliana] >gi 166682 (L08790)

protein kinase [Arabidopsis thaliana]



Seq. No. 11665

Contig ID 22024 1.R1040

5'-most EST uC-gmrominsoy165a12b1

Method BLASTX
NCBI GI g3319354
BLAST score 2127
E value 0.0e+00
Match length 509
% identity 81

NCBI Description (AF077407) contains similarity to sugar transporters (Pfam:

sugar\_tr.hmm, score: 395.39) [Arabidopsis thaliana]

Seq. No. 11666

Contig ID 22024 2.R1040

Method BLASTX
NCBI GI g3319354
BLAST score 483
E value 1.0e-48
Match length 137
% identity 72

NCBI Description (AF077407) contains similarity to sugar transporters (Pfam:

sugar tr.hmm, score: 395.39) [Arabidopsis thaliana]

Seq. No. 11667

Contig ID 22030 1.R1040

5'-most EST LIB3170-059-Q1-J1-B2

Method BLASTX
NCBI GI g4455169
BLAST score 261
E value 2.0e-22
Match length 80
% identity 59

NCBI Description (AL035521) putative aldehyde dehydrogenase [Arabidopsis

thaliana]

Seq. No. 11668

Contig ID 22030 2.R1040

5'-most EST LIB3051-088-Q1-K1-H1

Seq. No. 11669

22030 3.R1040 Contig ID 5'-most EST g4276926 Method BLASTX NCBI GI g4455169 BLAST score 162 E value 7.0e-11 Match length 62 % identity 48

NCBI Description (AL035521) putative aldehyde dehydrogenase [Arabidopsis

thaliana]

11670

Seq. No.

Contig ID 22030 4.R1040 5'-most EST uxk700670410.h1

Method BLASTX NCBI GI g4455169



```
BLAST score
                   804
E value
                   5.0e-86
Match length
                   246
% identity
NCBI Description (AL035521) putative aldehyde dehydrogenase [Arabidopsis
                  thaliana]
                  11671
Seq. No.
                  22032 1.R1040
Contig ID
5'-most EST
                  LIB3092-043-Q1-K1-C6
Method
                  BLASTX
NCBI GI
                  q4056437
BLAST score
                  1135
E value
                  1.0e-124
Match length
                   348
                   65
% identity
NCBI Description (AC005990) Strong similarity to PFAM PF 00069 Eukaryotic
                  protein kinase domain. [Arabidopsis thaliana]
Seq. No.
                  11672
Contig ID
                  22033 1.R1040
5'-most EST
                  LIB3106-064-Q1-K1-A3
Seq. No.
                  11673
Contig ID
                  22033 2.R1040
5'-most EST
                  LIB3138-061-Q1-N1-B4
Method
                  BLASTX
NCBI GI
                   g1653162
BLAST score
                   674
E value
                  2.0e-70
Match length
                  320
% identity
                   45
NCBI Description (D90911) (p)ppGpp 3-pyrophosphohydrolase [Synechocystis
                  sp.]
Seq. No.
                  11674
                  22035 1.R1040
Contig ID
5'-most EST
                  LIB3051-036-Q1-K1-E7
Method
                  BLASTX
NCBI GI
                  g2832625
BLAST score
                  585
                  3.0e-60
E value
Match length
                  269
% identity
                  43
NCBI Description (AL021711) putative protein [Arabidopsis thaliana]
Seq. No.
                  11675
                  22082 1.R1040
Contig ID
```

5'-most EST jex700909636.h1

Method BLASTX NCBI GI q2497486 BLAST score 591 E value 3.0e-61 Match length 140 83 % identity

NCBI Description URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE) >gi\_2121275 (AF000147) UMP/CMP kinase [Arabidopsis



## thaliana]

Seq. No. 11676

Contig ID 22085\_1.R1040 5'-most EST sat701012311.h1

Method BLASTX
NCBI GI g2462834
BLAST score 320
E value 4.0e-29
Match length 146
% identity 41

NCBI Description (AF000657) hypothetical protein [Arabidopsis thaliana]

Seq. No. 11677

Contig ID 22085\_2.R1040
5'-most EST g4302814
Method BLASTX
NCBI GI g2462834
BLAST score 306
E value 1.0e-27
Match length 141

NCBI Description (AF000657) hypothetical protein [Arabidopsis thaliana]

Seq. No. 11678

% identity

Contig ID 22087 1.R1040

5'-most EST LIB3051-049-Q1-K1-H12

41

 Method
 BLASTX

 NCBI GI
 g3080398

 BLAST score
 271

 E value
 9.0e-24

 Match length
 127

Match length 127 % identity 24

NCBI Description (AL022603) putative protein [Arabidopsis thaliana]

Seq. No. 11679

Contig ID 22087\_2.R1040 5'-most EST xpa700795215.h1

Seq. No. 11680

Contig ID 22088\_1.R1040

5'-most EST LIB3051-049-Q1-K1-A3

Seq. No. 11681

Contig ID 22088\_2.R1040

5'-most EST LIB3170-038-Q1-K1-H10

Method BLASTX
NCBI GI g2829887
BLAST score 145
E value 4.0e-09
Match length 67
% identity 54

NCBI Description (AC002396) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 11682

Contig ID 22130 1.R1040

5'-most EST LIB3051-040-Q1-K1-H11



Method BLASTX
NCBI GI g603890
BLAST score 216
E value 2.0e-17
Match length 64
% identity 62

NCBI Description (Z46949) pathogenesis-related protein PR-6 type [Sambucus

nigra]

Seq. No. 11683

Contig ID 22136\_1.R1040 5'-most EST zsg701123428.h1

Method BLASTX
NCBI GI g3540195
BLAST score 322
E value 2.0e-29
Match length 162
% identity 20

NCBI Description (AC004260) Unknown protein [Arabidopsis thaliana]

Seq. No. 11684

Contig ID 22143\_1.R1040 5'-most EST eep700867984.h1

Method BLASTX
NCBI GI g4455338
BLAST score 1340
E value 1.0e-148
Match length 348
% identity 76

NCBI Description (AL035525) putative protein [Arabidopsis thaliana]

Seq. No. 11685

Contig ID 22144 1.R1040 5'-most EST leu701155238.h1

Method BLASTX
NCBI GI g4455194
BLAST score 300
E value 5.0e-27
Match length 70
% identity 77

NCBI Description (AL035440) putative protein [Arabidopsis thaliana]

Seq. No. 11686

Contig ID 22144\_2.R1040

5'-most EST LIB3139-073-P1-N1-H2

Method BLASTX
NCBI GI g4455194
BLAST score 311
E value 1.0e-28
Match length 70
% identity 80

NCBI Description (AL035440) putative protein [Arabidopsis thaliana]

Seq. No. 11687

Contig ID 22146\_1.R1040 5'-most EST trc700565736.h1

Method BLASTX



```
NCBI GI g1644427
BLAST score 530
E value 5.0e-65
Match length 186
% identity 65
NCBI Description (U74610) glyoxalase II [Arabidopsis thaliana]
```

 Seq. No.
 11688

 Contig ID
 22148\_1.R1040

 5'-most EST
 g4397131

 Method
 BLASTN

 NCBI GI
 g18834

 BLAST score
 309

 E value
 1.0e-173

E value 1.0e-1
Match length 1136
% identity 84

NCBI Description H.brasiliensis HMGR1 mRNA for 3-hydroxy-3-methylglutaryl

coenzyme A reductase

Seq. No. 11689

Contig ID 22148\_2.R1040 5'-most EST sat701011586.h1

Seq. No. 11690

Contig ID 22148 3.R1040

5'-most EST jC-gmle01810042g12d1

Method BLASTN
NCBI GI g1763233
BLAST score 50
E value 6.0e-19
Match length 66
% identity 94

NCBI Description Camptotheca acuminata 3-hydroxy-3-methylglutaryl coenzyme A

reductase gene, complete cds

Seq. No. 11691

Contig ID 22148\_5.R1040

5'-most EST jC-gmf102220086e10a1

Method BLASTN
NCBI GI g21103
BLAST score 159
E value 7.0e-84
Match length 239
% identity 92

NCBI Description R.sativus mRNA for HMG-COA reductase (clone cRS8)

Seq. No. 11692

Contig ID 22149 1.R1040

5'-most EST LIB3170-076-Q1-K1-E11

Method BLASTX
NCBI GI g2739383
BLAST score 498
E value 3.0e-50
Match length 118
% identity 76

NCBI Description (AC002505) unknown protein [Arabidopsis thaliana]



```
Seq. No.
                  11693
                  22151 1.R1040
Contig ID
                  gsv701055942.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q2708749
BLAST score
                  396
E value
                  5.0e-38
Match length
                  117
                  62
% identity
                  (AC003952) putative senescence-assoc. rhodanese-like
NCBI Description
                  protein [Arabidopsis thaliana]
Seq. No.
                  11694
                  22151 2.R1040
Contig ID
5'-most EST
                  LIB3107-001-Q1-K1-F2
Method
                  BLASTX
NCBI GI
                  g2708749
BLAST score
                  322
E value
                  8.0e-30
Match length
                  110
                  53
% identity
NCBI Description (AC003952) putative senescence-assoc. rhodanese-like
                  protein [Arabidopsis thaliana]
Seq. No.
                  11695
Contig ID
                  22151 3.R1040
5'-most EST
                  uC-gmropic110a07b1
Seq. No.
                  11696
Contig ID
                  22156 1.R1040
5'-most EST
                  leu701150496.h1
Method
                  BLASTN
                  g3176077
NCBI GI
BLAST score
                   124
E value
                   3.0e-63
Match length
                   328
% identity
                  Medicago sativa mRNA for protein phosphatase 1, epsilon
NCBI Description
                  subunit
Seq. No.
                  11697
Contig ID
                  22157 1.R1040
5'-most EST
                  zsg701118069.h2
                  BLASTX
Method
NCBI GI
                  q4115931
BLAST score
                  1754
E value
                  0.0e + 00
```

Match length 380

88

NCBI Description (AF118223) contains similarity to Guillardia theta ABC transporter (GB:AF041468) [Arabidopsis thaliana]

Seq. No. 11698 Contig ID 22158 1.R1040 5'-most EST g4396314 Method BLASTX NCBI GI g4220462

% identity



BLAST score 1083 E value 1.0e-118 Match length 277 % identity 74

NCBI Description (AC006216) Strong similarity to gb\_Z50851 HD-zip (athb-8) gene from Arabidopsis thaliana containing Homeobox PF\_00046

and bZIP PF\_00170 domains. [Arabidopsis thaliana]

Seq. No. 11699

Contig ID 22164 1.R1040

5'-most EST LIB3051-109-Q1-K1-E5

Method BLASTX
NCBI GI g4097585
BLAST score 576
E value 2.0e-59
Match length 182
% identity 65

NCBI Description (U64925) NTGP4 [Nicotiana tabacum]

Seq. No. 11700

Contig ID 22193 1.R1040

5'-most EST LIB3107-039-Q1-K1-D6

Method BLASTX
NCBI GI g3377517
BLAST score 370
E value 3.0e-35
Match length 203
% identity 39

NCBI Description (AF073361) nitrate transporter NTL1 [Arabidopsis thaliana]

Seq. No. 11701

Contig ID 22193 2.R1040 5'-most EST kl1701212430.h1

Method BLASTX
NCBI GI g2760834
BLAST score 163
E value 3.0e-15
Match length 86
% identity 51

NCBI Description (AC003105) putative nitrate transporter [Arabidopsis

thaliana]

Seq. No. 11702

Contig ID 22195\_1.R1040 5'-most EST zzp700829817.h1

Method BLASTX
NCBI GI g4220462
BLAST score 804
E value 4.0e-86
Match length 211
% identity 73

NCBI Description (AC006216) Strong similarity to gb\_Z50851 HD-zip (athb-8)

gene from Arabidopsis thaliana containing Homeobox PF\_00046

and bZIP PF 00170 domains. [Arabidopsis thaliana]

Seq. No. 11703

Contig ID 22196 1.R1040

```
5'-most EST
                   leu701156235,h1
Method
                  BLASTX
NCBI GI
                   q2467274
BLAST score
                   392
E value
                   2.0e-37
Match length
                  140
                   59
% identity
NCBI Description
                  (Z99759) rna binding protein [Schizosaccharomyces pombe]
Seq. No.
                   11704
                   22202 1.R1040
Contig ID
                  LIB3051-014-Q1-E1-C4
5'-most EST
Method
                  BLASTX
NCBI GI
                   g3322947
BLAST score
                   358
                   2.0e-33
E value
Match length
                   211
                   38
% identity
NCBI Description (AE001239) hemolysin (tlyC) [Treponema pallidum]
                   11705
Seq. No.
Contig ID
                   22205 1.R1040
5'-most EST
                  LIB3051-034-Q1-K1-C6
Method
                   BLASTN
NCBI GI
                   g868002
BLAST score
                   356
                   0.0e + 00
E value
Match length
                   947
% identity
                   84
NCBI Description Pumpkin mRNA for aconitase, complete cds
                   11706
Seq. No.
                   22209 1.R1040
Contig ID
5'-most EST
                   sat701003325.h1
Method
                   BLASTX
                   q4580575
NCBI GI
BLAST score
                   747
                   4.0e-79
E value
Match length
                   373
                   46
% identity
                  (AF082176) auxin response factor 9 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   11707
Contig ID
                   22210 1.R1040
                   LIB3170-081-Q1-K1-C8
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2146746
BLAST score
                   462
E value
                   4.0e-46
Match length
                   101
% identity
                   89
                  protein kinase (EC 2.7.1.-) - Arabidopsis thaliana
NCBI Description
                   >gi_166819 (L05562) protein kinase [Arabidopsis thaliana]
```

Seq. No. 11708

Contig ID 22210 2.R1040

5'-most EST LIB3107-036-Q1-K1-C11

```
Method
                  BLASTX
NCBI GI
                  a2146746
BLAST score
                  297
E value
                  7.0e-27
Match length
                  69
% identity
                  86
                  protein kinase (EC 2.7.1.-) - Arabidopsis thaliana
NCBI Description
                  >gi 166819 (L05562) protein kinase [Arabidopsis thaliana]
Seq. No.
                  22217 1.R1040
Contig ID
                  jC-gmst02400026b01a1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q3482931
                  790
BLAST score
                  3.0e-84
E value
Match length
                  196
                  76
% identity
NCBI Description (AC003970) germin-like protein [Arabidopsis thaliana]
                  11710
Seq. No.
```

22231 1.R1040 Contig ID 5'-most EST LIB3051-045-Q1-K1-A1 Method BLASTX NCBI GI g4529972 BLAST score 342 4.0e-32 E value Match length 146

47

% identity (AC002330) putative chloroplast outer envelope 86-like NCBI Description protein [Arabidopsis thaliana]

Seq. No. 11711 Contig ID 22232\_1.R1040 5'-most EST LIB3051-048-Q1-K1-A1 Method BLASTN NCBI GI q3021356

BLAST score 85 E value 6.0e-40Match length 257 % identity 83

Cyamopsis tetragonoloba mRNA for UDP-galactose 4-epimerase, NCBI Description clone GEPI48

11712 Seq. No.

22233 1.R1040 Contig ID  $uaw70\overline{0}664464.h1$ 5'-most EST

BLASTX Method NCBI GI q4432854 BLAST score 325 E value 2.0e-29 Match length 308 % identity

NCBI Description (AC006300) hypothetical protein [Arabidopsis thaliana]

Seq. No. 11713

Contig ID 22238 1.R1040



5'-most EST zsq701126668.hl Method BLASTX NCBI GI q2288999 BLAST score 581 E value 5.0e-65 Match length 141 82 % identity

NCBI Description (AC002335) electron transfer flavoprotein ubiquinone oxidoreductase isolog [Arabidopsis thaliana]

11714 Seq. No.

Contig ID 22239 1.R1040

5'-most EST LIB3138-126-Q1-N1-G12

Method BLASTX NCBI GI g1449179 BLAST score 1860 0.0e+00E value Match length 436 81 % identity

(D86506) N-ethylmaleimide sensitive fusion protein NCBI Description

[Nicotiana tabacum]

11715 Seq. No.

Contig ID 22240 1.R1040

5'-most EST LIB3051-009-Q1-E1-B12

Method BLASTX NCBI GI g266323 BLAST score 191 2.0e-14 E value Match length 108 % identity 40

NCBI Description ALPHA-AMYLASE/SUBTILISIN INHIBITOR (RASI)

>gi\_100651\_pir\_\_S24131 subtilisin/alpha-amylase inhibitor, 20K - rice >gi\_254616\_bbs\_112376 bifunctional subtilisin/alpha-amylase inhibitor, RASI [Oryza sativa=rice, seeds, bran, Peptide, 176 aa]

Seq. No. 11716

22242 1.R1040 Contig ID

LIB3051-044-Q1-K1-B7 5'-most EST

Method BLASTX NCBI GI g2494132 BLAST score 440 E value 3.0e-43 Match length 213 % identity 42

NCBI Description (AC002376) Contains similarity to human dimethylaniline

monooxygenase (gb\_M64082). [Arabidopsis thaliana]

Seq. No. 11717

22243 2.R1040 Contig ID

5'-most EST jC-gmle01810063f12a1

Method BLASTX g4127461 NCBI GI BLAST score 655 E value 1.0e-68 Match length 180

2031

5'-most EST

BLAST score

Method

NCBI GI

E value



% identity NCBI Description (AJ011674) receptor-like protein kinase, RLK3 [Arabidopsis thaliana] 11718 Seq. No. Contig ID 22244 1.R1040 5'-most EST LIB3051-025-Q1-K1-A5 Method BLASTX NCBI GI g2213583 BLAST score 515 E value 3.0e-52 Match length 169 60 % identity (AC000348) T7N9.3 [Arabidopsis thaliana] NCBI Description Seq. No. 11719 Contig ID 22249 1.R1040  $jex70\overline{0}904158.h1$ 5'-most EST Method BLASTX g4455323 NCBI GI BLAST score 631 E value 8.0e-66 Match length 168 % identity NCBI Description (AL035525) aminopeptidase-like protein [Arabidopsis thaliana] Seq. No. 11720 Contig ID 22251 1.R1040 5'-most EST LIB3051-004-Q1-E1-A3 Method BLASTX g2494144 NCBI GI BLAST score 187 5.0e-14 E value Match length 73 58 % identity NCBI Description (AC002329) predicted leucine-rich protein [Arabidopsis thaliana] Seq. No. 11721 Contig ID 22252 1.R1040 5'-most EST fua701043059.h1 Method BLASTX NCBI GI g3367596 BLAST score 818 E value 1.0e-87 Match length 198 78 % identity NCBI Description (AL031135) putative protein [Arabidopsis thaliana] Seq. No. 11722 Contig ID 22276 1.R1040

LIB3107-011-Q1-K1-F7

BLASTX

388 3.0e-37

g4454026



```
Match length
                  120
% identity
NCBI Description (AL035394) phosphatase like protein [Arabidopsis thaliana]
Seq. No.
                  11723
                  22276 2.R1040
Contig ID
5'-most EST
                  zpv700757969.hl
                  BLASTX
Method
NCBI GI
                  g4454026
BLAST score
                  220
E value
                  3.0e-18
                  64
Match length
                  70
% identity
NCBI Description (AL035394) phosphatase like protein [Arabidopsis thaliana]
Seq. No.
                  11724
                  22278 1.R1040
Contig ID
5'-most EST
                  LIB3051-007-Q1-E1-G2
                  BLASTX
Method
NCBI GI
                  g2245091
BLAST score
                  245
E value
                  2.0e-20
Match length
                  114
% identity
                  52
NCBI Description (Z97343) hypothetical protein [Arabidopsis thaliana]
                  11725
Seq. No.
Contig ID
                  22279 1.R1040
5'-most EST
                  uC-gmropic090a03b1
Method
                  BLASTX
                  g2738248
NCBI GI
BLAST score
                  1256
E value
                  1.0e-139
Match length
                  287
% identity
                  85
                  (U97200) cobalamin-independent methionine synthase
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  11726
Contig ID
                  22285 1.R1040
5'-most EST
                  bth700845369.h1
Method
                  BLASTX
NCBI GI
                  q3757521
BLAST score
                  526
                  1.0e-53
E value
Match length
                  169
% identity
NCBI Description (AC005167) unknown protein [Arabidopsis thaliana]
```

Seq. No. 11727

22286 1.R1040 Contig ID 5'-most EST jC-qmst02400057e10a1

Method BLASTN NCBI GI g400531

BLAST score 365 E value 0.0e + 00Match length 745



% identity

NCBI Description V.sativa mRNA for NADPH-ferrihemoprotein reductase

11728 Seq. No.

22286 2.R1040 Contig ID

LIB3051-066-Q1-K1-C9 5'-most EST

Method BLASTN NCBI GI q400531 BLAST score 122 E value 7.0e-62 Match length 222 % identity 89

NCBI Description V.sativa mRNA for NADPH-ferrihemoprotein reductase

Seq. No. 11729

22286 3.R1040 Contig ID

5'-most EST LIB3051-015-Q1-E1-G2

Method BLASTN NCBI GI g295447 BLAST score 172 1.0e-91 E value Match length 568 % identity 89

NCBI Description Vigna radiata NADPH cytochrome P450 mRNA, complete cds

11730 Seq. No.

Contig ID 22288 1.R1040

5'-most EST LIB3107-017-Q1-K1-A3

Method BLASTX NCBI GI q3668091 BLAST score 332 E value 4.0e-30 345 Match length % identity 6

NCBI Description (AC004667) hypothetical protein [Arabidopsis thaliana]

Seq. No. 11731

Contig ID 22290 1.R1040 5'-most EST leu701155978.hl

Method BLASTX NCBI GI q3413717 BLAST score 677 E value 4.0e-71 Match length 171 76 % identity

(AC004747) unknown protein [Arabidopsis thaliana] NCBI Description

>gi 3643590 (AC005395) unknown protein [Arabidopsis

thaliana]

Seq. No. 11732

Contig ID 22292 1.R1040

5'-most EST jC-gmf102220102e05a1

Method BLASTX NCBI GI q3201624 BLAST score 261 E value 2.0e-22 100 Match length

Seq. No.



% identity NCBI Description (AC004669) hypothetical protein [Arabidopsis thaliana] Seq. No. 11733 Contig ID 22293 1.R1040 5'-most EST q4313608 Method BLASTX NCBI GI q4204293 BLAST score 609 E value 4.0e-63 Match length 140 80 % identity (AC003027) 1cl prt seq No definition line found NCBI Description [Arabidopsis thaliana] Seq. No. 11734 22293 2.R1040 Contig ID 5'-most EST hrw701063093.h1 BLASTX Method g4204293 1170 1.0e-170

NCBI GI BLAST score E value Match length 405 % identity NCBI Description

(AC003027) 1cl prt seq No definition line found

[Arabidopsis thaliana]

Contig ID 22297 1.R1040 5'-most EST pxt700941687.h1 Method BLASTX g2760332 NCBI GI BLAST score 655 E value 1.0e-68 239 Match length

11735

% identity 15

NCBI Description (AC002130) F1N21.17 [Arabidopsis thaliana]

Seq. No. 11736

22298 1.R1040 Contig ID 5'-most EST  $uxk70\overline{0}671023.h1$ 

Method BLASTX g4455359 NCBI GI BLAST score 423 E value 2.0e-41 Match length 148 59 % identity

NCBI Description (AL035524) putative protein [Arabidopsis thaliana]

Seq. No. 11737

Contig ID 22298 2.R1040 5'-most EST crh700852843.h1

Method BLASTX NCBI GI g4455359 BLAST score 602 E value 2.0e-62 Match length 143



% identity 83

NCBI Description (AL035524) putative protein [Arabidopsis thaliana]

Seq. No. 11738

Contig ID 22299 1.R1040

5'-most EST LIB3087-008-Q1-K1-F11

Method BLASTX
NCBI GI g3386615
BLAST score 957
E value 1.0e-104
Match length 214
% identity 84

NCBI Description (AC004665) putative phosphomannomutase [Arabidopsis

thaliana]

Seq. No. 11739

Contig ID 22299 2.R1040

5'-most EST LIB3109-053-Q1-K1-A11

Method BLASTX
NCBI GI g3386615
BLAST score 307
E value 1.0e-28
Match length 84
% identity 76

NCBI Description (AC004665) putative phosphomannomutase [Arabidopsis

thaliana]

Seq. No. 11740

Contig ID 22302 1.R1040

5'-most EST LIB3051-085-Q1-K1-B7

Method BLASTX
NCBI GI g114950
BLAST score 224
E value 3.0e-18
Match length 68

% identity 66

NCBI Description GLU S.GRISEUS PROTEASE INHIBITOR (BGIA)

>gi\_81581\_pir\_\_A41174 endopeptidase inhibitor - balsam pear >gi\_234607\_bbs\_53154 BGIA=acidic amino acid-specific endopeptidase inhibitor [Momordica charantia L.=bitter

gourd, Peptide, 68 aa]

Seq. No. 11741

Contig ID 22313\_1.R1040 5'-most EST hrw70\overline{10}60805.h1

Seq. No. 11742

Contig ID 22313 2.R1040 5'-most EST fua701040140.h1

Method BLASTX
NCBI GI g3935150
BLAST score 750
E value 1.0e-79
Match length 215
% identity 69

NCBI Description (AC005106) T25N20.14 [Arabidopsis thaliana]



Seq. No. 11743

Contig ID 22313\_3.R1040 5'-most EST uaw700667096.h1

Method BLASTX
NCBI GI g3935150
BLAST score 212
E value 1.0e-16
Match length 62

% identity 28

NCBI Description (AC005106) T25N20.14 [Arabidopsis thaliana]

Seq. No. 11744

Contig ID 22316 1.R1040

5'-most EST LIB $30\overline{5}1-019-Q1-E1-G12$  Method BLASTX

Method BLASTX
NCBI GI g2262177
BLAST score 472
E value 3.0e-47
Match length 130
% identity 68

NCBI Description (AC002329) hypothetical protein similar to T18A10.3

[Arabidopsis thaliana]

Seq. No. 11745

Contig ID 22316\_2.R1040 5'-most EST leu701147372.h1

Method BLASTX
NCBI GI g2262177
BLAST score 655
E value 9.0e-69
Match length 176
% identity 68

NCBI Description (AC002329) hypothetical protein similar to T18A10.3

[Arabidopsis thaliana]

Seq. No. 11746

Contig ID 22318 1.R1040

5'-most EST jC-gmf102220102f08a1

Method BLASTX
NCBI GI g2529668
BLAST score 1355
E value 1.0e-150
Match length 388
% identity 68

NCBI Description (AC002535) putative photolyase/blue-light receptor

[Arabidopsis thaliana] >gi 3319288 (AF053366)

photolyase/blue light photoreceptor PHR2 [Arabidopsis

thaliana]

Seq. No. 11747

Contig ID 22321 1.R1040

5'-most EST LIB3051-053-Q1-K2-D3

Method BLASTX
NCBI GI g2780192
BLAST score 151
E value 1.0e-09
Match length 74



% identity 47
NCBI Description (AJ222713) unnamed protein product [Arabidopsis thaliana]

Seq. No. 11748

Contig ID 22322\_1.R1040 5'-most EST uC-gmropic063e04b1

Method BLASTN
NCBI GI 94376087
BLAST score 51
E value 2.0e-19
Match length 75
% identity 92

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig

fragment No

Seq. No. 11749

Contig ID 22322 2.R1040 5'-most EST sat701012193.h1

Method BLASTX
NCBI GI g2493318
BLAST score 266
E value 1.0e-22
Match length 205
% identity 44

NCBI Description BLUE COPPER PROTEIN PRECURSOR >gi 562779 emb CAA80963

(Z25471) blue copper protein [Pisum sativum]

>gi\_1098264\_prf\_\_2115352A blue Cu protein [Pisum sativum]

Seq. No. 11750

Contig ID 22322 3.R1040

5'-most EST uC-gmrominsoy153a03b1

Method BLASTX
NCBI GI g2493318
BLAST score 296
E value 3.0e-26
Match length 104
% identity 53

NCBI Description BLUE COPPER PROTEIN PRECURSOR >gi\_562779\_emb\_CAA80963\_

(Z25471) blue copper protein [Pisum sativum]

>gi 1098264 prf 2115352A blue Cu protein [Pisum sativum]

Seq. No. 11751

Contig ID 22322\_5.R1040 5'-most EST dpv701102983.h1

Seq. No. 11752

Contig ID 22327\_1.R1040 5'-most EST LIB3107-062-Q1-K1-G2

Method BLASTX
NCBI GI g3080400
BLAST score 889
E value 9.0e-96
Match length 208
% identity 81

NCBI Description (AL022603) putative protein [Arabidopsis thaliana]

>gi\_4455264\_emb\_CAB36800.1\_ (AL035527) putative protein

[Arabidopsis thaliana]



Seq. No. 11753

Contig ID 22328\_1.R1040 5'-most EST dpv701099215.h1

Method BLASTX
NCBI GI g3046815
BLAST score 1698
E value 0.0e+00
Match length 436
% identity 74

NCBI Description (AL021687) cytochrome P450 [Arabidopsis thaliana]

Seq. No. 11754

Contig ID 22328\_2.R1040 5'-most EST txt700735469.h1

Method BLASTX
NCBI GI g3046815
BLAST score 197
E value 4.0e-15
Match length 73
% identity 52

NCBI Description (AL021687) cytochrome P450 [Arabidopsis thaliana]

Seq. No. 11755

Contig ID 22328 3.R1040

5'-most EST LIB3139-044-P1-N1-B2

Method BLASTX
NCBI GI g3046815
BLAST score 316
E value 3.0e-29
Match length 99
% identity 65

NCBI Description (AL021687) cytochrome P450 [Arabidopsis thaliana]

Seq. No. 11756

Contig ID 22328\_4.R1040 5'-most EST zsg701126320.h1

Method BLASTX
NCBI GI g3080353
BLAST score 208
E value 2.0e-16
Match length 61
% identity 74

NCBI Description (AL022580) cytochrome P450 [Arabidopsis thaliana]

Seq. No. 11757

Contig ID 22328\_5.R1040 5'-most EST smc700746253.h1

Method BLASTX
NCBI GI g3046815
BLAST score 491
E value 2.0e-49
Match length 129
% identity 73

NCBI Description (AL021687) cytochrome P450 [Arabidopsis thaliana]

Seq. No. 11758



Contig ID 22328\_6.R1040 5'-most EST gsv701052031.h1

Seq. No. 11759

Contig ID 22331 1.R1040

5'-most EST LIB3051-058-Q1-K2-D3

Seq. No. 11760

Contig ID 22332 1.R1040

5'-most EST jC-gmro02910038f06a1

Method BLASTX
NCBI GI g4006873
BLAST score 299
E value 2.0e-27
Match length 236
% identity 35

NCBI Description (Z99707) hypothetical protein [Arabidopsis thaliana]

Seq. No. 11761

Contig ID 22333 1.R1040

5'-most EST LIB3051-091-Q1-K1-H5

Method BLASTX
NCBI GI g1071874
BLAST score 402
E value 4.0e-39
Match length 169
% identity 50

NCBI Description chitinase (EC 3.2.1.14) / lysozyme (EC 3.2.1.17) PZ

precursor, pathogenesis-related - common tobacco
>gi\_467689\_emb\_CAA55128\_ (X78325) chitinase/lysozyme

[Nicotiana tabacum]

Seq. No. 11762

Contig ID 22337\_1.R1040 5'-most EST crh700850254.h1

Method BLASTX
NCBI GI g3395441
BLAST score 405
E value 3.0e-39
Match length 156
% identity 49

NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]

Seq. No. 11763

Contig ID 22383 1.R1040

5'-most EST LIB3051-081-Q1-K1-F3

Method BLASTX
NCBI GI g3249109
BLAST score 635
E value 6.0e-66
Match length 193
% identity 63

NCBI Description (AC003114) Contains similarity to pre-mRNA splicing factor

(SF2), P33 subunit gb M72709 from Homo sapiens. ESTs

gb T42588 and gb R65514 come from this gene. [Arabidopsis

thaliana]



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11764
Seq. No.
                   22383 2.R1040
Contig ID
5'-most EST
                  jC-qmle01810032d12d1
Seq. No.
                   11765
                   22383 3.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy115h06b1
Method
                  BLASTX
NCBI GI
                  g2129717
BLAST score
                  288
                   7.0e-26
E value
Match length
                  70
                   76
% identity
                  ribonucleoprotein - Arabidopsis thaliana >gi 166844
NCBI Description
                   (M98340) ribonucleoprotein [Arabidopsis thalīana]
                   >gi_1582992_prf__2119375A Ser/Arg-rich protein [Arabidopsis
                  thaliana]
Seq. No.
                  11766
Contig ID
                  22383 4.R1040
                  awf700842864.h1
5'-most EST
Seq. No.
                  11767
Contig ID
                  22404 1.R1040
5'-most EST
                   zpv700762592.h1
Method
                  BLASTX
NCBI GI
                   g3738325
BLAST score
                   679
E value
                   5.0e-77
                  284
Match length
% identity
                  (AC005170) putative CaMB-channel protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                   11768
Contig ID
                   22405_1.R1040
5'-most EST
                   uC-gmrominsoy117a09b1
Method
                   BLASTX
NCBI GI
                   g4510376
BLAST score
                   420
E value
                   3.0e-41
Match length
                   118
% identity
                   69
NCBI Description
                   (AC007017) unknown protein [Arabidopsis thaliana]
                   11769
Seq. No.
                   22407 1.R1040
Contig ID
5'-most EST
                  LIB3051-047-Q1-K1-A6
Method
                  BLASTX
```

NCBI GI g4206122 BLAST score 426 E value 9.0e-42 Match length 170 % identity 52

NCBI Description (AF097667) protein phosphatase 2C homolog [Mesembryanthemum

crystallinum]



Seq. No. 11770

Contig ID 22407\_2.R1040 5'-most EST rlr700902318.h1

Seq. No. 11771

Contig ID 22408\_1.R1040

5'-most EST LIB3051-037-Q1-K1-D11

Method BLASTX
NCBI GI g2384673
BLAST score 619
E value 2.0e-64
Match length 195
% identity 59

NCBI Description (AF012658) putative potassium transporter AtKT3p

[Arabidopsis thaliana]

Seq. No. 11772

Contig ID 22409\_1.R1040 5'-most EST awf700839749.h1

Method BLASTX
NCBI GI g3080393
BLAST score 1190
E value 1.0e-131
Match length 336
% identity 68

NCBI Description (AL022603) NADH dehydrogenase like protein [Arabidopsis

thaliana]

Seq. No. 11773

Contig ID 22417\_1.R1040

5'-most EST LIB3051-063-Q1-K1-C7

Method BLASTX
NCBI GI g4415941
BLAST score 507
E value 3.0e-51
Match length 168
% identity 44

NCBI Description (AC006418) putative arginine-serine rich splicing factor

[Arabidopsis thaliana]

Seq. No. 11774

Contig ID 22461\_1.R1040 5'-most EST kl1701209310.h1

Method BLASTX
NCBI GI g3122572
BLAST score 2275
E value 0.0e+00
Match length 543
% identity 79

NCBI Description NADH-UBIQUINONE OXIDOREDUCTASE 75 KD SUBUNIT PRECURSOR

(COMPLEX I-75KD) (CI-75KD) (76 KD MITOCHONDRIAL COMPLEX I SUBUNIT) >gi 1084434\_pir\_ S52737 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 76K chain precursor - potato >gi 758340 emb CAA59818 (X85808) 76 kDa mitochondrial

complex I subunit [Solanum tuberosum]

Seq. No. 11775

NCBI GI BLAST score

E value



```
22484 1.R1040
Contig ID
5'-most EST
                   dpv701101986.h1
                   BLASTX
Method
NCBI GI
                   q3540201
BLAST score
                   397
E value
                   7.0e-68
Match length
                   183
% identity
                   74
NCBI Description
                  (AC004260) Putative nuclear protein [Arabidopsis thaliana]
                   11776
Seq. No.
                   22485 1.R1040
Contig ID
                   zhf700952062.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                   g1653767
BLAST score
                   386
E value
                   6.0e-37
                   169
Match length
% identity
                   46
NCBI Description
                   (D90916) oligopeptidase A [Synechocystis sp.]
Seq. No.
                   11777
                   22487 1.R1040
Contig ID
5'-most EST
                   LIB3109-044-Q1-K1-B4
Method
                   BLASTX
NCBI GI
                   q280401
BLAST score
                   608
E value
                   5.0e-63
Match length
                   175
% identity
                   66
                  H+-transporting ATPase (EC 3.6.1.35) - curled-leaved
NCBI Description
                   tobacco >qi 170206 (M27888) H+-translocating ATPase
                   [Nicotiana plumbaginifolia]
Seq. No.
                   11778
Contig ID
                   22488 1.R1040
5'-most EST
                   LIB3107-037-Q1-K1-H2
                   BLASTN
Method
NCBI GI
                   g2264318
BLAST score
                   43
E value
                   9.0e-15
                   90
Match length
                   93
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MUP24, complete sequence [Arabidopsis thaliana]
                   11779
Seq. No.
                   22488 3.R1040
Contig ID
                   fde700873091.h1
5'-most EST
                   11780
Seq. No.
Contig ID
                   22489 1.R1040
5'-most EST
                   LIB3051-094-Q1-K1-C8
Method
                   BLASTX
```

g3080443

9.0e-36



Match length 127 % identity 58

NCBI Description (AL022605) putative protein [Arabidopsis thaliana]

Seq. No. 11781

Contig ID 22490\_1.R1040 5'-most EST gsv701051573.h1

Method BLASTN
NCBI GI g732912
BLAST score 215
E value 1.0e-117
Match length 582
% identity 84

NCBI Description P.vulgaris mRNA for pectinesterase

Seq. No. 11782

Contig ID 22490 2.R1040 5'-most EST gsv701046458.h1

Method BLASTN
NCBI GI g732912
BLAST score 176
E value 3.0e-94
Match length 368
% identity 87

NCBI Description P.vulgaris mRNA for pectinesterase

Seq. No. 11783

Contig ID 22502 1.R1040

5'-most EST uC-gmrominsoy182f02b1

Method BLASTX
NCBI GI g3036805
BLAST score 958
E value 1.0e-104
Match length 263
% identity 68

NCBI Description (AL022373) thaumatin-like protein [Arabidopsis thaliana]

Seq. No. 11784

Contig ID 22502\_3.R1040 5'-most EST dpv701098060.h1

Seq. No. 11785

Contig ID 22505\_1.R1040

5'-most EST LIB3106-102-Q1-K1-E6

Method BLASTX
NCBI GI g2833311
BLAST score 253
E value 2.0e-21
Match length 68
% identity 65

NCBI Description HYPOTHETICAL 18.9 KD PROTEIN R07E5.13 IN CHROMOSOME III >gi 630728 pir \$43605 R07E5.13 protein (clone R07E5) -

Caenorhabditis elegans >gi 3878946 emb CAA83622 (Z32683)

R07E5.13 [Caenorhabditis elegans]

Seq. No. 11786

Contig ID 22506 1.R1040



```
5'-most EST
                  uaw700664374.h1
Method
                  BLASTX
NCBI GI
                  g3021409
                  173
BLAST score
                  2.0e-12
E value
Match length
                  91
                  15
% identity
                  (Y12781) transducin (beta) like 1 protein [Homo sapiens]
NCBI Description
Seq. No.
                  11787
                  22507_1.R1040
Contig ID
5'-most EST
                  LIB3051-111-Q1-K1-E7
Method
                  BLASTX
NCBI GI
                  q2576361
BLAST score
                  499
E value
                  2.0e-50
Match length
                  106
                  82
% identity
                  (U39782) lysine and histidine specific transporter
NCBI Description
                   [Arabidopsis thaliana]
                  11788
Seq. No.
                  22509 1,R1040
Contig ID
5'-most EST
                  LIB3051-061-Q1-K1-E5
Method
                  BLASTX
NCBI GI
                  q3894176
BLAST score
                  165
E value
                  2.0e-11
Match length
                  94
% identity
                  40
                  (AC005312) putative NAM (no apical meristem) protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  11789
                  22510 1.R1040
Contig ID
5'-most EST
                  txt700735828.h1
Method
                  BLASTX
NCBI GI
                  g3193284
BLAST score
                  1200
                  1.0e-139
E value
                  340
Match length
                  72
% identity
                  (AF069298) No definition line found [Arabidopsis thaliana]
NCBI Description
                  11790
Seq. No.
Contig ID
                  22511 1.R1040
5'-most EST
                  LIB3051-093-Q1-K1-C5
Method
                  BLASTX
NCBI GI
                  g3080434
BLAST score
                  333
E value
                  3.0e-31
```

Match length 107 % identity

NCBI Description (AL022605) putative gamma-glutamyltransferase [Arabidopsis

thaliana]

11791 Seq. No.



22512 1.R1040 Contig ID

5'-most EST LIB3051-009-Q1-E1-A11

Method BLASTX NCBI GI q464520 BLAST score 168 2.0e-11 E value Match length 84 38 % identity

NCBI Description TRANSCRIPTION INITIATION FACTOR IIF, BETA SUBUNIT

(TFIIF-BETA) (TRANSCRIPTION INITIATION FACTOR RAP30)

>gi\_422624\_pir\_\_S30220 transcription factor RAP30 - African

clawed frog (fragment) >gi\_65135\_emb\_CAA78835\_ (Z15132)
transcription factor RAP30 [Xenopus laevis]

Seq. No. 11792

22513 1.R1040 Contig ID

5'-most EST LIB3065-020-Q1-N1-A12

Method BLASTX NCBI GI g1871185 BLAST score 1051 E value 1.0e-115 Match length 236 % identity

NCBI Description (U90439) seven in absentia isolog [Arabidopsis thaliana]

Seq. No. 11793

Contig ID 22514 1.R1040

 $LIB31\overline{3}9-005-P1-N1-E5$ 5'-most EST

Method BLASTX NCBI GI g2827536 BLAST score 268 E value 3.0e-23 Match length 86 % identity 55

NCBI Description (AL021633) hypothetical protein [Arabidopsis thaliana]

Seq. No. 11794

22514 2.R1040 Contig ID

5'-most EST LIB3073-020-Q1-K1-G5

Seq. No. 11795

22514 3.R1040 Contig ID

5'-most EST jC-gmst02400073g06a1

Method BLASTX NCBI GI g2827536 BLAST score 267 E value 2.0e-23 Match length 66 % identity

NCBI Description (AL021633) hypothetical protein [Arabidopsis thaliana]

Seq. No. 11796

Contig ID 22515 1.R1040

5'-most EST LIB3087-010-Q1-K1-E5

Method BLASTX NCBI GI g2352828 BLAST score 367



```
E value
                   1.0e-34
Match length
                   139
% identity
                   57
                   (AF009228) NaCl-inducible Ca2+-binding protein [Arabidopsis
NCBI Description
                   thaliana]
                   11797
Seq. No.
                   22515_2.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy244g11b1
Method
                   BLASTX
                   g2352828
NCBI GI
BLAST score
                   345
E value
                   3.0e-32
Match length
                   139
% identity
                   55
```

NCBI Description (AF009228) NaCl-inducible Ca2+-binding protein [Arabidopsis thaliana]

 Seq. No.
 11798

 Contig ID
 22519\_1.R1040

 5'-most EST
 kmv700740228.h1

 Method
 BLASTX

 NCBI GI
 g2129929

 BLAST score
 2125

BLAST score 2125
E value 0.0e+00
Match length 418
% identity 97
NCRI Description DNA-dir

NCBI Description DNA-directed RNA polymerase (EC 2.7.7.6) II chain RPB2 - tomato >qi 1049068 (U28403) RNA polymerase II subunit 2

[Solanum lyconersicum]

[Solanum lycopersicum]

Seq. No. 11799

Contig ID 22521\_1.R1040 5'-most EST fua701040386.h1

Method BLASTN
NCBI GI g4159708
BLAST score 47
E value 4.0e-17
Match length 95
% identity 87

% identity 87
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MKP6, complete sequence [Arabidopsis thaliana]

Seq. No. 11800

Contig ID 22522 1.R1040

5'-most EST LIB3139-045-P1-N1-A5

Method BLASTX
NCBI GI g100099
BLAST score 157
E value 2.0e-10
Match length 52
% identity 60

NCBI Description DNA-binding protein VBP1 - fava bean >gi 1372966 (M81827)

CREB-like protein [Vicia faba]

Seq. No. 11801

Contig ID 22522 2.R1040



5'-most EST LIB3109-013-Q1-K1-B5

Method BLASTN
NCBI GI g1372965
BLAST score 59

E value 2.0e-24
Match length 149
% identity 90

NCBI Description Vicia faba CREB-like protein mRNA, complete cds

Seq. No. 11802

Contig ID 22522 3.R1040 5'-most EST rlr700899007.h1

Seq. No. 11803

Contig ID 22523 1.R1040

5'-most EST LIB3051-107-Q1-K1-C5

Seq. No. 11804

Contig ID 22523 2.R1040 5'-most EST kl1701212729.h1

Method BLASTX
NCBI GI g2789660
BLAST score 351
E value 6.0e-33
Match length 155
% identity 50

NCBI Description (AF040102) p105 [Arabidopsis thaliana]

Seq. No.

Contig ID 22523 3.R1040

5'-most EST LIB3087-009-Q1-K1-C4

11805

Method BLASTX
NCBI GI g2789660
BLAST score 395
E value 6.0e-57
Match length 254
% identity 52

NCBI Description (AF040102) p105 [Arabidopsis thaliana]

Seq. No. 11806

Contig ID 22523 4.R1040

5'-most EST LIB3109-047-Q1-K1-H3

Method BLASTX
NCBI GI g2789660
BLAST score 466
E value 1.0e-46
Match length 174
% identity 56

NCBI Description (AF040102) p105 [Arabidopsis thaliana]

Seq. No. 11807

Contig ID 22524\_1.R1040 5'-most EST uxk700672077.h1

Method BLASTX
NCBI GI g4455359
BLAST score 1014
E value 1.0e-110



Match length 332 % identity 64

NCBI Description (AL035524) putative protein [Arabidopsis thaliana]

Seq. No.

11808

Contig ID 5'-most EST 22525\_1.R1040 zsg701122823.h1

Method BLASTX
NCBI GI g1245182
BLAST score 964
E value 1.0e-105
Match length 227

% identity 78

NCBI Description (U49398) sterol delta-7 reductase [Arabidopsis thaliana]

Seq. No.

11809

Contig ID

22525 2.R1040

5'-most EST

LIB3051-069-Q1-K1-C8

Method BLASTX
NCBI GI g1245182
BLAST score 258
E value 4.0e-31
Match length 103
% identity 69

NCBI Description (U49398) sterol delta-7 reductase [Arabidopsis thaliana]

Seq. No.

11810

Contig ID 22526\_1.R1040

5'-most EST LIB3109-018-Q1-K1-B3

Method BLASTX
NCBI GI g4204294
BLAST score 460
E value 7.0e-46
Match length 141
% identity 71

NCBI Description (AC003027) lcl prt seq No definition line found

[Arabidopsis thaliana]

Seq. No. 11811

Contig ID 22575\_1.R1040

5'-most EST LIB3051-070-Q1-K1-A2

Method BLASTX
NCBI GI g514324
BLAST score 915
E value 7.0e-99
Match length 265
% identity 68

NCBI Description (L34773) RNA polymerase subunit [Arabidopsis thaliana]

>gi\_2462755 (AC002292) RNA polymerase subunit (isoform B)
[Arabidopsis thaliana] >gi\_1586550 prf \_2204246B RNA

polymerase [Arabidopsis thaliana]

Seq. No. 11812

Contig ID 22575\_2.R1040 5'-most EST eep700865145.h1

Method BLASTX NCBI GI g514324



BLAST score 182 E value 1.0e-13 Match length 60 % identity 53

NCBI Description (L34773) RNA polymerase subunit [Arabidopsis thaliana] >gi\_2462755 (AC002292) RNA polymerase subunit (isoform B) [Arabidopsis thaliana] >gi\_1586550\_prf\_\_2204246B RNA

polymerase [Arabidopsis thaliana]

Seg. No. 11813

Contig ID 22578 1.R1040

5'-most EST uC-gmrominsoy173b06b1

Method BLASTX
NCBI GI g2213587
BLAST score 234
E value 2.0e-19
Match length 109
% identity 49

NCBI Description (AC000348) T7N9.7 [Arabidopsis thaliana]

Seq. No. 11814

Contig ID 22578 2.R1040

5'-most EST LIB3094-090-Q1-K1-F2

Method BLASTX
NCBI GI g2213587
BLAST score 291
E value 3.0e-29
Match length 111
% identity 59

NCBI Description (AC000348) T7N9.7 [Arabidopsis thaliana]

Seq. No. 11815

Contig ID 22579\_1.R1040 5'-most EST leu701146288.h1

Method BLASTX
NCBI GI g1168609
BLAST score 519
E value 2.0e-55
Match length 140
% identity 79

NCBI Description AUXIN-RESISTANCE PROTEIN AXR1 >gi\_479664\_pir\_\_S35071 auxin-resistance protein AXR1 - Arabidopsis thaliana >gi\_304104 (L13922) ubiquitin-activating enzyme E1 [Arabidopsis thaliana] >gi\_2388579 (AC000098) Match to Arabidopsis AXR1 (gb ATHAXR1122). [Arabidopsis thaliana]

>gi\_448755\_prf\_\_1917337A ubiquitin-activating enzyme E1

[Arabidopsis thaliana]

Seq. No. 11816

Contig ID 22582\_1.R1040 5'-most EST fde700876020.h1

Method BLASTX
NCBI GI g2498882
BLAST score 414
E value 5.0e-40
Match length 292
% identity 38



NCBI Description SPLICEOSOME ASSOCIATED PROTEIN 114 (SAP 114) (SF3A120) 
>gi\_2146975\_pir\_\_S60735 splicing factor SF3a 120K chain - human >gi\_899298\_emb\_CAA59494 (X85237) human splicing factor [Homo sapiens] >gi\_3212998 (AC004997) spliceosome associated protein 114 (SF3a) [Homo sapiens]

Seq. No. 11817

Contig ID 22582 2.R1040 5'-most EST uC-gmropic049a06b1

Method BLASTX
NCBI GI g4538923
BLAST score 366
E value 8.0e-35
Match length 97
% identity 72

NCBI Description (AL049483) predicted protein destination factor

[Arabidopsis thaliana]

Seq. No. 11818

Contig ID 22582\_3.R1040

5'-most EST LIB3051-072-Q1-K1-E1

Method BLASTX
NCBI GI 94538923
BLAST score 341
E value 5.0e-32
Match length 91
% identity 71

NCBI Description (AL049483) predicted protein destination factor

[Arabidopsis thaliana]

Seq. No. 11819

Contig ID 22584\_1.R1040

5'-most EST uC-gmrominsoy047f01b1

Method BLASTX
NCBI GI g3047080
BLAST score 258
E value 4.0e-22
Match length 115
% identity 77

NCBI Description (AF058914) contains similarity to Arabidopsis thaliana

DNA-damage-repair/tolerance resistance protein DRT111

(SW:P42698) [Arabidopsis thaliana]

Seq. No. 11820

Contig ID 22584 2.R1040 5'-most EST sat701003057.h1

Method BLASTX
NCBI GI g3047080
BLAST score 586
E value 2.0e-60
Match length 177
% identity 65

NCBI Description (AF058914) contains similarity to Arabidopsis thaliana

DNA-damage-repair/tolerance resistance protein DRT111

(SW:P42698) [Arabidopsis thaliana]

Seq. No. 11821



Contig ID 22586\_1.R1040 5'-most EST LIB3051-060-Q1-K1-C3

Method BLASTX
NCBI GI g4309738
BLAST score 299
E value 6.0e-27
Match length 93
% identity 57

NCBI Description (AC006439) putative tubby protein [Arabidopsis thaliana]

Seq. No. 11822

Contig ID 22586\_2.R1040 5'-most EST jsh701067196.h1 Method BLASTX

NCBI GI g3738302 BLAST score 183 E value 2.0e-13 Match length 60 % identity 50

NCBI Description (AC005309) tubby-like protein [Arabidopsis thaliana]

>gi\_4249398 (AC006072) putative tubby protein [Arabidopsis

thaliana]

Seq. No. 11823

Contig ID 22589 1.R1040

5'-most EST uC-gmflminsoy054b12b1

Method BLASTX
NCBI GI g3152587
BLAST score 937
E value 1.0e-101
Match length 231
% identity 73

NCBI Description (AC002986) Similar to CREB-binding protein homolog

gb\_U88570 from D. melanogaster and contains similarity to callus-associated protein gb\_U01961 from Nicotiana tabacum. EST gb\_W43427 comes from this gene. [Arabidopsis thaliana]

Seq. No. 11824

Contig ID 22590 1.R1040 5'-most EST fjg700968389.h1

Method BLASTX
NCBI GI g2947060
BLAST score 1136
E value 1.0e-125
Match length 245
% identity 85

NCBI Description (AC002521) putative membrane protein [Arabidopsis thaliana]

Seq. No. 11825

Contig ID 22590\_2.R1040 5'-most EST fde700873556.h1

Method BLASTX
NCBI GI g2947060
BLAST score 205
E value 2.0e-16
Match length 51
% identity 76



NCBI Description (AC002521) putative membrane protein [Arabidopsis thaliana]

Seq. No.

11826

Contig ID

22597 1.R1040

5'-most EST

LIB3051-074-Q1-K1-C11

Seq. No.

11827

Contig ID 5'-most EST 22597 2.R1040 gsv701054819.hl

Seq. No.

11828

Contig ID 5'-most EST 22601 1.R1040 leu701148093.hl

Method NCBI GI BLASTX q2213614

BLAST score E value

861 2.0e-92 418

Match length % identity

59

NCBI Description (AC000103) F21J9.8 [Arabidopsis thaliana]

Seq. No.

11829

Contig ID

22601 2.R1040

5'-most EST

uC-gmrominsoy089f02b1

Method NCBI GI BLASTX g2213614

BLAST score E value Match length 380 2.0e-36 145

% identity NCBI Description

(AC000103) F21J9.8 [Arabidopsis thaliana]

Seq. No.

11830

Contig ID

22612 1.R1040

5'-most EST

jC-gmro02910057d08a1

Method NCBI GI BLASTX q3123161

BLAST score E value

219 1.0e-17

Match length % identity

94 16

NCBI Description

HYPOTHETICAL 77.0 KD TRP-ASP REPEATS CONTAINING PROTEIN

F35G12.4 IN CHROMOSOME III >gi 3876723 emb CAA86335

(Z46242) similar to beta-transducin; cDNA EST EMBL: Z14703 comes from this gene; cDNA EST EMBL:D67532 comes from this gene; cDNA EST EMBL:D69055 comes from this gene; cDNA EST

EMBL: D64515 comes from this gene; cDNA EST EMBL: D655

Seq. No.

11831

Contig ID 5'-most EST 22613 1.R1040  $uxk70\overline{0}671879.h1$ 

Method NCBI GI BLAST score BLASTX q481812

E value Match length

% identity

365 8.0e-35

NCBI Description DNA-binding protein GT-2 - Arabidopsis thaliana

>gi 416490 emb CAA51289 (X72780) GT-2 factor [Arabidopsis

thaliana]

11832 Seq. No.

22614 1.R1040 Contig ID bth700848344.h1 5'-most EST

Method BLASTX NCBI GI q3269288 BLAST score 845 1.0e-90 E value Match length 201 % identity 82

(AL030978) putative protein [Arabidopsis thaliana] NCBI Description

11833 Seq. No.

22626 1.R1040 Contig ID crh700850830.hl 5'-most EST

Method BLASTX NCBI GI g4138583 702 BLAST score E value 5.0e-74 Match length 226 % identity 68

NCBI Description (Y10821) plastidic ATP/ADP-transporter [Solanum tuberosum]

Seq. No.

11834 22631 1.R1040 Contig ID 5'-most EST gsv701047795.hl

BLASTX Method NCBI GI g1362086 BLAST score 883 E value 3.0e-95 Match length 188 % identity 89

NCBI Description 5-methyltetrahydropteroyltriglutamate--homocysteine

S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle

>gi 2129919 pir S65957

5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi\_886471\_emb\_CAA58474\_ (X83499) methionine synthase

[Catharanthus roseus]

Seq. No. 11835

22633\_1.R1040 Contig ID

5'-most EST LIB3170-042-Q1-J1-F10

BLASTX Method NCBI GI q3738312 BLAST score 844 E value 1.0e-90 234 Match length % identity

NCBI Description (AC005309) hypothetical protein [Arabidopsis thaliana]

11836 Seq. No.

22636 1.R1040 Contig ID  $zhf70\overline{0}964194.h1$ 5'-most EST



Method BLASTX
NCBI GI g3269288
BLAST score 820
E value 1.0e-87
Match length 203
% identity 79

NCBI Description (AL030978) putative protein [Arabidopsis thaliana]

Seq. No. 11837

Contig ID 22636\_2.R1040

5'-most EST LIB3074-011-Q1-E1-C8

Method BLASTX
NCBI GI g3269288
BLAST score 462
E value 3.0e-46
Match length 114
% identity 80

NCBI Description (AL030978) putative protein [Arabidopsis thaliana]

Seq. No. 11838

Contig ID 22638 1.R1040 5'-most EST fua701043379.h1

Method BLASTX
NCBI GI 94262186
BLAST score 1028
E value 1.0e-131
Match length 269
% identity 86

NCBI Description (AC005508) Highly similar to cullin 3 [Arabidopsis

thaliana]

Seq. No. 11839

Contig ID 22643\_1.R1040

5'-most EST LIB3051-084-Q1-K1-F11

Method BLASTX
NCBI GI g3702121
BLAST score 753
E value 1.0e-104
Match length 317
% identity 72

NCBI Description (AJ011681) retinoblastoma-related protein [Chenopodium

rubrum]

Seq. No. 11840

Contig ID 22644 1.R1040

5'-most EST LIB3051-013-Q1-E1-C7

Method BLASTX
NCBI GI g3549667
BLAST score 1116
E value 1.0e-122
Match length 278
% identity 77

NCBI Description (AL031394) Arabidopsis dynamin-like protein ADL2

[Arabidopsis thaliana]

Seq. No. 11841

Contig ID 22646 1.R1040



5'-most EST LIB3087-011-Q1-K1-D9

Method BLASTX
NCBI GI g2827526
BLAST score 449
E value 2.0e-44
Match length 166
% identity 56

NCBI Description (AL021633) AIG2-like protein [Arabidopsis thaliana]

Seq. No. 11842

Contig ID 22646\_2.R1040 5'-most EST jsh701068472.h1

Method BLASTX
NCBI GI g2827537
BLAST score 428
E value 5.0e-42
Match length 108
% identity 72

NCBI Description (AL021633) putative zinc finger protein [Arabidopsis

thaliana]

Seq. No. 11843

Contig ID 22646 3.R1040

5'-most EST LIB3051-039-Q1-K1-E5

Method BLASTX
NCBI GI g2827526
BLAST score 197
E value 9.0e-19
Match length 81
% identity 61

NCBI Description (AL021633) AIG2-like protein [Arabidopsis thaliana]

Seq. No. 11844

Contig ID 22646\_5.R1040

5'-most EST uC-gmflminsoy022g10b1

Method BLASTX
NCBI GI g4337197
BLAST score 112
E value 2.0e-12
Match length 78
% identity 64

NCBI Description (AC006403) putative AIG2 protein [Arabidopsis thaliana]

Seq. No. 11845

Contig ID 22648 1.R1040

5'-most EST LIB3051-019-Q1-E1-C11

Method BLASTX
NCBI GI g3006142
BLAST score 207
E value 2.0e-16
Match length 100
% identity 43

NCBI Description (AL022299) hypothetical protein [Schizosaccharomyces pombe]

Seq. No. 11846

Contig ID 22649\_1.R1040 5'-most EST uC-gmropic026h08b1

```
Method
                  BLASTN
NCBI GI
                  q2921318
                  658
BLAST score
                  0.0e+00
E value
                  707
Match length
                  98
% identity
NCBI Description Glycine max beta-1,3-glucanase 4 (SGlu4) gene, partial
                  sequence
Seq. No.
                  11847
                  22655 1.R1040
Contig ID
5'-most EST
                  LIB3051-046-Q1-K1-E9
                  BLASTX
Method
                  g2443755
NCBI GI
BLAST score
                  397
                  7.0e-59
E value
Match length
                  152
                  75
% identity
NCBI Description (AF020433) cyclophilin [Arabidopsis thaliana]
                  11848
Seq. No.
                  22656 1.R1040
Contig ID
5'-most EST
                  uC-gmflminsoy080c08b1
Method
                  BLASTX
NCBI GI
                  g1449179
BLAST score
                  416
E value
                  8.0e-41
Match length
                  122
% identity
                  67
NCBI Description (D86506) N-ethylmaleimide sensitive fusion protein
                  [Nicotiana tabacum]
                  11849
Seq. No.
                  22656 2.R1040
Contig ID
5'-most EST
                  ujr700646566.hl
                  BLASTX
Method
NCBI GI
                  g1449179
BLAST score
                  401
                  5.0e-39
E value
Match length
                  131
% identity
NCBI Description
                  (D86506) N-ethylmaleimide sensitive fusion protein
                   [Nicotiana tabacum]
                  11850
Seq. No.
                  22658 1.R1040
Contig ID
5'-most EST
                  LIB3051-012-Q1-E1-D12
Method
                  BLASTX
NCBI GI
                  g2262100
```

BLAST score 400 E value 5.0e-39

Match length 110 75 % identity

NCBI Description (AC002343) unknown protein [Arabidopsis thaliana]

Seq. No. 11851

Contig ID 22659 1.R1040



```
LIB3051-107-Q1-K1-F7
5'-most EST
                  11852
Seq. No.
                  22660 1.R1040
Contig ID
                  seb700652168.hl
5'-most EST
Method
                  BLASTX
                  g3549672
NCBI GI
BLAST score
                  1054
                  1.0e-124
E value
Match length
                  277
                  85
% identity
NCBI Description (AL031394) putative protein [Arabidopsis thaliana]
                  11853
Seq. No.
Contig ID
                  22660 2.R1040
5'-most EST
                  jC-qmf102220096f05a1
Method
                  BLASTX
NCBI GI
                  g4263821
BLAST score
                  309
                  4.0e-28
E value
                  106
Match length
                  65
% identity
NCBI Description (AC006067) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  11854
Contig ID
                  22690 1.R1040
5'-most EST
                  LIB3051-005-Q1-E1-H3
Method
                  BLASTX
NCBI GI
                  g3212848
BLAST score
                  432
E value
                  8.0e-43
Match length
                  125
% identity
                  69
                  (AC004005) putative inositol polyphosphate-5-phosphatase
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  11855
Contig ID
                  22691 1.R1040
5'-most EST
                  leu701152652.h1
Method
                  BLASTX
                  g3047104
NCBI GI
BLAST score
                  761
E value
                  6.0e-81
Match length
                  206
% identity
NCBI Description (AF058919) No definition line found [Arabidopsis thaliana]
Seq. No.
                  11856
                  22691 2.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy040g04b1
```

Seq. No. 11857

Contig ID 22692 1.R1040

5'-most EST LIB3051-019-Q1-K1-H11

Method BLASTX
NCBI GI g2262136
BLAST score 617



```
E value
                  2.0e-64
Match length
                  139
% identity
                  87
NCBI Description
                  (AC002330) predicted protein of unknown function
                  [Arabidopsis thaliana] >gi_4263520_gb_AAD15346_ (AC004044)
                  predicted protein of unknown function [Arabidopsis
                  thaliana]
                  11858
Seq. No.
                  22694 1.R1040
Contig ID
5'-most EST
                  LIB3107-040-Q1-K1-E1
Method
                  BLASTX
NCBI GI
                  g4406780
BLAST score
                  1836
                  0.0e+00
E value
Match length
                  428
                  82
% identity
                  (AC006532) putative multispanning membrane protein
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  11859
Contig ID
                  22695 1.R1040
5'-most EST
                  jC-gmf102220050b10d1
Method
                  BLASTX
                  g2316016
NCBI GI
BLAST score
                  607
                  4.0e-63
E value
Match length
                  196
% identity
                  43
                  (U92650) MRP-like ABC transporter [Arabidopsis thaliana]
NCBI Description
                  11860
Seq. No.
Contig ID
                  22696 1.R1040
                  hyd700725518.h1
5'-most EST
Method
                  BLASTX
```

g1076715 NCBI GI BLAST score 419 6.0e-41E value 128 Match length 59 % identity

NCBI Description abscisic acid-induced protein HVA22 - barley >gi\_404589

(L19119) A22 [Hordeum vulgare]

11861 Seq. No.

22697 1.R1040 Contig ID

5'-most EST LIB3051-039-Q1-K1-H11

BLASTX Method NCBI GI g1220453 BLAST score 1056 E value 1.0e-115 Match length 247 % identity 76

NCBI Description (M79328) alpha-amylase [Solanum tuberosum]

Seq. No. 11862

Contig ID 22701 1.R1040 dpv701098608.h1 5'-most EST



Method BLASTX
NCBI GI g2213629
BLAST score 495
E value 2.0e-89
Match length 221
% identity 74

NCBI Description (AC000103) F21J9.21 [Arabidopsis thaliana]

Seq. No. 11863

Contig ID 22702\_2.R1040 5'-most EST rca701002056.h1

Method BLASTX
NCBI GI g544250
BLAST score 738
E value 4.0e-78
Match length 168
% identity 80

NCBI Description ER LUMEN PROTEIN RETAINING RECEPTOR (HDEL RECEPTOR)

>gi 541860 pir A49677 endoplasmic reticulum retention

receptor Erd2 - Arabidopsis thaliana

Seq. No. 11864

Contig ID 22704\_1.R1040

5'-most EST uC-gmrominsoy058e02b1

Method BLASTX
NCBI GI g3901012
BLAST score 668
E value 5.0e-70
Match length 146
% identity 83

NCBI Description (AJ130885) xyloglucan endotransglycosylase 1 [Fagus

sylvatica]

Seq. No. 11865

Contig ID 22704 2.R1040 5'-most EST gsv70\overline{10}47788.h1

Method BLASTX
NCBI GI g3901012
BLAST score 312
E value 1.0e-28
Match length 77
% identity 81

NCBI Description (AJ130885) xyloglucan endotransglycosylase 1 [Fagus

sylvatica]

Seq. No. 11866

Contig ID 22704 3.R1040 5'-most EST ssr700557082.h1

Method BLASTX
NCBI GI g3901012
BLAST score 873
E value 5.0e-94
Match length 207
% identity 74

NCBI Description (AJ130885) xyloglucan endotransglycosylase 1 [Fagus

sylvatica]



Seq. No. 11867

Contig ID 22706\_1.R1040 5'-most EST bth700844079.h1

Method BLASTX
NCBI GI g1361983
BLAST score 1203
E value 1.0e-132
Match length 328
% identity 71

NCBI Description ARP protein - Arabidopsis thaliana >gi\_886434\_emb\_CAA89858\_

(Z49776) ARP protein [Arabidopsis thaliana]

Seq. No. 11868

Contig ID 22707 1.R1040

5'-most EST LIB3170-050-Q1-K1-F3

Method BLASTX
NCBI GI g4115922
BLAST score 336
E value 4.0e-36
Match length 144
% identity 60

NCBI Description (AF118222) contains similarity to ubiquitin

carboxyl-terminal hydrolase family 2 (Pfam: PF00443,

score=48.3, E=3.5e-13, N=2) and (Pfam:PF00442, Score=40.0

E=5.2e-08, N=1) [Arabidopsis thaliana]

Seq. No. 11869

Contig ID 22708\_1.R1040 5'-most EST hyd700728881.h1

Method BLASTX
NCBI GI g2388911
BLAST score 444
E value 8.0e-44
Match length 181
% identity 48

NCBI Description (Z98974) hypothetical protein [Schizosaccharomyces pombe]

Seq. No. 11870

Contig ID 22708 2.R1040 5'-most EST kl1701204858.h1

Method BLASTX
NCBI GI g2388911
BLAST score 163
E value 3.0e-11
Match length 79
% identity 41

NCBI Description (298974) hypothetical protein [Schizosaccharomyces pombe]

Seq. No. 11871

Contig ID 22711 1.R1040 5'-most EST hyd700725741.h1

Method BLASTX
NCBI GI g4138581
BLAST score 474
E value 1.0e-47
Match length 128
% identity 27



NCBI Description (X98474) mitochondrial energy transfer protein [Solanum tuberosum]

Seq. No. 11872

Contig ID 22712\_1.R1040 5'-most EST leu701152787.h1

Method BLASTX
NCBI GI g2253583
BLAST score 357
E value 1.0e-33
Match length 135
% identity 61

NCBI Description (U78721) hypothetical protein [Arabidopsis thaliana]

Seq. No. 11873

Contig ID 22712 2.R1040

5'-most EST LIB3138-029-Q1-N1-E9

Seq. No. 11874

Contig ID 22713 1.R1040

5'-most EST LIB3051-077-Q1-K1-E3

Method BLASTX
NCBI GI g2388970
BLAST score 385
E value 2.0e-37
Match length 108
% identity 71

NCBI Description (Z98979) tat binding homolog [Schizosaccharomyces pombe]

Seq. No. 11875

Contig ID 22714\_1.R1040 5'-most EST sat701004519.h1

Method BLASTX
NCBI GI g4102839
BLAST score 446
E value 5.0e-44
Match length 182
% identity 48

NCBI Description (AF016713) LeOPT1 [Lycopersicon esculentum]

Seq. No. 11876

Contig ID 22716\_1.R1040 5'-most EST dpv701097324.h1

Method BLASTX
NCBI GI g4262182
BLAST score 915
E value 1.0e-98
Match length 366
% identity 49

NCBI Description (AC005508) 44123 [Arabidopsis thaliana]

Seq. No. 11877

Contig ID 22716 2.R1040

5'-most EST uC-gmrominsoy201d05b1

Seq. No. 11878

Contig ID 22719 1.R1040



```
5'-most EST
                  LIB3051-066-Q1-K1-D9
Method
                  BLASTX
NCBI GI
                  q2160163
BLAST score
                  257
                  5.0e-22
E value
Match length
                  97
                  37
% identity
NCBI Description
                  (AC000132) No definition line found [Arabidopsis thaliana]
Seq. No.
                  11879
                  22726 1.R1040
Contig ID
5'-most EST
                  jC-gmst02400045a08a1
Method
                  BLASTX
NCBI GI
                  g3548815
                  253
BLAST score
E value
                  2.0e-21
Match length
                  143
% identity
NCBI Description
                  (AC005313) similar to axoneme-associated protein mst101
                  [Arabidopsis thaliana]
Seq. No.
                  11880
                  22726 2.R1040
Contig ID
5'-most EST
                  LIB3051-077-Q1-K1-D1
Seq. No.
                  11881
Contig ID
                  22731 1.R1040
                  pmv700890575.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2801442
BLAST score
                  589
E value
                  1.0e-72
Match length
                  161
% identity
                  75
NCBI Description
                  (AF028338) ubiquitin-conjugating enzyme 15 [Arabidopsis
                  thaliana]
Seq. No.
                  11882
Contig ID
                  22734 1.R1040
5'-most EST
                  jC-qmro02910054e09a1
Method
                  BLASTX
NCBI GI
                  g1730621
BLAST score
                  583
E value
                  7.0e-60
Match length
                  228
                  50
% identity
                  HYPOTHETICAL 48.1 KD PROTEIN IN TUB1-CPR3 INTERGENIC REGION
NCBI Description
```

>gi\_630106\_pir\_\_S48817 hypothetical protein YML079w - yeast

(Saccharomyces cerevisiae) >gi\_587531\_emb\_CAA86498

(Z46373) orf, len: 423, CAI: 0.18, 27.4% identity in 307 aa

overlap with S36201 S36201 hypothetical protein 1 -Rhizobium leguminosarum [Saccharomyces cerevisiae]

Seq. No. 11883 Contig ID 22750 1.R1040 5'-most EST q5606442

Method BLASTX



NCBI GI g166410 BLAST score 647 E value 2.0e-67 Match length 237 % identity 54

NCBI Description (L07291) Alfin-1 [Medicago sativa]

Seq. No. 11884

Contig ID 22750\_2.R1040 5'-most EST seb700652312.h1

Method BLASTX
NCBI GI g166410
BLAST score 172
E value 4.0e-12
Match length 46
% identity 65

NCBI Description (L07291) Alfin-1 [Medicago sativa]

Seq. No. 11885

Contig ID 22750 3.R1040 5'-most EST kl1701208244.h1

Method BLASTN
NCBI GI g4091116
BLAST score 56
E value 1.0e-22
Match length 140
% identity 85

NCBI Description Oryza sativa nucleic acid binding protein mRNA, complete

cds

Seq. No. 11886

Contig ID 22750 4.R1040 5'-most EST fua701043546.h1

Method BLASTX
NCBI GI g166410
BLAST score 389
E value 2.0e-37
Match length 195
% identity 44

NCBI Description (L07291) Alfin-1 [Medicago sativa]

Seq. No. 11887

Contig ID 22752\_1.R1040

5'-most EST LIB3051-064-Q1-K1-E7

Method BLASTX
NCBI GI g2980806
BLAST score 373
E value 2.0e-35
Match length 102
% identity 62

NCBI Description (AL022197) putative protein [Arabidopsis thaliana]

Seq. No. 11888

Contig ID 22753\_1.R1040

5'-most EST LIB3051-066-Q1-K1-E7

Method BLASTX NCBI GI g1174470



BLAST score 338 E value 9.0e-32 Match length 117 % identity 54

NCBI Description OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5)

(INTEGRAL MEMBRANE PROTEIN 1) >gi\_508543 (L34260) integral membrane protein 1 [Mus musculus] >gi\_1588285\_prf\_\_2208301A

integral membrane protein [Mus musculus]

Seq. No. 11889

Contig ID 22759 1.R1040

5'-most EST LIB3093-029-Q1-K1-G8

Method BLASTX
NCBI GI g3169180
BLAST score 1576
E value 1.0e-176
Match length 346
% identity 85

NCBI Description (AC004401) putative casein kinase II catalytic subunit

[Arabidopsis thaliana]

Seq. No. 11890

Contig ID 22764\_1.R1040 5'-most EST bnh700764516.h1

Method BLASTN
NCBI GI g1771194
BLAST score 38
E value 7.0e-12
Match length 153
% identity 86

NCBI Description L.japonicus gene encoding RING finger protein

Seq. No.

11891

Contig ID 22764 2.R1040

5'-most EST jC-gmro02910023f08d1

Method BLASTN
NCBI GI g558544
BLAST score 94
E value 3.0e-45
Match length 258
% identity 84

NCBI Description L.japonicus (Gifu B-129) mRNA for RING finger protein (C

terminal)

Seq. No.

11892

Contig ID 22764\_3.R1040 5'-most EST zhf700956451.h1

Method BLASTN
NCBI GI g558544
BLAST score 115
E value 7.0e-58
Match length 235
% identity 87

NCBI Description L.japonicus (Gifu B-129) mRNA for RING finger protein (C

terminal)

Seq. No.



22769 1.R1040 Contig ID 5'-most EST uC-gmropic024d10b1 Method BLASTX NCBI GI g3413712 BLAST score 354 E value 1.0e-33 Match length 90 70 % identity (AC004747) hypothetical protein [Arabidopsis thaliana] NCBI Description Seq. No. 11894 Contig ID 22771 1.R1040 5'-most EST jC-gmst02400066d06a2 Method BLASTX NCBI GI g4432860 BLAST score 813 6.0e-87 E value Match length 296 19 % identity (AC006300) putative glucose-induced repressor protein NCBI Description [Arabidopsis thaliana] Seq. No. 11895 Contig ID 22773 1.R1040 5'-most EST LIB3093-018-Q1-K1-C10 Method BLASTX g3184283 NCBI GI BLAST score 936 1.0e-101 E value Match length 237 % identity (AC004136) putative TBP-binding protein [Arabidopsis NCBI Description thaliana] Seq. No. 11896 Contig ID 22774 1.R1040  $zpv70\overline{0}759175.h1$ 5'-most EST Seq. No. 11897 22775 1.R1040 Contig ID LIB3051-084-Q1-K1-E11 5'-most EST Method BLASTX NCBI GI g2911052 BLAST score 541 2.0e-55 E value 169 Match length % identity 66 (AL021961) putative protein [Arabidopsis thaliana] NCBI Description Seq. No. 11898 22776 1.R1040 Contig ID 5'-most EST jC-gmro02910023d10d1

Method BLASTX

 NCBI GI
 g2655098

 BLAST score
 818

 E value
 1.0e-87

 Match length
 217



% identity 69

NCBI Description (AF023472) peptide transporter [Hordeum vulgare]

Seq. No. 1

11899

Contig ID

22777\_1.R1040

5'-most EST

LIB3051-005-Q1-E1-G11

Method NCBI GI BLAST score BLASTX g4455225

E value Match length 1.0e-64 178

622

60

% identity NCBI Description

(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.

11900

Contig ID 5'-most EST 22777\_2.R1040 rca700997594.h1

Method BLASTX
NCBI GI g4455225
BLAST score 387
E value 3.0e-37
Match length 141

% identity 46

NCBI Description (AL035440) putative protein [Arabidopsis thaliana]

Seq. No.

11901

Contig ID

22778 1.R1040

5'-most EST

LIB3051-088-Q1-K1-E11

Method BLASTX
NCBI GI g3986172
BLAST score 462
E value 4.0e-46
Match length 140
% identity 60

NCBI Description

(AB015428) EXGT1 [Pisum sativum]

Seq. No.

11902

Contig ID

22781\_1.R1040

5'-most EST

uC-gmronoir031d11b1

Method BLASTX
NCBI GI g549010
BLAST score 1927
E value 0.0e+00
Match length 421
% identity 88

NCBI Description

EUKARYOTIC PEPTIDE CHAIN RELEASE FACTOR SUBUNIT 1 (ERF1) (OMNIPOTENT SUPPRESSOR PROTEIN 1 HOMOLOG) (SUP1 HOMOLOG) >gi\_322554\_pir\_\_S31328 omnipotent suppressor protein SUP1

homolog (clone G18) - Arabidopsis thaliana

>gi\_16514\_emb\_CAA49172\_ (X69375) similar to yeast

omnipotent suppressor protein SUP1 (SUP45) [Arabidopsis thaliana] >gi\_1402882\_emb\_CAA66813\_ (X98130) eukaryotic early release factor subunit 1-like protein [Arabidopsis thaliana] >gi\_1495249\_emb\_CAA66118\_ (X97486) eRF1-3

[Arabidopsis thaliana]

Seq. No.



22781 3.R1040 Contig ID pcp700994108.hl 5'-most EST

11904 Seq. No.

22781 4.R1040 Contig ID  $k1170\overline{1}213390.h1$ 5'-most EST

11905 Seq. No.

22782 1.R1040 Contig ID hyd700728673.h1 5'-most EST

BLASTX Method g3885334 NCBI GI 921 BLAST score 1.0e-100 E value Match length 209 81 % identity

(AC005623) putative argonaute protein [Arabidopsis NCBI Description

thaliana]

11906 Seq. No.

22783 1.R1040 Contig ID zzp700831966.h1 5'-most EST

BLASTX Method g2576411 NCBI GI 646 BLAST score 1.0e-67 E value 159 Match length 79 % identity

(AF012833) similar to dynamin-like protein encoded by NCBI Description

GenBank Accession Number X99669 [Arabidopsis thaliana]

11907 Seq. No.

22784 1.R1040 Contig ID

LIB3093-058-Q1-K1-G11 5'-most EST

BLASTN Method q3941321 NCBI GI 560 BLAST score 0.0e + 00E value 860 Match length % identity

Medicago truncatula gamma-glutamylcysteine synthetase mRNA, NCBI Description

nuclear gene encoding putative plastid protein, complete

cds

11908 Seq. No.

22785 1.R1040 Contig ID qsv701049335.h1 5'-most EST

BLASTX Method NCBI GI q3402692 172 BLAST score E value 3.0e-12 46 Match length 72 % identity

(AC004697) putative NCBI Description

CDP-diacylglycerol--glycerol-3-phosphate

3-phosphatidyltransferase [Arabidopsis thaliana]



Seq. No. 11909

Contig ID 22787\_1.R1040

5'-most EST LIB3139-036-P1-N1-H9

Method BLASTX
NCBI GI g1916290
BLAST score 290
E value 1.0e-25
Match length 112
% identity 51

NCBI Description (U89876) ALY [Mus musculus]

Seq. No. 11910

Contig ID 22803\_1.R1040 5'-most EST uC-gmropic024e01b1

Method BLASTX
NCBI GI g1362009
BLAST score 659
E value 7.0e-69
Match length 153
% identity 45

NCBI Description ubiquitin-like protein 7 - Arabidopsis thaliana

Seq. No. 11911

Contig ID 22803\_3.R1040 5'-most EST fua701039520.h1

Method BLASTN
NCBI GI g2760346
BLAST score 105
E value 6.0e-52
Match length 210
% identity 18

NCBI Description Arabidopsis thaliana ubiquitin (UBQ11) gene, complete cds

Seq. No. 11912

Contig ID 22868\_1.R1040 5'-most EST cks700764771.h1

Method BLASTN
NCBI GI g312559
BLAST score 147
E value 4.0e-77
Match length 191
% identity 94

NCBI Description G.max 26S rRNA (partial)

Seq. No. 11913

Contig ID 22868\_2.R1040 5'-most EST awf700837946.h1

Method BLASTN
NCBI GI g2687435
BLAST score 205
E value 1.0e-112
Match length 249
% identity 96

NCBI Description Hamamelis virginiana large subunit 26S ribosomal RNA gene,

partial sequence

Seq. No. 11914



```
22874 1.R1040
Contig ID
                  uC-gmflminsoy064h12b1
5'-most EST
                  BLASTX
Method
                  g2815493
NCBI GI
BLAST score
                  1716
E value
                  0.0e + 00
                  491
Match length
                   65
% identity
                  SERINE CARBOXYPEPTIDASE I PRECURSOR (CARBOXYPEPTIDASE C)
NCBI Description
                   (CP-MI) >gi_1731988_emb_CAA70816_ (Y09603) serine
                   carboxypeptidase I, CP-MI [Hordeum vulgare]
                   11915
Seq. No.
                   22946 1.R1040
Contig ID
                   LIB3051-064-Q1-K1-A3
5'-most EST
Method
                   BLASTN
                   q3452177
NCBI GI
BLAST score
                   542
                   0.0e + 00
E value
                   562
Match length
% identity
                   99
                   Glycine max cv Ransom clone 3 26S-18S ribosomal RNA
NCBI Description
                   intergenic spacer region
                   11916
Seq. No.
                   22954 1.R1040
Contig ID
                   LIB3051-041-Q1-K1-H6
5'-most EST
                   BLASTN
Method
                   g169980
NCBI GI
BLAST score
                   242
                   1.0e-133
E value
                   368
Match length
                   93
% identity
                   Soybean heat-shock protein (Gmhsp26-A) gene, complete cds
NCBI Description
                   11917
Seq. No.
                   22990 1.R1040
Contig ID
                   LIB3065-019-Q1-N1-D2
 5'-most EST
                   BLASTX
Method
                   g3413716
NCBI GI
                   201
 BLAST score
                   5.0e-15
 E value
                   291
 Match length
 % identity
                   (AC004747) unknown protein [Arabidopsis thaliana]
 NCBI Description
                   >gi_3643589 (AC005395) unknown protein [Arabidopsis
                    thaliana]
                    11918
 Seq. No.
                    22990 2.R1040
 Contig ID
                    sat701003222.h1
 5'-most EST
 Method
                    BLASTX
```

q3413716 NCBI GI BLAST score 681

3.0e-82

E value Match length 306 18 % identity



NCBI Description (AC004747) unknown protein [Arabidopsis thaliana] >gi 3643589 (AC005395) unknown protein [Arabidopsis thaliana]

Seq. No. Contig ID 11919

5'-most EST

22990 4.R1040

Method

LIB3051-050-Q1-K1-C10

NCBI GI BLAST score BLASTX g3413716

E value Match length

1.0e-22 189

% identity

181

NCBI Description

(AC004747) unknown protein [Arabidopsis thaliana] >gi 3643589 (AC005395) unknown protein [Arabidopsis

thaliana]

Seq. No.

11920

Contig ID

23001 1.R1040

5'-most EST

LIB3170-039-Q1-K2-F10

Method NCBI GI BLASTN g210811

BLAST score E value

536 0.0e + 00

Match length % identity

572 98

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No.

11921

Contig ID

23002 1.R1040

5'-most EST

LIB3051-051-Q1-K1-H5

Method NCBI GI

BLASTX g3875246

BLAST score

558

E value

4.0e-57

Match length % identity

195 56

NCBI Description

(Z81490) similar to WD domain, G-beta repeats (2 domains);

cDNA EST EMBL: T00482 comes from this gene; cDNA EST

EMBL: T00923 comes from this gene; cDNA EST yk449d4.3 comes from this gene; cDNA EST yk449d4.5 comes from this gene;

Seq. No.

11922

Contig ID 5'-most EST 23154 1.R1040 leu701145548.h1

Method NCBI GI BLASTX q3236242

BLAST score

425

E value

1.0e-41

Match length % identity

103

NCBI Description

(AC004684) putative ribosomal protein L36 [Arabidopsis

thaliana]

Seq. No.

11923

Contig ID

23154 2.R1040

```
jsh701065078.h1
5'-most EST
                  BLASTN
Method
NCBI GI
                  g1276966
BLAST score
                  48
                  5.0e-18
E value
Match length
                  113
% identity
                  91
NCBI Description Daucus carota putative ribosomal protein mRNA, somatic
                  embryo clone Gea42, partial cds
Seq. No.
                  11924
Contig ID
                  23231 1.R1040
5'-most EST
                  LIB3051-117-Q1-K1-B11
Method
                  BLASTN
NCBI GI
                  q170091
BLAST score
                  439
                  0.0e+00
E value
Match length
                  451
                  100
% identity
NCBI Description Glycine max vegetative storage protein (vspB) gene,
                  complete cds
                  11925
Seq. No.
                  23239_1.R1040
Contig ID
5'-most EST
                  LIB3093-006-Q1-K1-C2
Method
                  BLASTX
                  q3033382
NCBI GI
                  171
BLAST score
E value
                  6.0e-12
Match length
                  126
% identity
NCBI Description (AC004238) unknown protein [Arabidopsis thaliana]
                  11926
Seq. No.
                  23240 1.R1040
Contig ID
                  LIB3106-015-Q1-K1-F5
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3435196
BLAST score
                  2868
                  0.0e+00
E value
Match length
                  727
% identity
                  74
NCBI Description (AF067773) glutamyl-tRNA synthetase [Arabidopsis thaliana]
Seq. No.
                  11927
Contig ID
                  23241 4.R1040
5'-most EST
                  uxk700670057.h1
```

Method BLASTX
NCBI GI g3786009
BLAST score 1903
E value 0.0e+00
Match length 476
% identity 79

NCBI Description (AC005499) unknown protein [Arabidopsis thaliana]

Seq. No. 11928

Contig ID 23241 5.R1040



```
5'-most EST
                  gsv701055860.hl
Method
                  BLASTX
NCBI GI
                  q3786009
BLAST score
                  257
E value
                  3.0e-22
Match length
                  70
% identity
                  77
                 (AC005499) unknown protein [Arabidopsis thaliana]
NCBI Description
                  11929
Seq. No.
Contig ID
                  23242 1.R1040
5'-most EST
                  jC-qmle01810082d08a1
Method
                  BLASTX
NCBI GI
                  g4567286
BLAST score
                  510
E value
                  1.0e-67
                  143
Match length
% identity
                  83
NCBI Description
                  (AC006841) putative coatomer alpha subunit [Arabidopsis
                  thaliana]
                  11930
Seq. No.
                  23246 1.R1040
Contig ID
5'-most EST
                  LIB3055-011-Q1-N1-D12
Method
                  BLASTX
NCBI GI
                  q3953478
                  407
BLAST score
                  2.0e-41
E value
Match length
                  121
                  75
% identity
NCBI Description
                 (AC002328) F2202.23 [Arabidopsis thaliana]
Seq. No.
                  11931
                  23247 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy233c12b1
Method
                  BLASTX
NCBI GI
                  g1944407
BLAST score
                  688
                  1.0e-72
E value
Match length
                  163
                  75
% identity
NCBI Description (D86988) KIAA0221 [Homo sapiens]
Seq. No.
                  11932
Contig ID
                  23249 1.R1040
5'-most EST
                  LIB3051-004-Q1-E1-B6
Method
                  BLASTX
NCBI GI
                  g4469015
BLAST score
                  576
E value
                  1.0e-59
Match length
                  141
% identity
                  78
                 (AL035602) putative protein [Arabidopsis thaliana]
NCBI Description
```

Seq. No. 11933

Contig ID 23251\_1.R1040 5'-most EST LIB3170-036-Q1-K1-C1



```
BLASTX
Method
                  q3668089
NCBI GI
                  831
BLAST score
                  6.0e-89
E value
                  299
Match length
                  52
% identity
NCBI Description (AC004667) unknown protein [Arabidopsis thaliana]
                  11934
Seq. No.
```

23251 4.R1040 Contig ID LIB3092-053-Q1-K1-A4 5'-most EST BLASTX Method q3668089 NCBI GI 225 BLAST score 2.0e-18

E value 73 Match length 53 % identity

(AC004667) unknown protein [Arabidopsis thaliana] NCBI Description

11935 Seq. No. 23252 1.R1040 Contig ID LIB3051-004-Q1-E1-F2 5'-most EST BLASTX Method

a133356 NCBI GI BLAST score 401 4.0e-39 E value 147 Match length 53 % identity

DNA-DIRECTED RNA POLYMERASE III LARGEST SUBUNIT (C160) NCBI Description >gi\_66978\_pir\_\_RNBY3L DNA-directed RNA polymerase (EC

2.7.7.6) III 160K chain - yeast (Saccharomyces cerevisiae) >gi\_4400\_emb\_CAA26905\_ (X03129) RNA polymerase III largest subunit [Saccharomyces cerevisiae]

>gi\_1050828\_emb\_CAA62123\_ (X90518) ORF 03254 [Saccharomyces cerevisiae] > gi\_1164961\_emb\_CAA64036\_ (X94335) YOR3254c

[Saccharomyces cerevisiae] >gi\_1420309 emb\_CAA99314

(Z75024) ORF YOR116c [Saccharomyces cerevisiae]

Seq. No. 11936

23254 1.R1040 Contig ID

jC-gmro02910060e09a1 5'-most EST

BLASTX Method g2435519 NCBI GI 1124 BLAST score E value 1.0e-123 316 Match length 72 % identity

(AF024504) similar to mouse MEM3 (GB:U47024 and S. NCBI Description

cerevisiae vacuolar sorting protein 35 (SW; P34110)

[Arabidopsis thaliana]

11937 Seq. No.

23254 2.R1040 Contia ID fC-gmf170090643511 5'-most EST

BLASTX Method g2435519 NCBI GI 468 BLAST score



2.0e-86 E value 236 Match length % identity 71

(AF024504) similar to mouse MEM3 (GB:U47024 and S. NCBI Description cerevisiae vacuolar sorting protein 35 (SW; P34110)

[Arabidopsis thaliana]

11938 Seq. No.

23257 1.R1040 Contig ID g4307102 5'-most EST BLASTX Method g2317901 NCBI GI 988 BLAST score 1.0e-107 E value Match length 267 70

% identity (U89959) Similar to vesicle transport protein, PIR NCBI Description

Accession Number A55931 [Arabidopsis thaliana]

11939 Seq. No.

23257 2.R1040 Contia ID

LIB3170-072-Q1-K1-G6 5'-most EST

11940 Seq. No.

23258 1.R1040 Contig ID uC-gmronoir024e05b1 5'-most EST

BLASTX Method g2501231 NCBI GI BLAST score 415 1.0e-40 E value 143 Match length 59 % identity

HYPOTHETICAL 38.1 KD PROTEIN >gi\_99505\_pir\_\_S24930 NCBI Description

hypothetical protein - pink corydalis >gi\_18258 emb\_CAA45139\_(X63595) protein of unknown

function [Corydalis sempervirens] >gi\_444333\_prf\_\_1906382A

pCSC71 protein [Corydalis sempervirens]

11941 Seq. No.

23260 1.R1040 Contig ID

LIB3170-064-Q1-K1-E8 5'-most EST

BLASTX Method q577309 NCBI GI 590 BLAST score 5.0e-61 E value 197 Match length 50 % identity

(D42053) KIAA0091 gene product is related to subtilisin. NCBI Description [Homo sapiens] >gi\_4506775\_ref\_NP\_003782.1\_pS1P\_ UNKNOWN

Seq. No. 11942

23262 1.R1040 Contig ID fC-qmse700672488b1 5'-most EST

11943 Seq. No.

23262 2.R1040 Contig ID sat701008570.hl 5'-most EST



```
Method
                   BLASTX
NCBI GI
                   g2245124
BLAST score
                   536
                   9.0e-55
E value
Match length
                   158
 % identity
                   62
NCBI Description (Z97343) protein kinase [Arabidopsis thaliana]
Seq. No.
                   11944
Contig ID
                   23264 1.R1040
5'-most EST
                   LIB3051-015-Q1-E1-A6
Method
                   BLASTX
                   g100099
NCBI GI
BLAST score
                   412
E value
                   2.0e-40
                   153
Match length
                   57
% identity
NCBI Description
                  DNA-binding protein VBP1 - fava bean >gi 1372966 (M81827)
                   CREB-like protein [Vicia faba]
                   11945
Seq. No.
Contig ID
                   23274 1.R1040
 5'-most EST
                   uxk700672037.h1
Method
                   BLASTX
                   g2723477
NCBI GI
BLAST score
                   375
                   6.0e-36
E value
Match length
                   113
 % identity
                   69
NCBI Description (D89824) GTP-binding protein [Arabidopsis thaliana]
                   11946
Seq. No.
Contig ID
                   23279 1.R1040
5'-most EST
                   LIB3170-075-Q1-K2-F4
Method
                   BLASTX
NCBI GI
                   g4006848
BLAST score
                   707
                   8.0e-89
E value
Match length
                   321
                   57
 % identity
NCBI Description
                   (AJ131433) selenocysteine methyltransferase [Astragalus
                   bisulcatus]
Seq. No.
                   11947
Contig ID
                   23279 2.R1040
 5'-most EST
                   LIB3051-017-Q1-E1-H5
Method
                   BLASTX
NCBI GI
                   g4006848
BLAST score
                   278
E value
                   8.0e-25
Match length
                   71
 % identity
                   73
NCBI Description
                   (AJ131433) selenocysteine methyltransferase [Astragalus
```

Seq. No. 11948

Contig ID 23283 1.R1040

bisulcatus]



```
5'-most EST
                  LIB3051-018-Q1-E1-E8
Method
                  BLASTX
NCBI GI
                  q576509
BLAST score
                  1640
E value
                  0.0e + 00
Match length
                  528
% identity
                  76
NCBI Description (L36857) GTP-binding protein [Pisum sativum]
Seq. No.
                  11949
                  23284 1.R1040
Contig ID
                  LIB3109-052-Q1-K1-D3
5'-most EST
                  BLASTX
Method
NCBI GI
                  g3402673
BLAST score
                  791
                  1.0e-119
E value
                  337
Match length
% identity
                  64
NCBI Description (AC004697) unknown protein [Arabidopsis thaliana]
                  11950
Seq. No.
Contig ID
                  23286_1.R1040
5'-most EST
                  LIB3051-018-Q1-E1-H1
Method
                  BLASTX
NCBI GI
                  q481812
BLAST score
                  200
E value
                  3.0e-15
Match length
                  84
% identity
                  49
                  DNA-binding protein GT-2 - Arabidopsis thaliana
NCBI Description
                  >gi 416490 emb CAA51289 (X72780) GT-2 factor [Arabidopsis
                  thaliana]
Seq. No.
                  11951
                  23289 1.R1040
Contig ID
5'-most EST
                  zhf700957710.h1
Method
                  BLASTX
                  g3551247
NCBI GI
BLAST score
                  1250
                  1.0e-138
E value
Match length
                  236
                  99
% identity
NCBI Description (AB012703) 181 [Daucus carota]
Seq. No.
                  11952
Contig ID
                  23298 1.R1040
5'-most EST
                  zsg701122657.h1
Method
                  BLASTX
NCBI GI
                  g3056581
BLAST score
                  292
E value
                  4.0e-26
                  131
Match length
% identity
                  43
```

Contig ID 23300 1.R1040

11953

Seq. No.

NCBI Description (AC004255) T1F9.2 [Arabidopsis thaliana]



5'-most EST LIB3051-028-Q1-K1-F7 Method BLASTX

NCBI GI g124198 BLAST score 289 E value 1.0e-25 Match length 70 % identity 74

NCBI Description TRANSLATION INITIATION FACTOR IF-1, CHLOROPLAST

>gi\_81508\_pir\_\_A23525 translation initiation factor IF-1
homolog - spinach chloroplast >gi\_12263\_emb\_CAA27212\_
(X03496) pot. initiation factor IF-1 (aa 1-77) [Spinacia

oleracea]

Seq. No. 11954

Contig ID 23303\_1.R1040

5'-most EST LIB3051-029-Q1-K1-A4

Method BLASTX
NCBI GI g1177405
BLAST score 561
E value 2.0e-57
Match length 193
% identity 55

NCBI Description (X89855) citrate binding protein [Hevea brasiliensis]

Seq. No. 11955

Contig ID 23304\_1.R1040 5'-most EST uC-gmropic022e02b1

Method BLASTX
NCBI GI g3242783
BLAST score 2828
E value 0.0e+00
Match length 735
% identity 72

NCBI Description (AF055354) respiratory burst oxidase protein B [Arabidopsis

thaliana]

Seq. No. 11956

Contig ID 23304\_2.R1040 5'-most EST uC-gmropic038h09b1

Method BLASTX
NCBI GI g2342676
BLAST score 369
E value 3.0e-35
Match length 87
% identity 76

NCBI Description (AC000106) Strong similarity to Oryza NADPH oxidase

(gb\_X93301). [Arabidopsis thaliana]

Seq. No. 11957

Contig ID 23304 3.R1040

5'-most EST LIB3170-080-Q1-K1-B12

Method BLASTX
NCBI GI g3242783
BLAST score 215
E value 1.0e-32
Match length 107
% identity 70



```
NCBI Description
                  (AF055354) respiratory burst oxidase protein B [Arabidopsis
                  thaliana]
Seq. No.
                  11958
Contig ID
                  23304 5.R1040
5'-most EST
                  LIB3107-079-Q1-K1-F11
Method
                  BLASTX
NCBI GI
                  q3242783
BLAST score
                  408
E value
                  4.0e-70
Match length
                  187
                  74
% identity
                  (AF055354) respiratory burst oxidase protein B [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  11959
                  23304 7.R1040
Contig ID
5'-most EST
                  zsq701119889.h1
                  BLASTX
Method
NCBI GI
                  q3242783
BLAST score
                  410
E value
                  3.0e-40
Match length
                  131
% identity
                   61
                  (AF055354) respiratory burst oxidase protein B [Arabidopsis
NCBI Description
                  thalianal
Seq. No.
                  11960
                  23308 2.R1040
Contig ID
5'-most EST
                  LIB3051-029-Q1-K1-F7
Method
                  BLASTX
                  q4539301
NCBI GI
BLAST score
                  295
E value
                  9.0e-27
Match length
                  119
% identity
                  54
NCBI Description (AL049480) putative mitochondrial protein [Arabidopsis
                  thaliana]
                  11961
Seq. No.
                  23310 1.R1040
Contig ID
5'-most EST
                  sat701012472.h1
Method
                  BLASTX
NCBI GI
                  g3355471
BLAST score
                  399
E value
                  2.0e-38
Match length
                  223
% identity
                   46
                  (AC004218) putative lysophospholipase [Arabidopsis
NCBI Description
                  thaliana]
```

Seq. No. 11962

Contig ID 23315\_1.R1040

5'-most EST LIB3051-110-Q1-K1-H6

Seq. No. 11963

Contig ID 23315 2.R1040



```
LIB3051-030-Q1-K1-F10
5'-most EST
                   11964
Seq. No.
                   23318 1.R1040
Contig ID
                   LIB3051-030-Q1-K1-H10
5'-most EST
                   BLASTX
Method
NCBI GI
                   q1620970
                   413
BLAST score
                   2.0e-40
E value
                   100
Match length
```

% identity 85
NCBI Description (Y08887) L-lactate dehydrogenase [Lycopersicon esculentum]
>gi\_1806117\_emb\_CAA71611\_ (Y10602) L-lactate dehydrogenase
[Lycopersicon esculentum]

 Seq. No.
 11965

 Contig ID
 23328\_1.R1040

 5'-most EST
 g5606112

 Method
 BLASTX

 NCBI GI
 g3913425

 BLAST score
 390

 E value
 3.0e-61

E value 3.0e Match length 177 % identity 69

NCBI Description PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE >gi 2275203 (AC002337) RNA helicase isolog

[Arabidopsis thaliana]

Seq. No. 11966

Contig ID 23328\_2.R1040 5'-most EST zzp700830332.h1

Method BLASTX
NCBI GI g3913425
BLAST score 184
E value 2.0e-17
Match length 74
% identity 69

NCBI Description PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE >gi 2275203 (AC002337) RNA helicase isolog

[Arabidopsis thaliana]

Seq. No. 11967

Contig ID 23329\_1.R1040
5'-most EST g5058367
Method BLASTX
NCBI GI g2924515
BLAST score 442
E value 4.0e-48
Match length 172

Match length 1/2 % identity 62

NCBI Description (AL022023) putative protein [Arabidopsis thaliana]

Seq. No. 11968

Contig ID 23329\_2.R1040 5'-most EST uxk700668313.h1

Method BLASTN NCBI GI g2924505



BLAST score 33 E value 4.0e-09 Match length 49 % identity 92

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone M4E13

(ESSAII project)

Seq. No. 11969

Contig ID 23342\_1.R1040

5'-most EST uC-gmrominsoy109h04b1

Method BLASTX
NCBI GI g2979560
BLAST score 632
E value 1.0e-65
Match length 186
% identity 68

NCBI Description (AC003680) unknown protein [Arabidopsis thaliana]

Seq. No. 11970

Contig ID 23351\_1.R1040 5'-most EST seb700649132.h1

Method BLASTN
NCBI GI g295447
BLAST score 250
E value 1.0e-138
Match length 416
% identity 93

NCBI Description Vigna radiata NADPH cytochrome P450 mRNA, complete cds

Seq. No. 11971

Contig ID 23356\_1.R1040 5'-most EST uC-gmropic031g06b1

Method BLASTX
NCBI GI g2160188
BLAST score 363
E value 1.0e-34
Match length 76
% identity 88

NCBI Description (AC000132) Similar to Vicia sucrose transport protein

(gb\_Z93774). [Arabidopsis thaliana]

Seq. No. 11972

Contig ID 23364\_1.R1040

5'-most EST LIB3051-043-Q1-K1-B10

Seq. No. 11973

Contig ID 23372\_1.R1040
5'-most EST g4396854
Method BLASTX
NCBI GI g1703168
BLAST score 284
E value 5.0e-25
Match length 168
% identity 40

% identity 40
NCBI Description BETA-ADAPTIN 1 (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN
BETA SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 BETA

LARGE CHAIN) (AP105A) >gi\_482950\_pir\_\_B32105



clathrin-associated protein complex 2, beta chain minor component - rat >gi 203113 (M77245) beta'-chain clathrin associated protein complex AP-1 [Rattus norvegicus]

11974 Seq. No.

23373 1.R1040 Contig ID

5'-most EST LIB3051-050-Q1-K1-C6

Method BLASTX q1680686 NCBI GI 305 BLAST score 2.0e-27 E value 113 Match length % identity

(U51330) rust resistance kinase Lr10 [Triticum aestivum] NCBI Description

11975 Seq. No.

23374 1.R1040 Contig ID

5'-most EST LIB3051-050-Q1-K1-C7

Method BLASTX q728905 NCBI GI BLAST score 282 4.0e-25 E value 118 Match length % identity 47

PROBABLE CALCIUM-TRANSPORTING ATPASE 3 (ENDOPLASMIC NCBI Description

RETICULUM CA2+-ATPASE) >gi\_1078206\_pir\_\_S51995 probable ATPase (EC 3.6.1.-) DRS2 - yeast (Saccharomyces cerevisiae) >gi\_171114 (L01795) ATPase [Saccharomyces cerevisiae]

>gi\_595560 (U12980) Drs2p: Membrane spanning

Ca-ATPase(P-type), member of the cation transport(E1-E2)

ATPase [Saccharomyces cerevisiae]

11976 Seq. No.

23375 1.R1040 Contig ID

LIB3170-040-Q1-K1-C9 5'-most EST

Method BLASTX NCBI GI g2982455 301 BLAST score 3.0e-27 E value Match length 63 % identity

(AL022223) putative uracil phosphoribosyl transferase NCBI Description

[Arabidopsis thaliana]

11977 Seq. No.

23376 1.R1040 Contig ID

 $LIB31\overline{7}0-037-Q1-K1-F9$ 5'-most EST

Method BLASTX q3402694 NCBI GI 352 BLAST score 6.0e-33 E value 170 Match length % identity

(AC004697) putative Mlo-hi protein [Arabidopsis thaliana] NCBI Description

11978 Seq. No.

23377\_1.R1040 Contig ID



```
LIB3051-050-Q1-K1-F11
5'-most EST
                  BLASTX
Method
                  g1008904
NCBI GI
                  98
BLAST score
                  7.0e-14
E value
Match length
                  96
% identity
                   49
                  (L43094) xyloglucan endotransglycosylase [Tropaeolum majus]
NCBI Description
                   11979
Seq. No.
                   23379 1.R1040
Contig ID
                   LIB3170-039-Q1-K1-F9
5'-most EST
Method
                   BLASTX
                   g172383
NCBI GI
                   345
BLAST score
                   2.0e-32
E value
                   153
Match length
% identity
                   52
                   (M38723) RNA polymerase III [Saccharomyces cerevisiae]
NCBI Description
                   11980
Seq. No.
                   23383 1.R1040
Contig ID
5'-most EST
                   LIB3170-038-Q1-K1-C10
Method
                   BLASTX
                   q1888527
NCBI GI
                   554
BLAST score
                   2.0e-56
E value
                   308
Match length
% identity
                   (U88667) ATP-binding cassette transporter [Homo sapiens]
NCBI Description
                   >gi 4557876 ref NP 000341.1_pABCR_ ATP binding cassette
                   transporter
                   11981
Seq. No.
                   23387 1.R1040
Contig ID
                   LIB30\overline{5}1-053-Q1-K2-C1
5'-most EST
                   11982
Seq. No.
                   23390 1.R1040
Contig ID
                   LIB3170-039-Q1-K2-H11
5'-most EST
                   BLASTX
Method
                   g477819
NCBI GI
                   614
BLAST score
                   5.0e-64
E value
                   158
Match length
                   75
 % identity
                   mitochondrial processing peptidase (EC 3.4.99.41) beta
NCBI Description
                   chain precursor - potato >gi 410634 bbs 136741 cytochrome c
                   reductase-processing peptidase subunit II, MPP subunit II,
                   P53 [potatoes, var. Marfona, tuber, Peptide Mitochondrial,
                   530 aa]
                   11983
 Seq. No.
                   23397 1.R1040
 Contig ID
                   uC-gmrominsoy286e04b1
 5'-most EST
```

2083

BLASTX

g2129539

Method NCBI GI



```
BLAST score
E value
                  1.0e-21
                  71
Match length
                  65
% identity
                  AtJ1 protein - Arabidopsis thaliana >gi 564030 (U16246)
NCBI Description
                  AtJ1 [Arabidopsis thaliana]
                  11984
Seq. No.
                  23397 3.R1040
Contig ID
                  qsv701049713.h1
5'-most EST
                  11985
Seq. No.
```

Contig ID 23398\_1.R1040
5'-most EST fde700876642.h1
Method BLASTX
NCBI GI g3482972
BLAST score 518
E value 3.0e-52

BLAST score 518 E value 3.0e-5 Match length 321 % identity 40

NCBI Description (AL031369) putative protein [Arabidopsis thaliana]

Seq. No. 11986

Contig ID 23401\_1.R1040

5'-most EST LIB3170-042-Q1-K1-G2

Method BLASTX
NCBI GI g3413700
BLAST score 928
E value 1.0e-100
Match length 292
% identity 64

NCBI Description (AC004747) putative YME1 protein [Arabidopsis thaliana]

Seq. No. 11987

Contig ID 23407\_1.R1040

5'-most EST LIB3051-058-Q1-K2-B3

Method BLASTX
NCBI GI 94468993
BLAST score 179
E value 4.0e-13
Match length 84
% identity 45

NCBI Description (AL035605) putative protein [Arabidopsis thaliana]

Seq. No.

11988

Contig ID 23412\_1.R1040 5'-most EST uaw700662189.h1

Method BLASTX
NCBI GI g2342685
BLAST score 213
E value 7.0e-17
Match length 113
% identity 42

NCBI Description (AC000106) Contains similarity to Rhodococcus amidase (gb D16207). ESTs gb T20504, gb H36650, gb N97423, gb H36595

come from this gene. [Arabidopsis thaliana]



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Seq. No.
                  11989
                  23414 1.R1040
Contig ID
                  LIB3051-063-Q1-K1-H1
5'-most EST
                  11990
Seq. No.
                  23417 2.R1040
Contig ID
                  LIB3051-064-Q1-K1-B1
5'-most EST
                  BLASTX
Method
                  q2827558
NCBI GI
                  191
BLAST score
                  2.0e-14
E value
Match length
                  90
% identity
                  (AL021635) putative DNA binding protein [Arabidopsis
NCBI Description
                  thaliana]
                   11991
Seq. No.
                   23421 1.R1040
Contig ID
                  LIB3094-044-Q1-K1-A4
5'-most EST
                  BLASTX
Method
                   g3128174
NCBI GI
BLAST score
                   271
                   1.0e-23
E value
Match length
                   76
% identity
NCBI Description (AC004521) hypothetical protein [Arabidopsis thaliana]
                   11992
Seq. No.
                   23421 2.R1040
Contig ID
                   has700548280.hl
5'-most EST
                   BLASTX
Method
                   g3128174
NCBI GI
BLAST score
                   246
                   6.0e-21
E value
Match length
                   80
                   69
% identity
NCBI Description (AC004521) hypothetical protein [Arabidopsis thaliana]
                   11993
Seq. No.
                   23421 3.R1040
Contig ID
                   g5606780
5'-most EST
                   BLASTX
Method
                   g3128174
NCBI GI
                   246
BLAST score
                   6.0e-21
E value
                   67
Match length
                   79
 % identity
                   (AC004521) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   11994
Seq. No.
                   23424 1.R1040
Contig ID
                   LIB3051-064-Q1-K1-E10
 5'-most EST
                   BLASTX
Method
                   g3341684
NCBI GI
 BLAST score
                   283
                   3.0e-25
 E value
```

2085

118

Match length



% identity NCBI Description (AC003672) hypothetical protein [Arabidopsis thaliana] 11995 Seq. No. 23429 1.R1040 Contig ID LIB3051-065-Q1-K1-B8 5'-most EST Method BLASTX g2980641 NCBI GI 344 BLAST score 2.0e-58 E value Match length 140 81 % identity NCBI Description (Y11250) multi resistance protein [Arabidopsis thaliana] 11996 Seq. No. 23430 1.R1040 Contig ID LIB3051-065-Q1-K1-E1 5'-most EST BLASTX Method g2245131 NCBI GI 175 BLAST score 1.0e-12 E value 108 Match length 42 % identity (Z97344) hypothetical protein [Arabidopsis thaliana] NCBI Description 11997 Seq. No. 23433 1.R1040 Contig ID uC-gmropic023c12b1 5'-most EST BLASTX Method q4530126 NCBI GI 668 BLAST score 4.0e-70 E value 247 Match length % identity 51 (AF078082) receptor-like protein kinase homolog RK20-1 NCBI Description [Phaseolus vulgaris] 11998 Seq. No. 23435 1.R1040 Contig ID LIB3051-066-Q1-K1-D12 5'-most EST 11999 Seq. No. 23436 1.R1040 Contig ID  $V4L-0\overline{1}-Q1-B1-H8$ 5'-most EST BLASTN Method g3873174 NCBI GI BLAST score 53 1.0e-20 E value 148 Match length 89 % identity Genomic sequence for Arabidopsis thaliana BAC F14N23, NCBI Description complete sequence [Arabidopsis thaliana]

Seq. No. 12000

Contig ID 23438\_1.R1040

5'-most EST LIB3107-062-Q1-K1-A6

Method BLASTX



q4325324 NCBI GI BLAST score 733 1.0e-77 E value Match length 266 % identity (AF125574) lysyl-tRNA synthetase; LysRS [Arabidopsis NCBI Description thaliana] 12001 Seq. No. 23442 1.R1040 Contig ID 5'-most EST LIB3170-051-Q1-K1-A4 BLASTX Method q2583113 NCBI GI 244 BLAST score 1.0e-20 E value Match length 48 90 % identity (AC002387) hypothetical protein [Arabidopsis thaliana] NCBI Description 12002 Seq. No. 23445 1.R1040 Contig ID LIB3051-067-Q1-K1-C5 5'-most EST 12003 Seq. No. 23449 1.R1040 Contig ID LIB3051-067-Q1-K1-F3 5'-most EST BLASTX Method q3097056 NCBI GI BLAST score 264 E value 7.0e-45 97 Match length 94 % identity (AJ003139) dihydrofolate reductase-thymidylate synthetase NCBI Description [Daucus carota] 12004 Seq. No. 23450 1.R1040 Contig ID LIB3170-049-Q1-K1-C11 5'-most EST Method BLASTX g2578365 NCBI GI 471 BLAST score 2.0e-47 E value 104 Match length % identity 88 (AJ002298) GTP cyclohydrolase II / NCBI Description 3,4-dihydroxy-2-butanone-4-phosphate synthase [Lycopersicon esculentum]

12005 Seq. No.

23451 1.R1040 Contig ID

LIB3170-051-Q1-J1-B5 5'-most EST

BLASTX Method NCBI GI g3152880 266 BLAST score 3.0e-23 E value 59 Match length % identity 85



(AF063246) cell wall invertase; beta-fructofuranosidase NCBI Description [Pisum sativum]

12006 Seq. No.

23451 2.R1040 Contig ID  $q4396\overline{2}99$ 5'-most EST BLASTX Method g2500930 NCBI GI 1083 BLAST score 1.0e-118

E value 250 Match length 78 % identity

BETA-FRUCTOFURANOSIDASE PRECURSOR (SUCROSE-6-PHOSPHATE NCBI Description HYDROLASE) (INVERTASE) >gi 1160488 emb\_CAA59677\_ (X85327)

beta-fructofuranosidase [Pisum sativum]

12007 Seq. No.

23452 1.R1040 Contig ID

LIB3051-067-Q1-K1-H2 5'-most EST

BLASTX Method q2827663 NCBI GI 158 BLAST score 1.0e-10 E value 121 Match length % identity

(AL021637) membrane-associated salt-inducible-like protein NCBI Description

[Arabidopsis thaliana]

12008 Seq. No.

23454 1.R1040 Contig ID ncj700985601.hl 5'-most EST

BLASTX Method g2791278 NCBI GI BLAST score 676 1.0e-70 E value Match length 373 39 % identity

(Z69257) beta-xylosidase [Hypocrea jecorina] NCBI Description

12009 Seq. No.

23454 2.R1040 Contig ID fC-gmse700851725h1 5'-most EST

12010 Seq. No.

23455 1.R1040 Contig ID

LIB3051-068-Q1-K1-C7 5'-most EST

BLASTX Method NCBI GI q2317901 246 BLAST score 3.0e-26 E value 131 Match length 56 % identity

(U89959) Similar to vesicle transport protein, PIR NCBI Description

Accession Number A55931 [Arabidopsis thaliana]

12011 Seq. No.

23456 1.R1040 Contig ID



5'-most EST LIB3051-068-Q1-K1-D5

Method BLASTX
NCBI GI g2494165
BLAST score 853
E value 9.0e-92
Match length 202
% identity 79

NCBI Description DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE (ATP))

>gi\_2129574\_pir\_\_S71278 DNA ligase - Arabidopsis thaliana >gi\_1359495\_emb\_CAA66599\_ (X97924) DNA ligase [Arabidopsis

thaliana]

Seq. No. 12012

Contig ID 23460\_1.R1040

5'-most EST LIB3170-056-Q1-K1-C4

Method BLASTX
NCBI GI g3021265
BLAST score 302
E value 2.0e-27
Match length 111
% identity 56

NCBI Description (AL022347) protein kinase - like protein [Arabidopsis

thaliana] >gi\_3292839\_emb\_CAA19829\_ (AL031018) protein

kinase - like protein [Arabidopsis thaliana]

Seq. No. 12013

Contig ID 23462\_1.R1040

5'-most EST LIB3051-078-Q1-K1-D8

Seq. No. 12014

Contig ID 23471\_1.R1040

5'-most EST LIB3170-054-Q1-K1-C6

Method BLASTX
NCBI GI g2459415
BLAST score 289
E value 1.0e-25
Match length 146
% identity 53

NCBI Description (AC002332) hypothetical protein [Arabidopsis thaliana]

Seq. No. 12015

Contig ID 23473\_1.R1040 5'-most EST uxk700670974.h1

Method BLASTX
NCBI GI g4262233
BLAST score 252
E value 2.0e-21
Match length 131
% identity 47

NCBI Description (AC006200) hypothetical protein [Arabidopsis thaliana]

Seq. No. 12016

Contig ID 23477\_1.R1040

5'-most EST LIB3051-086-Q1-K1-C4

Method BLASTX NCBI GI g1854443 BLAST score 1038

1.0e-113 E value 295 Match length % identity 66 NCBI Description (D83970) CPRD8 protein [Vigna unguiculata] 12017 Seq. No. 23483 1.R1040 Contig ID LIB3170-054-Q1-K1-E7 5'-most EST BLASTX Method g4567227 NCBI GI 1103 BLAST score 1.0e-121 E value 312 Match length 67 % identity (AC007119) putative transport protein [Arabidopsis NCBI Description thaliana] 12018 Seq. No. 23485 1.R1040 Contig ID

5'-most EST LIB3138-101-Q1-N1-B5
Method BLASTX
NCBI GI g4263722
BLAST score 451
E value 5.0e-51
Match length 192
% identity 59

NCBI Description (AC006223) putative glucan synthase [Arabidopsis thaliana]

Seq. No. 12019

Contig ID 23486\_1.R1040

5'-most EST LIB3170-053-Q1-K1-C8

Method BLASTN

NCBI GI g3318610

BLAST score 92 E value 6.0e-44 Match length 220 % identity 85

NCBI Description Glycine max mRNA for mitochondrial phosphate transporter,

complete cds

Seq. No. 12020

Contig ID 23487\_1.R1040

5'-most EST LIB3051-082-Q1-K1-F4

Method BLASTX
NCBI GI g3021512
BLAST score 265
E value 3.0e-46
Match length 135
% identity 73

NCBI Description (X96728) isocitrate dehydrogenase (NADP+) [Nicotiana

tabacum]

Seq. No. 12021

Contig ID 23488\_1.R1040

5'-most EST LIB3170-053-Q1-K1-F8

Method BLASTX NCBI GI g2262115



```
BLAST score
                   9.0e-27
E value
                  171
Match length
% identity
                   35
                  (AC002343) cellulose synthase isolog [Arabidopsis thaliana]
NCBI Description
                  12022
Seq. No.
                   23490 1.R1040
Contig ID
                  LIB3170-055-Q1-K1-D8
5'-most EST
Seq. No.
                   12023
                   23494 1.R1040
Contig ID
                   LIB3051-083-Q1-K1-E4
5'-most EST
                   BLASTX
Method
                   q3925363
NCBI GI
                   259
BLAST score
E value
                   2.0e-25
                   154
Match length
                   48
% identity
                   (AF067961) homeodomain protein [Malus domestica]
NCBI Description
                   12024
Seq. No.
                   23495 1.R1040
Contig ID
                   LIB3051-083-Q1-K1-F8
5'-most EST
                   BLASTX
Method
                   q3668088
NCBI GI
BLAST score
                   335
E value
                   3.0e-31
Match length
                   155
                   43
% identity
                  (AC004667) G9a-like protein [Arabidopsis thaliana]
NCBI Description
                   12025
Seq. No.
                   23499 1.R1040
Contig ID
5'-most EST
                   g5126819
                   BLASTX
Method
                   q2702269
NCBI GI
                   412
BLAST score
                   3.0e-40
E value
                   126
Match length
                   67
% identity
                   (AC003033) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   12026
Seq. No.
                   23503 1.R1040
Contig ID
                   LIB3051-090-Q1-K1-E8
5'-most EST
                   BLASTX
Method
                   g2462935
NCBI GI
                   323
BLAST score
                   6.0e-30
E value
                   139
Match length
                   45
 % identity
NCBI Description (Y12321) open reading frame 1 [Brassica oleracea]
                   12027
Seq. No.
```

Contig ID 23505\_1.R1040

5'-most EST LIB3051-090-Q1-K1-F3



Method BLASTX
NCBI GI g3212863
BLAST score 540
E value 2.0e-55
Match length 150
% identity 71

NCBI Description (AC004005) putative translation initiation factor

[Arabidopsis thaliana]

Seq. No. 12028

Contig ID 23516\_1.R1040

5'-most EST LIB3051-091-Q1-K1-E5

Method BLASTX
NCBI GI g1223579
BLAST score 696
E value 2.0e-73
Match length 218
% identity 65

NCBI Description (X96481) cDNA101 [Arabidopsis thaliana]

Seq. No. 12029

Contig ID 23519\_1.R1040

5'-most EST LIB3051-091-Q1-K1-H6

Method BLASTX
NCBI GI g1353135
BLAST score 242
E value 2.0e-20
Match length 135
% identity 43

NCBI Description PUTATIVE SERINE/THREONINE-PROTEIN KINASE C41C4.4 IN

CHROMOSOME II PRECURSOR >gi\_3874887\_emb\_CAA88100\_ (Z48045) similar to serine/threonine kinase; cDNA EST EMBL:D26974 comes from this gene; cDNA EST EMBL:D26978 comes from this gene; cDNA EST EMBL:D26977 comes from this gene; cDNA EST

EMBL:D26976 comes from this gene; cDNA EST E

Seq. No. 12030

Contig ID 23523\_1.R1040

5'-most EST LIB3170-057-Q1-K1-H5

Method BLASTX
NCBI GI g1209756
BLAST score 150
E value 2.0e-09
Match length 75
% identity 49

NCBI Description (U43629) integral membrane protein [Beta vulgaris]

Seq. No. 12031

Contig ID 23526 1.R1040

5'-most EST uC-gmrominsoy058c10b1

Seq. No. 12032

Contig ID 23530 1.R1040

5'-most EST LIB3051-093-Q1-K1-D6

Seq. No. 12033

Contig ID 23532 1.R1040



5'-most EST LIB3051-093-Q1-K1-F6

Method BLASTX
NCBI GI g2500724
BLAST score 1862
E value 0.0ef00
Match length 404
% identity 89

NCBI Description PREPROTEIN TRANSLOCASE SECA SUBUNIT PRECURSOR

>gi\_2129894\_pir\_\_S72453 secA protein precursor - garden pea >gi\_1122325\_emb\_CAA57798\_ (X82404) chloroplast SecA protein

[Pisum sativum]

Seq. No. 12034

Contig ID 23537 1.R1040

5'-most EST LIB3106-040-Q1-K1-A12

Seq. No. 12035

Contig ID 23539\_1.R1040 5'-most EST uC-gmropic011f07b1

Method BLASTX
NCBI GI g1438877
BLAST score 406
E value 3.0e-39
Match length 251
% identity 18

NCBI Description (U41287) zinc finger protein [Mus musculus]

Seq. No. 12036

Contig ID 23541\_1.R1040

5'-most EST LIB3170-058-Q1-K1-B8

Method BLASTX
NCBI GI g132521
BLAST score 562
E value 1.0e-57
Match length 132
% identity 81

NCBI Description RAS-RELATED PROTEIN RGP1 (GTP-BINDING REGULATORY PROTEIN

RGP1) >gi\_100684\_pir\_\_S16554 GTP-binding protein rgp1 - rice >gi\_20356\_emb\_CAA41966\_ (X59276) GTP-binding protein [Oryza sativa] >gi\_228209\_prf\_\_1718315A GTP-binding protein [Oryza sativa]

- -

Seq. No. 12037

Contig ID 23544\_1.R1040

5'-most EST jC-gmro02910046a02a1

Method BLASTN
NCBI GI g295447
BLAST score 99
E value 3.0e-48
Match length 286
% identity 85

NCBI Description Vigna radiata NADPH cytochrome P450 mRNA, complete cds

Seq. No. 12038

Contig ID 23544\_2.R1040

5'-most EST LIB3051-095-Q1-K1-D2

Method BLASTN



```
NCBI GI
                   q295447
BLAST score
                  83
E value
                  9.0e-39
Match length
                  179
% identity
                  87
NCBI Description Vigna radiata NADPH cytochrome P450 mRNA, complete cds
                  12039
Seq. No.
                  23553 1.R1040
Contig ID
5'-most EST
                  uC-gmropic039d05b1
Method
                  BLASTX
NCBI GI
                  q2801536
BLAST score
                  475
E value
                   3.0e-47
Match length
                  162
% identity
                  58
NCBI Description (AF039531) lysophospholipase homolog [Oryza sativa]
                  12040
Seq. No.
Contig ID
                  23556 1.R1040
5'-most EST
                  LIB3051-103-Q1-K1-A8
Method
                  BLASTX
NCBI GI
                  q3413707
BLAST score
                  563
E value
                   9.0e-72
Match length
                  190
% identity
NCBI Description (AC004747) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  12041
Contig ID
                  23558 1.R1040
                  LIB3170-064-Q1-K1-B4
5'-most EST
Method
                  BLASTX
NCBI GI
                  q1184075
BLAST score
                   354
E value
                   2.0e-33
Match length
                  178
% identity
NCBI Description
                  (U42444) Cf-2.1 [Lycopersicon pimpinellifolium]
                   >gi 1587673 prf 2207203A Cf-2 gene [Lycopersicon
                   esculentum]
                  12042
Seq. No.
                   23561 1.R1040
Contig ID
5'-most EST
                  LIB3051-103-Q1-K1-D10
Method
                  BLASTX
                  g3688173
NCBI GI
BLAST score
                  201
E value
                  1.0e-15
Match length
                   113
% identity
NCBI Description (AL031804) putative protein [Arabidopsis thaliana]
Seq. No.
                   12043
```

2094

23567 1.R1040

q5606259

BLASTX

Contig ID

5'-most EST Method



NCBI GI g1223579 BLAST score 450 E value 1.0e-44 Match length 169 % identity 60

NCBI Description (X96481) cDNA101 [Arabidopsis thaliana]

Seq. No. 12044

Contig ID 23568\_1.R1040

5'-most EST LIB3170-064-Q1-K1-A5

Seq. No. 12045

Contig ID 23574\_1.R1040 5'-most EST rca700996304.h1

Method BLASTX
NCBI GI g2262100
BLAST score 374
E value 6.0e-48
Match length 140
% identity 62

NCBI Description (AC002343) unknown protein [Arabidopsis thaliana]

Seq. No. 12046

Contig ID 23574\_2.R1040

5'-most EST LIB3051-091-Q1-K1-F5

Method BLASTX
NCBI GI g2262100
BLAST score 530
E value 5.0e-54
Match length 149
% identity 70

NCBI Description (AC002343) unknown protein [Arabidopsis thaliana]

Seq. No. 12047

Contig ID 23574\_3.R1040 5'-most EST uaw700661744.h1

Method BLASTX
NCBI GI g2262100
BLAST score 148
E value 1.0e-09
Match length 40
% identity 65

NCBI Description (AC002343) unknown protein [Arabidopsis thaliana]

Seq. No. 12048

Contig ID 23575\_1.R1040 5'-most EST zpv700761096.h1

Method BLASTX
NCBI GI g4539301
BLAST score 792
E value 3.0e-84
Match length 381
% identity 43

NCBI Description (AL049480) putative mitochondrial protein [Arabidopsis

thaliana]

Seq. No. 12049



Contig ID 23575 2.R1040 5'-most EST LIB3051-046-Q1-K1-H7 Seq. No. 12050 23575 3.R1040 Contig ID uaw700664916.h1 5'-most EST 12051 Seq. No. Contig ID 23577 1.R1040 5'-most EST uC-gmropic029g01b1 Method BLASTX NCBI GI g1843462 BLAST score 414 E value 2.0e-40 Match length 218 % identity 43 (L10211) isoliquiritigenin 2'-O-methyltransferase [Medicago NCBI Description sativa] Seq. No. 12052 23580 1.R1040 Contig ID 5'-most EST trc700564387.h1 Method BLASTN NCBI GI g1786114 BLAST score 493 E value 0.0e + 00Match length 788 % identity 91 Vigna unguiculata phosphoinositide-specific phospholipase C NCBI Description mRNA, complete cds Seq. No. 12053 23580 2.R1040 Contig ID 5'-most EST LIB3170-064-Q1-K1-F6 Method BLASTN NCBI GI q1786114 BLAST score 129 3.0e-66 E value Match length 367 % identity 88 NCBI Description Vigna unguiculata phosphoinositide-specific phospholipase C mRNA, complete cds 12054 Seq. No. Contig ID 23582 1.R1040 5'-most EST LIB3170-062-Q1-K1-C6

Method BLASTN NCBI GI g1065907 BLAST score 44 E value 1.0e-15 Match length 84 88 % identity

NCBI Description Pisum sativum chloroplast processing enzyme mRNA, nuclear

gene encoding chloroplast protein, complete cds

12055 Seq. No.

23588 1.R1040 Contig ID



```
5'-most EST
                  LIB3051-105-Q1-K1-H5
Method
                  BLASTX
NCBI GI
                  g395330
BLAST score
                  187
E value
                  5.0e-14
Match length
                  54
                  61
% identity
NCBI Description (X69789) cytochrome P450 [Catharanthus roseus]
                  12056
Seq. No.
                  23590 1.R1040
Contig ID
5'-most EST
                  LIB3051-111-Q1-K1-G7
Method
                  BLASTN
NCBI GI
                  g3449322
BLAST score
                  49
                  3.0e-18
E value
                  146
Match length
                  87
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MXC17, complete sequence [Arabidopsis thaliana]
Seq. No.
                  12057
Contig ID
                  23591 1.R1040
5'-most EST
                  xpa700795573.h1
Method
                  BLASTX
NCBI GI
                  q4056425
BLAST score
                  520
                  1.0e-52
E value
                  152
Match length
% identity
                  64
                  (AC005322) ESTs gb H36249, gb AA59732 and gb AA651219 come
NCBI Description
                  from this gene. [Arabidopsis thaliana]
                  12058
Seq. No.
                  23591 2.R1040
Contig ID
5'-most EST
                  gsv701044812.h1
                  BLASTX
Method
NCBI GI
                  q4056425
BLAST score
                  365
E value
                   1.0e-34
Match length
                  103
% identity
                  68
NCBI Description (AC005322) ESTs gb H36249, gb AA59732 and gb AA651219 come
                  from this gene. [Arabidopsis thaliana]
Seq. No.
                  12059
                  23595 1.R1040
Contig ID
5'-most EST
                  LIB3170-067-Q1-K1-F2
Method
                  BLASTX
NCBI GI
                  g1930149
BLAST score
                  251
                  2.0e-21
E value
Match length
                  150
% identity
                   37
NCBI Description (U96629) unknown protein CIT987SK 2A8 1 [Homo sapiens]
```

2097

12060

Seq. No.

```
23597 1.R1040
Contig ID
                  LIB3139-107-P1-N1-B2
5'-most EST
                  BLASTX
Method
                  g4432839
NCBI GI
                  449
BLAST score
                  1.0e-44
E value
                  107
Match length
% identity
                  45
NCBI Description (AC006283) unknown protein [Arabidopsis thaliana]
                  12061
Seq. No.
                   23598 1.R1040
Contig ID
                  LIB3170-067-Q1-J1-G2
5'-most EST
                  BLASTX
Method
                   q3935168
NCBI GI
                   195
BLAST score
                   7.0e-15
E value
Match length
                   44
                   86
% identity
NCBI Description (AC004557) F17L21.11 [Arabidopsis thaliana]
                   12062
Seq. No.
                   23604 1.R1040
Contig ID
                   LIB3170-068-Q1-K1-E5
5'-most EST
                   12063
Seq. No.
                   23609 1.R1040
Contig ID
                   LIB3170-067-Q1-K1-G5
5'-most EST
                   BLASTX
Method
                   q4539662
NCBI GI
                   211
BLAST score
                   3.0e-33
E value
Match length
                   143
                   56
% identity
NCBI Description (AF061282) polyprotein [Sorghum bicolor]
                   12064
Seq. No.
                   23611 1.R1040
Contiq ID
                   LIB3170-065-Q1-K1-B6
 5'-most EST
                   BLASTX
Method
                   g2827699
NCBI GI
                   562
BLAST score
                   7.0e-58
 E value
                   163
 Match length
                   67
 % identity
NCBI Description (AL021684) predicted protein [Arabidopsis thaliana]
                   12065
 Seq. No.
                   23614 1.R1040
 Contig ID
                   LIB3051-115-Q1-K1-E7
 5'-most EST
                   BLASTX
 Method
                   g2829886
 NCBI GI
                    404
 BLAST score
                    2.0e-51
 E value
                    197
 Match length
                    59
 % identity
 NCBI Description (AC002396) Hypothetical protein [Arabidopsis thaliana]
```

NCBI Description



```
12066
Seq. No.
                   23615 1.R1040
Contig ID
                   LIB30\overline{5}1-115-Q1-K1-F2
5'-most EST
                  BLASTX
Method
                   g2920666
NCBI GI
BLAST score
                   179
                   4.0e-13
E value
                   81
Match length
% identity
                   (AF048978) 2,4-D inducible glutathione S-transferase
NCBI Description
                   [Glycine max]
                   12067
Seq. No.
                   23617 1.R1040
Contig ID
                   uC-qmrominsoy0001c09b1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2832632
                   498
BLAST score
                   3.0e-50
E value
                   187
Match length
                   57
% identity
                   (AL021711) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   12068
Seq. No.
                   23618 1.R1040
Contig ID
                   ssr700556428.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2462838
                   585
BLAST score
                   1.0e-60
E value
Match length
                   167
                   72
% identity
                   (AF000657) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   12069
                   23624 1.R1040
Contig ID
                   q4285481
5'-most EST
                   BLASTX
Method
                   q3386604
NCBI GI
                   264
BLAST score
                   7.0e-23
E value
                   62
Match length
                   77
% identity
                   (AC004665) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                    12070
Seq. No.
                    23626 1.R1040
Contig ID
                   LIB3170-066-Q1-K1-F7
5'-most EST
                   BLASTX
Method
                    g3643271
NCBI GI
                    230
BLAST score
E value
                    5.0e-19
                    134
Match length
                    29
 % identity
```

(AF090872) 33 kDa secretory protein [Oryza sativa]

>gi 3851590 (AF093570) 33 kDa secretory protein [Oryza



sativa] >gi\_4249681 (AF097724) 33 kDa secretory protein
[Oryza sativa]

Seq. No. 12071

Contig ID 23629 1.R1040

5'-most EST LIB3051-117-Q1-K1-B10

Seq. No. 12072

Contig ID 23630\_1.R1040

5'-most EST LIB3065-010-Q1-N1-H12

Method BLASTX
NCBI GI g2244987
BLAST score 421
E value 4.0e-41
Match length 209
% identity 43

NCBI Description (Z97340) similarity to protein kinase - slime mold

(Dictyostelium) [Arabidopsis thaliana]

Seq. No. 12073

Contig ID 23654 1.R1040

5'-most EST LIB3094-069-Q1-K1-D11

Method BLASTX
NCBI GI g3894168
BLAST score 482
E value 3.0e-48
Match length 241
% identity 41

NCBI Description (AC005312) similar to phloem-specific lectin [Arabidopsis

thaliana]

Seq. No. 12074

Contig ID 23655 1.R1040

5'-most EST LIB30 $\overline{5}1$ -063-Q1-K1-F1

Method BLASTX
NCBI GI g2780192
BLAST score 838
E value 8.0e-90
Match length 216
% identity 72

NCBI Description (AJ222713) unnamed protein product [Arabidopsis thaliana]

Seq. No. \_ 12075

Contig ID 23674\_1.R1040 5'-most EST wrg700789655.h2

Method BLASTX
NCBI GI g3510538
BLAST score 220
E value 2.0e-37
Match length 124
% identity 60

NCBI Description (U93167) expansin [Prunus armeniaca]

Seq. No. 12076

Contig ID 23676\_1.R1040

5'-most EST LIB $30\overline{5}1-034-Q1-K1-F5$ 

Method BLASTX



```
NCBI GI
                  q4191791
BLAST score
                  640
                  7.0e-67
E value
Match length
                  163
% identity
                  73
                  (AC005917) putative sf21 {Helianthus annuus} protein
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  12077
                  23677_1.R1040
Contig ID
5'-most EST
                  hrw701060737.h1
                  BLASTX
Method
NCBI GI
                  g1842111
BLAST score
                  559
E value
                  2.0e~57
Match length
                  181
% identity
                  61
NCBI Description
                  (U87586) decoy [Arabidopsis thaliana] >gi 1931612 (U93308)
                  decoy [Arabidopsis thaliana]
                  12078
Seq. No.
Contig ID
                  23677 2.R1040
5'-most EST
                  jC-qmf102220086e05a1
Method
                  BLASTX
NCBI GI
                  g1842111
                  266
BLAST score
                  2.0e-23
E value
Match length
                  74
                  70
% identity
                  (U87586) decoy [Arabidopsis thaliana] >gi_1931612 (U93308)
NCBI Description
                  decoy [Arabidopsis thaliana]
Seq. No.
                  12079
                  23679 1.R1040
Contig ID
5'-most EST
                  awf700838726.h1
Method
                  BLASTX
NCBI GI
                  g3434967
BLAST score
                  534
                  4.0e-54
E value
Match length
                  242
% identity
                  50
NCBI Description (AB008103) ethylene responsive element binding factor 1
                  [Arabidopsis thaliana]
                  12080
Seq. No.
                  23679 2.R1040
Contig ID
5'-most EST
                  LIB3051-017-Q1-E1-H8
                  BLASTN
Method
                  g3821780
NCBI GI
BLAST score
                  36
                  1.0e-10
E value
```

Match length 39 % identity 45

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 12081

Contig ID 23692\_1.R1040



5'-most EST LIB3051-059-Q1-K2-B12 Method BLASTX

NCBI GI g1070655
BLAST score 256
E value 7.0e-22
Match length 169
% identity 40

NCBI Description lectin precursor - lentil

Seq. No. 12082

Contig ID 23693\_1.R1040

5'-most EST LIB30 $\overline{5}$ 1-061-Q1-K1-G8

Method BLASTX
NCBI GI g3335345
BLAST score 1005
E value 1.0e-109
Match length 255
% identity 81

NCBI Description (AC004512) Contains similarity to ABC transporter

gb\_1651790 from Synechocystis sp. gb\_D90900. [Arabidopsis

thaliana]

Seq. No. 12083

Contig ID 23694\_1.R1040

5'-most EST uC-gmrominsoy227d01b1

Method BLASTX
NCBI GI g2618731
BLAST score 964
E value 1.0e-104
Match length 301
% identity 68

NCBI Description (U49077) IAA21 [Arabidopsis thaliana]

Seq. No. 12084

Contig ID 23695\_1.R1040 5'-most EST txt700735514.h1

Method BLASTX
NCBI GI g1706277
BLAST score 155
E value 2.0e-10
Match length 80
% identity 45

NCBI Description CYSTEINE PROTEINASE INHIBITOR B (CYSTATIN B) (SCB)

>gi\_2118421\_pir\_\_JC4792 cysteine proteinase inhibitor Scb -

common sunflower

Seq. No. 12085

Contig ID 23697\_1.R1040 5'-most EST zsg701124223.h1

Method BLASTX
NCBI GI g3482974
BLAST score 726
E value 3.0e-85
Match length 186
% identity 88

NCBI Description (AL031369) ATP-dependent Clp proteinase-like protein

[Arabidopsis thaliana]

Match length



```
12086
Seq. No.
                  23698 1.R1040
Contig ID
                  awf700840753.h1
5'-most EST
Seq. No.
                  12087
                  23699 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy313f05b1
Method
                  BLASTX
NCBI GI
                  g2245087
BLAST score
                  196
                  8.0e-15
E value
Match length
                  76
                  51
% identity
NCBI Description (297343) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  12088
                  23699 2.R1040
Contig ID
5'-most EST
                  gsv701054503.hl
Method
                  BLASTX
                  g2245087
NCBI GI
                  176
BLAST score
E value
                  9.0e-13
Match length
                  63
                  52
% identity
NCBI Description (Z97343) hypothetical protein [Arabidopsis thaliana]
                  12089
Seq. No.
                  23701 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy081c12b1
Method
                  BLASTX
NCBI GI
                  q1619300
BLAST score
                  643
E value
                  6.0e-67
Match length
                  189
% identity
                  64
NCBI Description
                  (X95269) LRR protein [Lycopersicon esculentum]
Seq. No.
                  12090
                  23701 3.R1040
Contig ID
5'-most EST
                  fua701039134.hl
Method
                  BLASTX
                  g1619300
NCBI GI
BLAST score
                  403
E value
                  2.0e-39
Match length
                  99
% identity
NCBI Description (X95269) LRR protein [Lycopersicon esculentum]
                  12091
Seq. No.
Contig ID
                  23701 4.R1040
5'-most EST
                  uC-gmrominsoy029d03b1
Method
                  BLASTX
NCBI GI
                  g1619300
BLAST score
                  391
E value
                  8.0e-38
```



% identity 73
NCBI Description (X95269) LRR protein [Lycopersicon esculentum]
Seq. No. 12092
Contig ID 23701 6.R1040

5'-most EST lus701015783.h1
Method BLASTX
NCBI GI g3860323
BLAST score 282
E value 2.0e-25
Match length 62
% identity 89

NCBI Description (AJ012688) hypothetical protein [Cicer arietinum]

Seq. No. 12093

Contig ID 23702\_1.R1040 5'-most EST jex700907695.h1 Method BLASTX

Method BLASTX
NCBI GI g3212865
BLAST score 812
E value 1.0e-110
Match length 246
% identity 83

NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]

Seq. No. 12094

Contig ID 23703\_1.R1040 5'-most EST ssr700560361.h1 Method BLASTX

Method BLASTX
NCBI GI g1857419
BLAST score 173
E value 3.0e-12
Match length 151
% identity 32

NCBI Description (U80213) protein arginine N-methyltransferase 2 [Homo

sapiens]  $>gi_4504495_ref_NP_001526.1_pHRMT1L1_ HMT1 (hnRNP)$ 

methyltransferase, S. cerevisiae)-like

Seq. No. 12095

Contig ID 23704\_1.R1040

5'-most EST LIB3051-087-Q1-K1-B8

Method BLASTX
NCBI GI g4539343
BLAST score 449
E value 2.0e-44
Match length 111
% identity 83

NCBI Description (AL035539) putative protein [Arabidopsis thaliana]

Seq. No. 12096

Contig ID 23705\_1.R1040 5'-most EST wvk700686611.h1

Method BLASTX
NCBI GI g1514643
BLAST score 2805
E value 0.0e+00
Match length 806



% identity (Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza] NCBI Description

Seq. No. 12097

Contig ID 23708 1.R1040 5'-most EST leu701145118.h1

Method BLASTN q4235150 NCBI GI BLAST score 38 9.0e-12 E value Match length 212 84 % identity

NCBI Description Arabidopsis thaliana chromosome I BAC T25B24 genomic sequence, complete sequence [Arabidopsis thaliana]

12098 Seq. No.

23709 1.R1040 Contig ID 5'-most EST sat701014322.h1

Method BLASTN g298018 NCBI GI BLAST score 185 2.0e-99 E value Match length 401 % identity 89

NCBI Description M.sativa mRNA msk7 for map kinase

Seq. No. 12099

23709 2.R1040 Contig ID

5'-most EST jC-gmle01810011e12a1

Method BLASTN NCBI GI g289124 BLAST score 245 1.0e-135 E value 353 Match length

92 % identity

NCBI Description Medicago sativa MAP kinase MsERK1 mRNA, complete cds

Seq. No. 12100

Contig ID 23709 3.R1040

5'-most EST LIB3051-071-Q1-K1-A6

Method BLASTN NCBI GI g20807 BLAST score 66 1.0e-28 E value Match length 138 87 % identity

NCBI Description P.sativum mRNA for MAP kinase homologue

12101 Seq. No.

Contig ID 23709 4.R1040 sat701008822.h1 5'-most EST

BLASTN Method NCBI GI q20807 BLAST score 34 E value 1.0e-09 Match length 46 % identity 93



NCBI Description P.sativum mRNA for MAP kinase homologue

Seq. No. 12102

Contig ID 23710 1.R1040

5'-most EST LIB3051-104-Q1-K1-B5

Method BLASTN
NCBI GI g510545
BLAST score 36
E value 1.0e-10
Match length 125
% identity 87

NCBI Description P.sativum mRNA for starch branching enzyme I

Seq. No. 12103

Contig ID 23713\_1.R1040 5'-most EST rlr700899203.h1

Method BLASTX
NCBI GI g2832697
BLAST score 202
E value 4.0e-32
Match length 99
% identity 73

NCBI Description (AL021713) putative protein [Arabidopsis thaliana]

Seq. No. 12104

Contig ID 23717\_1.R1040 5'-most EST eep700870019.h1

Method BLASTX
NCBI GI g3513451
BLAST score 233
E value 2.0e-19
Match length 136
% identity 42

NCBI Description (U78090) potassium channel regulator 1 [Rattus norvegicus]

Seq. No. 12105

Contig ID 23718 1.R1040

5'-most EST uC-gmrominsoy091b06b1

Method BLASTX
NCBI GI g116377
BLAST score 2009
E value 0.0e+00
Match length 388
% identity 100

NCBI Description CHALCONE SYNTHASE 1 (NARINGENIN-CHALCONE SYNTHASE 1)

>gi\_66552\_pir\_\_SYSYC1 naringenin-chalcone synthase (EC
2.3.1.74) 1 - soybean >gi\_18562\_emb\_CAA38456\_ (X54644)

naregenin-chalcone synthase [Glycine max]

Seq. No. 12106

Contig ID 23718 2.R1040

5'-most EST LIB3139-057-P1-N1-E2

Method BLASTN
NCBI GI g18751
BLAST score 156
E value 3.0e-82
Match length 367

% identity

58



```
% identity
NCBI Description Soybean Soychs gene for chalcone synthase (EC 2.3.1.74)
                  12107
Seq. No.
Contig ID
                  23718 5.R1040
5'-most EST
                  dpv701100769.h1
Method
                  BLASTN
NCBI GI
                  q169940
BLAST score
                  178
E value
                  2.0e-95
Match length
                  382
% identity
                  95
NCBI Description Glycine max chalcone synthase (chs6) gene, complete cds
Seq. No.
                  12108
                  23718 9.R1040
Contig ID
5'-most EST
                  rlr700898746.h1
Method
                  BLASTN
                  g18588
NCBI GI
BLAST score
                  207
E value
                  1.0e-113
Match length
                  239
% identity
                  96
NCBI Description Soybean gene 3 for chalcone synthetase protein
Seq. No.
                  12109
                  23720 1.R1040
Contig ID
5'-most EST
                  LIB3107-006-Q1-K1-F1
Method
                  BLASTX
NCBI GI
                  g2244973
BLAST score
                  352
E value
                  3.0e-33
                  98
Match length
% identity
                  67
NCBI Description (Z97340) similarity to extensin class 1 protein
                  [Arabidopsis thaliana]
Seq. No.
                  12110
Contig ID
                  23722 1.R1040
5'-most EST
                  LIB3051-054-Q1-K2-C2
Method
                  BLASTX
NCBI GI
                  g2583117
BLAST score
                  269
E value
                  2.0e-23
Match length
                  126
% identity
                  48
NCBI Description (AC002387) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  12111
Contig ID
                  23727 1.R1040
5'-most EST
                  LIB3051-037-Q1-K1-A4
Method
                  BLASTX
NCBI GI
                  q2245021
BLAST score
                  247
E value
                  1.0e-20
Match length
                  76
```



NCBI Description (Z97341) heat shock protein 110 homolog [Arabidopsis thaliana]

Seq. No. 12112

Contig ID 23730 1.R1040

5'-most EST LIB3051-030-Q1-K1-H9

Method BLASTX
NCBI GI g1502430
BLAST score 866
E value 2.0e-93
Match length 175
% identity 91

NCBI Description (U62331) phosphate transporter [Arabidopsis thaliana]

>gi\_2564661 (AF022872) phosphate transporter [Arabidopsis
thaliana] >gi\_3869206\_dbj\_BAA34398\_ (AB016166) Phosphate
Transporter 4 [Arabidopsis thaliana] >gi\_3928081 (AC005770)

phosphate transporter, AtPT2 [Arabidopsis thaliana]

Seq. No. 12113

Contig ID 23732 1.R1040

5'-most EST LIB3051-069-Q1-K1-C2

Method BLASTX
NCBI GI g1091678
BLAST score 232
E value 5.0e-19
Match length 140
% identity 33

NCBI Description activator-like transposable element [Pennisetum glaucum]

Seq. No. 12114

Contig ID 23733\_1.R1040

5'-most EST LIB3051-046-Q1-K1-A4

Method BLASTX
NCBI GI 9719291
BLAST score 635
E value 1.0e-82
Match length 265
% identity 68

NCBI Description (U19134) unknown [Arabidopsis thaliana]

>gi 1095007 prf 2107236A SABRE gene [Arabidopsis thaliana]

Seq. No. 12115

Contig ID 23736\_1.R1040

5'-most EST LIB3138-030-Q1-N1-A4

Method BLASTX
NCBI GI g3341692
BLAST score 419
E value 2.0e-40
Match length 143
% identity 60

NCBI Description (AC003672) unknown protein [Arabidopsis thaliana]

Seq. No. 12116

Contig ID 23736 3.R1040 5'-most EST asn701142401.h1



Contig ID 23737\_1.R1040 5'-most EST jex700908465.h1 Method BLASTX

NCBI GI g3461848 BLAST score 2314 E value 0.0e+00 Match length 570 % identity 80

NCBI Description (AC005315) putative ATPase [Arabidopsis thaliana]

Seq. No. 12118

Contig ID 23738\_1.R1040

5'-most EST jC-gmf102220148e08a1

Method BLASTX
NCBI GI g2626753
BLAST score 289
E value 3.0e-45
Match length 162
% identity 62

NCBI Description (AB008782) sulfate transporter [Arabidopsis thaliana]

Seq. No. 12119

Contig ID 23738\_2.R1040 5'-most EST gsv701056756.h1

Method BLASTX
NCBI GI g2626753
BLAST score 450
E value 1.0e-44
Match length 169
% identity 54

NCBI Description (AB008782) sulfate transporter [Arabidopsis thaliana]

Seq. No. 12120

Contig ID 23739\_1.R1040 5'-most EST ekl700968154.h1

Method BLASTX
NCBI GI g4191784
BLAST score 1216
E value 1.0e-142
Match length 363
% identity 47

NCBI Description (AC005917) putative WD-40 repeat protein [Arabidopsis

thaliana]

Seq. No. 12121

Contig ID 23740\_1.R1040 5'-most EST awf700838704.h1

Method BLASTX
NCBI GI g1708152
BLAST score 271
E value 2.0e-31
Match length 230
% identity 39

NCBI Description PROBABLE ATP-DEPENDENT RNA HELICASE DBP5 (HELICASE CA5/6) >gi 2133053 pir \_ S66920 probable RNA helicase CA5/6 - yeast

(Saccharomyces cerevisiae) >gi\_1353268 (U28135) Dbp5p [Saccharomyces cerevisiae] >gi\_1420175\_emb\_CAA99237\_



(Z74954) ORF YOR046c [Saccharomyces cerevisiae]

12122 Seq. No. 23741 1.R1040 Contig ID LIB3051-049-Q1-K1-H1 5'-most EST BLASTX Method q1136434 NCBI GI 506 BLAST score 3.0e-51 E value 150 Match length 62 % identity (D80009) KIAA0187 [Homo sapiens] NCBI Description 12123 Seq. No. 23743 1.R1040 Contig ID LIB3051-070-Q1-K1-A4 5'-most EST BLASTX Method g4038629 NCBI GI 207 BLAST score 2.0e-16 E value 107 Match length 38 % identity (AL023704) similar to E. coli DNA-damage-inducible protein NCBI Description [Schizosaccharomyces pombe] 12124 Seq. No. 23744 1.R1040 Contig ID pcp700992437.hl 5'-most EST BLASTX Method q2494264 NCBI GI 1098 BLAST score E value 1.0e-120 460 Match length 48 % identity HYPOTHETICAL 66.0 KD GTP-BINDING PROTEIN SLR1105 NCBI Description >gi 1651837\_dbj\_BAA16764\_ (D90900) elongation factor EF-G [Synechocystis sp.] 12125 Seq. No.

Contig ID 23745 1.R1040

5'-most EST uC-gmflminsoy063d03b1

Method BLASTX
NCBI GI g2244990
BLAST score 776
E value 1.0e-119
Match length 264
% identity 83

NCBI Description (Z97340) similarity to LIM homeobox protein -

Caenorhabditis [Arabidopsis thaliana]

Seq. No. 12126

Contig ID 23746\_1.R1040

5'-most EST LIB3170-056-Q1-K1-B3

Method BLASTX
NCBI GI g2244807
BLAST score 913
E value 9.0e-99

2110



Match length 256 % identity 49

NCBI Description (Z97336) hypothetical protein [Arabidopsis thaliana]

Seq. No. 12127

Contig ID 23754\_1.R1040 5'-most EST bth700847720.h1

Method BLASTX
NCBI GI g409756
BLAST score 233
E value 4.0e-19
Match length 144
% identity 34

NCBI Description (L25643) ATP/GTP nucleotide-binding protein [Leishmania

infantum]

Seq. No. 12128

Contig ID 23763\_1.R1040 5'-most EST uC-gmropic074b10b1

Method BLASTX
NCBI GI g3024898
BLAST score 756
E value 1.0e-133
Match length 404
% identity 59

NCBI Description PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA

HELICASE KIAA0224 (HA4657) >gi\_1504028\_dbj\_BAA13213\_ (D86977) similar to putative ATP-dependent RNA helicase K03H1.2 of C.elegans(S41025) [Homo sapiens] >gi\_3123906

(AF038391) pre-mRNA splicing factor [Homo sapiens]

Seq. No. 12129

Contig ID 23764\_1.R1040 5'-most EST jsh701067456.h1

Method BLASTX
NCBI GI 94415912
BLAST score 385
E value 5.0e-41
Match length 143
% identity 62

NCBI Description (AC006282) putative protease [Arabidopsis thaliana]

Seq. No. 12130

Contig ID 23765\_1.R1040 5'-most EST g4396405

Method BLASTX
NCBI GI g126201
BLAST score 879
E value 1.0e-94
Match length 219
% identity 76

NCBI Description 3-ISOPROPYLMALATE DEHYDROGENASE PRECURSOR (BETA-IPM

DEHYDROGENASE) (IMDH) (3-IPM-DH) >gi\_81676\_pir\_S20510 3-isopropylmalate dehydrogenase (EC 1.1.1.85) precursor -rape >gi\_17827\_emb\_CAA42596\_ (X59970) 3-isopropylmalate

dehydrogenase [Brassica napus]



Seq. No. 12131

Contig ID 23765\_2.R1040 5'-most EST fC-gmse700676027z1

Method BLASTX
NCBI GI g126201
BLAST score 275
E value 1.0e-27
Match length 81
% identity 83

NCBI Description 3-ISOPROPYLMALATE DEHYDROGENASE PRECURSOR (BETA-IPM DEHYDROGENASE) (IMDH) (3-IPM-DH) >gi\_81676\_pir\_S20510

3-isopropylmalate dehydrogenase (EC 1.1.1.85) precursor rape >gi\_17827\_emb\_CAA42596\_ (X59970) 3-isopropylmalate

dehydrogenase [Brassica napus]

Seq. No. 12132

Contig ID 23765\_3.R1040

5'-most EST LIB3170-064-Q1-K1-H9

Method BLASTX
NCBI GI g1903021
BLAST score 483
E value 2.0e-48
Match length 110
% identity 85

NCBI Description (Y10216) hypothetical 3-isopropylmalate dehydrogenase

[Arabidopsis thaliana]

Seq. No. 12133

Contig ID 23768\_1.R1040 5'-most EST epx701105453.h1

Method BLASTX
NCBI GI g4538939
BLAST score 1669
E value 0.0e+00
Match length 474
% identity 69

NCBI Description (AL049483) Col-O casein kinase I-like protein [Arabidopsis

thaliana]

Seq. No. 12134

Contig ID 23768\_2.R1040

5'-most EST LIB3051-111-Q1-K1-E4

Method BLASTX
NCBI GI 94538939
BLAST score 356
E value 1.0e-33
Match length 187
% identity 43

NCBI Description (AL049483) Col-O casein kinase I-like protein [Arabidopsis

thaliana]

Seq. No. 12135

Contig ID 23768\_4.R1040 5'-most EST jex700903401.h1

Seq. No. 12136

Contig ID 23769\_1.R1040



5'-most EST jC-gmst02400071f05a1 BLASTX Method NCBI GI q586441 BLAST score 340 E value 1.0e-31 Match length 114

52

% identity NCBI Description HYPOTHETICAL 13.6 KD PROTEIN IN NUP170-ILS1 INTERGENIC

REGION >gi 626483 pir S45432 hypothetical protein YBL078c - yeast (Saccharomyces cerevisiae) >qi 496705 emb CAA56032

(X79489) E-117 protein [Saccharomyces cerevisiae] >gi 536125 emb CAA84899 (Z35839) ORF YBL078c

[Saccharomyces cerevisiae]

Seq. No. 12137

Contig ID 23769 2.R1040 5'-most EST jsh701064635.h1

Seq. No. 12138

Contig ID 23772 1.R1040

5'-most EST  $LIB30\overline{5}1-059-Q1-K2-C6$ 

Method BLASTX NCBI GI g2702277 BLAST score 531 9.0e-54 E value 334 Match length % identity 42

NCBI Description (AC003033) putative cyclin g-associated kinase [Arabidopsis

thaliana] >gi 2914689 (AC003974) putative cyclin

g-associated kinase [Arabidopsis thaliana]

Seq. No. 12139

23773 1.R1040 Contig ID 5'-most EST kl1701205025.h1

Method BLASTX NCBI GI q124984 BLAST score 193 1.0e-14 E value Match length 66 % identity 56

NCBI Description INHIBITOR OF TRYPSIN AND HAGEMAN FACTOR (CMTI-V)

>gi 99624 pir S12897 serine proteinase inhibitor - winter

squash >gi 227289 prf\_1701295A trypsin inhibitor

[Cucurbita maxima]

12140 Seq. No.

Contig ID 23775 1.R1040

5'-most EST LIB3138-066-Q1-N1-F3

Method BLASTX NCBI GI q3550519 BLAST score 889 E value 6.0e-96 Match length 238 % identity 70

NCBI Description (AJ007630) oxygenase [Nicotiana tabacum]



Contig ID 23779\_1.R1040

5'-most EST uC-gmrominsoy314d10b1

Method BLASTX
NCBI GI g1732075
BLAST score 666
E value 1.0e-69
Match length 232
% identity 27

NCBI Description (U75309) TBP-associated factor [Homo sapiens]

Seq. No. 12142

Contig ID 23781 1.R1040

5'-most EST LIB3170-041-Q1-K1-E4

Method BLASTX
NCBI GI g3080398
BLAST score 421
E value 2.0e-41
Match length 155
% identity 35

NCBI Description (AL022603) putative protein [Arabidopsis thaliana]

Seq. No. 12143

Contig ID 23783\_1.R1040 5'-most EST rlr700895427.h1

Method BLASTX
NCBI GI g729273
BLAST score 955
E value 1.0e-103
Match length 212
% identity 85

NCBI Description CYPRO4 PROTEIN >gi\_322804\_pir\_\_S28592 cypro4 protein -

cardoon >gi 17959 emb CAA49354 (X69672) cypro4 [Cynara

cardunculus]

Seq. No. 12144

Contig ID 23785\_1.R1040

5'-most EST LIB3107-031-Q1-K1-C3

Method BLASTX
NCBI GI g1935000
BLAST score 278
E value 2.0e-24
Match length 113
% identity 43

NCBI Description (Y12314) GTPase [Schizosaccharomyces pombe]

Seq. No. 12145

Contig ID 23791\_1.R1040

5'-most EST jC-gmle01810054b11a1

Method BLASTX
NCBI GI g1184121
BLAST score 1021
E value 1.0e-111
Match length 315
% identity 63

NCBI Description (U20808) auxin-induced protein [Vigna radiata]



```
Contig ID
                  23792 1.R1040
5'-most EST
                  LIB3051-078-Q1-K1-H5
Method
                  BLASTX
NCBI GI
                  g2262115
BLAST score
                  310
E value
                  3.0e-28
                  148
Match length
% identity
                  41
NCBI Description (AC002343) cellulose synthase isolog [Arabidopsis thaliana]
Seq. No.
                  12147
                  23792 2.R1040
Contig ID
5'-most EST
                  sat701011611.h1
Seq. No.
                  12148
Contig ID
                  23796 1.R1040
5'-most EST
                  LIB3106-066-P1-K1-E1
                  BLASTX
Method
                  g4262153
NCBI GI
BLAST score
                  446
E value
                  3.0e-44
Match length
                  214
                  51
% identity
NCBI Description (AC005275) putative DNA-binding protein [Arabidopsis
                  thaliana]
                  12149
Seq. No.
Contig ID
                  23796 2.R1040
5'-most EST
                  uC-qmflminsoy064e05b1
Seq. No.
                  12150
Contig ID
                  23812 1.R1040
5'-most EST
                  LIB3051-102-Q1-K1-C4
Method
                  BLASTX
                  g2370595
NCBI GI
BLAST score
                  297
E value
                  7.0e-56
Match length
                  296
% identity
NCBI Description (AJ001414) GTPase activating protein [Yarrowia lipolytica]
Seq. No.
                  12151
                  23812 3.R1040
Contig ID
5'-most EST
                  jC-gmle01810049b07d1
Seq. No.
                  12152
                  23814 1.R1040
Contig ID
5'-most EST
                  jC-gmle01810021h09a1
Method
                  BLASTX
NCBI GI
                  q1001708
BLAST score
                  372
E value
                  2.0e-35
Match length
                  121
% identity
                  58
NCBI Description (D64004) NifS [Synechocystis sp.]
```

BLAST score

E value

247 2.0e-21



```
23818 1.R1040
Contig ID
                  fde700872768.h1
5'-most EST
                  BLASTN
Method
NCBI GI
                  g862479
BLAST score
                  211
                  1.0e-115
E value
                  759
Match length
                  83
% identity
NCBI Description Glycine max valosin-containing protein mRNA, complete cds
Seq. No.
                  12154
Contig ID
                  23819 1.R1040
5'-most EST
                  rca701002447.h1
Seq. No.
                  12155
Contig ID
                  23821 1.R1040
5'-most EST
                  xpa700797865.h1
Method
                  BLASTX
NCBI GI
                  g4455261
                  573
BLAST score
                  4.0e-59
E value
Match length
                  141
% identity
                  78
NCBI Description (AL035353) protein kinase-like protein [Arabidopsis
                  thaliana]
Seq. No.
                  12156
                  23821 2.R1040
Contig ID
5'-most EST
                  wrg700787326.h2
Method
                  BLASTX
NCBI GI
                  g4455261
BLAST score
                  577
                  1.0e-59
E value
Match length
                  141
% identity
NCBI Description (AL035353) protein kinase-like protein [Arabidopsis
                  thaliana]
Seq. No.
                  12157
Contig ID
                  23821 3.R1040
5'-most EST
                  sat701008435.h1
                  BLASTX
Method
NCBI GI
                  g4538939
BLAST score
                  184
E value
                  1.0e-13
Match length
                  51
% identity
                  71
NCBI Description (AL049483) Col-0 casein kinase I-like protein [Arabidopsis
                  thaliana]
                  12158
Seq. No.
                  23821 4.R1040
Contig ID
5'-most EST
                  zhf700964960.hl
Method
                  BLASTX
NCBI GI
                  g4538939
```



Match length 65 % identity 72

NCBI Description (AL049483) Col-O casein kinase I-like protein [Arabidopsis thaliana]

Seq. No. 12159

Contig ID 23823 1.R1040

5'-most EST LIB3170-057-Q1-K1-C11

Method BLASTX
NCBI GI g4467144
BLAST score 314
E value 1.0e-28
Match length 67
% identity 88

NCBI Description (AL035540) putative phosphatidylinositol synthase

[Arabidopsis thaliana]

Seq. No. 12160

Contig ID 23823\_2.R1040 5'-most EST fC-gmro700866722a1

Method BLASTX
NCBI GI g4467144
BLAST score 678
E value 2.0e-71
Match length 140
% identity 88

NCBI Description (AL035540) putative phosphatidylinositol synthase

[Arabidopsis thaliana]

Seq. No. 12161

Contig ID 23823 3.R1040

5'-most EST LIB3092-018-Q1-K1-B4

Method BLASTX
NCBI GI g3367632
BLAST score 420
E value 3.0e-41
Match length 99
% identity 79

NCBI Description (AJ000539) phosphatidylinositol synthase [Arabidopsis

thaliana]

Seq. No. 12162

Contig ID 23823\_4.R1040 5'-most EST vwf700679555.h1

Method BLASTX
NCBI GI g4467144
BLAST score 337
E value 1.0e-31
Match length 75
% identity 84

NCBI Description (AL035540) putative phosphatidylinositol synthase

[Arabidopsis thaliana]

Seg. No. 12163

Contig ID 23824 1.R1040

5'-most EST LIB3092-017-Q1-K1-E10

Method BLASTX



```
g4006878
NCBI GI
                  555
BLAST score
                  1.0e-56
E value
                  196
Match length
                  56
% identity
                  (Z99707) MAP3K-like protein kinase [Arabidopsis thaliana]
NCBI Description
                   12164
Seq. No.
                   23824 2.R1040
Contig ID
                  LIB3139-063-P1-N1-G3
5'-most EST
                   BLASTX
Method
                   g4006878
NCBI GI
                   339
BLAST score
                   1.0e-31
E value
Match length
                   124
                   53
% identity
                  (Z99707) MAP3K-like protein kinase [Arabidopsis thaliana]
NCBI Description
                   12165
Seq. No.
                   23825 1.R1040
Contig ID
                   pxt700941263.hl
5'-most EST
                   BLASTX
Method
```

5'-most EST pxt700941263.h1

Method BLASTX

NCBI GI g1174870

BLAST score 178

E value 8.0e-13

Match length 60

% identity 63

NCBI Description UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 8.0 KD PROTEIN >gi\_633685\_emb\_CAA55861\_ (X79274) ubiquinol--cytochrome c reductase [Solanum tuberosum]

eg. No. 12166

Seq. No. 12166
Contig ID 23825\_2.R1040
5'-most EST pxt700945709.h1

Method BLASTX
NCBI GI g1174870
BLAST score 258
E value 3.0e-22
Match length 73
% identity 70

NCBI Description UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 8.0 KD PROTEIN >gi\_633685\_emb\_CAA55861\_ (X79274) ubiquinol--cytochrome c

reductase [Solanum tuberosum]

Seq. No. 12167

Contig ID 23826\_1.R1040 5'-most EST bth700848406.h1

Method BLASTX
NCBI GI g4138853
BLAST score 3027
E value 0.0e+00
Match length 636
% identity 92

NCBI Description (AF098272) ethylene response sensor [Vigna radiata]

Seq. No. 12168

Contig ID 23827\_1.R1040

% identity

44



```
zsq701126834.hl
5'-most EST
                  BLASTX
Method
                  a2335108
NCBI GI
                  368
BLAST score
                  1.0e-35
E value
                  83
Match length
                  82
% identity
NCBI Description (AC002339) putative isulinase [Arabidopsis thaliana]
                  12169
Seq. No.
                  23828 1.R1040
Contig ID
                  leu701145260.hl
5'-most EST
                  BLASTX
Method
                  g322752
NCBI GI
                  291
BLAST score
                  7.0e-26
E value
                  131
Match length
                  44
% identity
                  auxin-independent growth promoter - Nicotiana tabacum
NCBI Description
                  >gi 559921_emb_CAA56570_ (X80301) axi 1 [Nicotiana tabacum]
                  12170
Seq. No.
                   23829 1.R1040
Contig ID
5'-most EST
                   fde700872266.hl
                  BLASTX
Method
                   q4371295
NCBI GI
                   595
BLAST score
                   3.0e-61
E value
                   156
Match length
                   82
% identity
                  (AC006260) putative CCAAT-binding transcription factor
NCBI Description
                   [Arabidopsis thaliana]
                   12171
Seq. No.
                   23829 2.R1040
Contig ID
                   r1r700902444.h1
5'-most EST
                   BLASTX
Method
                   q115840
NCBI GI
                   222
BLAST score
E value
                   8.0e-18
                   66
Match length
                   76
 % identity
                   CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A (CBF-A) (NF-Y
NCBI Description
                   PROTEIN CHAIN B) (NF-YB) (CAAT-BOX DNA BINDING PROTEIN
                   SUBUNIT B)
 Seq. No.
                   12172
                   23832 1.R1040
 Contig ID
 5'-most EST
                   uC-gmrominsoy154d06b1
                   BLASTX
 Method
                   q4567250
 NCBI GI
                   423
 BLAST score
                   2.0e-41
 E value
                   211
 Match length
```

NCBI Description (AC007070) hypothetical protein [Arabidopsis thaliana]



```
Seq. No.
Contig ID
                   23833 1.R1040
                   k11701206971.h1
5'-most EST
                   BLASTX
Method
                   q4063752
NCBI GI
                   386
BLAST score
                   4.0e-37
E value
Match length
                   117
% identity
                   61
                   (AC005851) unknown protein [Arabidopsis thaliana]
NCBI Description
                   >gi 4510410 gb AAD21496.1 (AC006929) unknown protein
                   [Arabidopsis thaliana]
```

12174 Seq. No.

23833 2.R1040 Contig ID uxk700669926.h1 5'-most EST

12175 Seq. No.

23835 1.R1040 Contig ID

LIB3051-002-Q1-E1-B6 5'-most EST

BLASTN Method g3241920 NCBI GI 53 BLAST score 2.0e-20 E value Match length 259 88 % identity

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MAE1, complete sequence [Arabidopsis thaliana]

12176 Seq. No.

23842 1.R1040 Contig ID

LIB3170-040-Q1-K1-F5 5'-most EST

BLASTX Method NCBI GI g3193291 451 BLAST score E value 7.0e-45 Match length 117 % identity 68

(AF069298) Similar to DNA mismatch repair protein; T14P8.6 NCBI Description

[Arabidopsis thaliana]

12177 Seq. No.

23844 1.R1040 Contig ID

LIB3107-016-Q1-K1-D2 5'-most EST

Method BLASTX q4185141 NCBI GI BLAST score 149 2.0e-09 E value Match length 62 58 % identity

(AC005724) putative calmodulin-binding protein [Arabidopsis NCBI Description

thaliana]

12178 Seq. No.

23844 2.R1040 Contig ID uC-gmropic078h07b1 5'-most EST

BLASTX Method



```
NCBI GI
                  q4185141
BLAST score
                  1298
E value
                  1.0e-143
Match length
                  399
% identity
                  (AC005724) putative calmodulin-binding protein [Arabidopsis
NCBI Description
                  thaliana]
                  12179
Seq. No.
Contig ID
                  23848 1.R1040
5'-most EST
                  jC-gmro02910021c03d1
                  BLASTX
Method
                  g1769898
NCBI GI
BLAST score
                  559
E value
                  2.0e-57
Match length
                  167
% identity
                  61
                  (Y08010) lectin receptor kinase [Arabidopsis thaliana]
NCBI Description
                  12180
Seq. No.
                  23849_1.R1040
Contig ID
5'-most EST
                  LIB3170-040-Q1-K1-D5
Method
                  BLASTX
                  g2244974
NCBI GI
                  325
BLAST score
                  4.0e-30
E value
                  113
Match length
                  59
% identity
NCBI Description
                  (Z97340) similarity to pore protein Pisum sativum
                  [Arabidopsis thaliana]
Seq. No.
                  12181
                  23849 2.R1040
Contig ID
                  LIB3072-049-Q1-K1-A4
5'-most EST
                  12182
Seq. No.
                  23850 1.R1040
Contig ID
                  hyd700725374.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q4262224
BLAST score
                  185
E value
                  7.0e-26
Match length
                  103
% identity
                  57
                  (AC006200) putative amino acid or GABA permease
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  12183
                  23851_1.R1040
Contig ID
5'-most EST
                  LIB3051-061-Q1-K1-G7
Method
                  BLASTX
                  g2621563
NCBI GI
```

BLAST score 344 E value 2.0e-32 Match length 126 52 % identity

NCBI Description (AE000833) ATP-dependent RNA helicase, eIF-4A family



## [Methanobacterium thermoautotrophicum]

```
Seq. No.
                  12184
Contig ID
                  23869 1.R1040
5'-most EST
                  zpv700759117.hl
                  BLASTX
Method
                  q4467147
NCBI GI
BLAST score
                  983
E value
                  1.0e-107
                  279
Match length
                  70
% identity
                 (AL035540) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  12185
                  23870 1.R1040
Contig ID
5'-most EST
                  LIB3051-078-Q1-K1-E12
                  BLASTX
Method
NCBI GI
                  g4455169
BLAST score
                  511
                  1.0e-51
E value
                  167
Match length
                  59
% identity
NCBI Description
                  (AL035521) putative aldehyde dehydrogenase [Arabidopsis
                  thaliana]
Seq. No.
                  12186
                  23872 1.R1040
Contig ID
5'-most EST
                  uC-qmropic005e05b1
Method
                  BLASTN
NCBI GI
                  g4115535
BLAST score
                  350
E value
                  0.0e + 00
                  809
Match length
                  86
% identity
NCBI Description Vigna mungo UFGlyT mRNA for UDP-glycose:flavonoid
                  glycosyltransferase, partial cds
Seq. No.
                  12187
Contig ID
                  23872 3.R1040
5'-most EST
                  uaw700662225.h1
Method
                  BLASTX
NCBI GI
                  g4115536
                  275
BLAST score
                   6.0e-35
E value
Match length
                  94
% identity
                  80
                  (AB012115) UDP-glycose:flavonoid glycosyltransferase [Vigna
NCBI Description
                  mungo]
Seq. No.
                  12188
Contig ID
                  23874_1.R1040
5'-most EST
                  LIB3051-102-Q1-K1-E4
```

Method BLASTX NCBI GI q3702324 BLAST score 149 E value 3.0e-09 Match length 145

```
% identity
                  (AC005397) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  12189
Seq. No.
                  23875 1.R1040
Contig ID
                  LIB3051-094-Q1-K1-H5
5'-most EST
                  BLASTX
Method
                  q2852447
NCBI GI
                  154
BLAST score
                  3.0e-14
E value
                  59
Match length
                  69
% identity
NCBI Description (D88206) protein kinase [Arabidopsis thaliana]
                  12190
Seq. No.
                  23877 1.R1040
Contig ID
                  uC-gmropic041h12b1
5'-most EST
                  BLASTX
Method
                  q2909583
NCBI GI
                  276
BLAST score
                  3.0e-24
E value
                  147
Match length
                   42
% identity
                  (AL021926) oxcA [Mycobacterium tuberculosis]
NCBI Description
                   12191
Seq. No.
                   23878 2.R1040
Contig ID
5'-most EST
                  LIB3167-023-P4-K4-A3
                   BLASTX
Method
NCBI GI
                   g4314370
                   375
BLAST score
E value
                   3.0e-55
                   210
Match length
% identity
                   59
                  (AC006340) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   12192
Seq. No.
                   23878 3.R1040
Contig ID
                   LIB3051-117-Q1-K1-E4
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4314370
BLAST score
                   248
                   2.0e-21
E value
                   102
Match length
% identity
                   49
                   (AC006340) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   12193
                   23879 1.R1040
Contig ID
                   uC-qmrominsoy222h03b1
 5'-most EST
                   BLASTX
Method
                   g418596
NCBI GI
 BLAST score
                   482
                   2.0e-48
 E value
                   165
Match length
```

52

NCBI Description PUTATIVE 40S RIBOSOMAL PROTEIN YHR148W

% identity



12194

>gi\_485540\_pir\_\_S33911 hypothetical protein YHR148w - yeast
(Saccharomyces cerevisiae) >gi\_4014\_emb\_CAA49237\_ (X69480)
uORF1 [Saccharomyces cerevisiae] >gi\_500654 (U10397)
Yhr148wp [Saccharomyces cerevisiae]

23879 2.R1040 Contig ID 5'-most EST LIB3051-069-01-K1-D2 Method BLASTX NCBI GI g418596 BLAST score 208 E value 2.0e-16 Match length 76 % identity 47

NCBI Description PUTATIVE 40S RIBOSOMAL PROTEIN YHR148W

>gi\_485540\_pir\_\_S33911 hypothetical protein YHR148w - yeast
(Saccharomyces cerevisiae) >gi\_4014\_emb\_CAA49237\_ (X69480)
uORF1 [Saccharomyces cerevisiae] >gi\_500654 (U10397)

Yhr148wp [Saccharomyces cerevisiae]

Seq. No. 12195

Seq. No.

Contig ID 23883 1.R1040

5'-most EST LIB $30\overline{5}1-113-Q1-K1-D2$ 

Method BLASTX
NCBI GI g3080426
BLAST score 221
E value 2.0e-27
Match length 116
% identity 50

NCBI Description (AL022604) putative protein [Arabidopsis thaliana]

Seq. No. 12196

Contig ID 23884\_1.R1040
5'-most EST g5057446
Method BLASTN
NCBI GI g2605509
BLAST score 63

E value 1.0e-26
Match length 123
% identity 89

NCBI Description Glycine max mRNA for alpha subunit of beta conglycinin,

complete cds

Seq. No. 12197

Contig ID 23885\_1.R1040 5'-most EST fde700876309.h1

Method BLASTX
NCBI GI g2492512
BLAST score 983
E value 1.0e-106
Match length 390
% identity 54

NCBI Description CELL DIVISION PROTEIN FTSH HOMOLOG 3

>gi\_1652556\_dbj\_BAA17477\_ (D90906) cell division protein

FtsH [Synechocystis sp.]



Contig ID 23906 1.R1040 5'-most EST LIB3170-037-Q1-K1-B9 Method BLASTX

NCBI GI g1669655
BLAST score 540
E value 6.0e-55
Match length 123
% identity 78

NCBI Description (X95962) CER3 [Arabidopsis thaliana]

Seq. No. 12199

Contig ID 23908\_1.R1040

5'-most EST LIB $30\overline{5}1-054-Q1-K2-D4$ 

Method BLASTX
NCBI GI g3193300
BLAST score 389
E value 1.0e-37
Match length 158
% identity 52

NCBI Description (AF069298) No definition line found [Arabidopsis thaliana]

Seq. No. 12200

Contig ID 23910\_1.R1040

5'-most EST LIB3051-114-Q1-K1-F2

Method BLASTX
NCBI GI g3287693
BLAST score 946
E value 1.0e-103
Match length 200
% identity 88

NCBI Description (AC003979) Similar to LIM17 gene product gb 1653769 from

the genome of Synechocystis sp. gb\_D90916. [Arabidopsis

thaliana]

Seq. No. 12201

Contig ID 23911\_1.R1040 5'-most EST awf700836848.h1

Method BLASTX
NCBI GI g3695408
BLAST score 208
E value 3.0e-16
Match length 85
% identity 47

NCBI Description (AF096373) contains similarity to Solanum lycopersicum

(tomato) wound-induced protein (GB:X59882) [Arabidopsis thaliana] >gi\_4538956\_emb\_CAB39780.1\_ (AL049488) probable

wound-induced protein [Arabidopsis thaliana]

Seq. No. 12202

Contig ID 23912\_1.R1040

5'-most EST LIB3051-066-Q1-K1-D4

Method BLASTX
NCBI GI g3021270
BLAST score 405
E value 6.0e-39
Match length 224
% identity 38



NCBI Description (AL022347) serine/threonine kinase -like protein [Arabidopsis thaliana]

Seq. No. 12203

Contig ID 23915\_1.R1040

5'-most EST LIB3106-043-Q1-K1-F12

Method BLASTX
NCBI GI g2191145
BLAST score 326
E value 1.0e-29
Match length 246
% identity 39

NCBI Description (AF007269) A\_IG002N01.4 gene product [Arabidopsis thaliana]

Seq. No. 12204

Contig ID 23916\_1.R1040

5'-most EST LIB3093-033-Q1-K1-B3

Method BLASTX
NCBI GI 94455345
BLAST score 379
E value 2.0e-41
Match length 143
% identity 64

NCBI Description (AL035522) putative protein [Arabidopsis thaliana]

Seq. No. 12205

Contig ID 23917\_1.R1040

5'-most EST LIB3138-127-Q1-N1-H7

Method BLASTX
NCBI GI g3096935
BLAST score 307
E value 3.0e-45
Match length 210
% identity 50

NCBI Description (AL023094) putative protein [Arabidopsis thaliana]

Seq. No. 12206

Contig ID 23917\_2.R1040 5'-most EST vwf700677978.h1

Method BLASTX
NCBI GI g3096935
BLAST score 153
E value 3.0e-10
Match length 54
% identity 59

NCBI Description (AL023094) putative protein [Arabidopsis thaliana]

Seq. No. 12207

Contig ID 23918\_1.R1040 5'-most EST bth700846355.h1

Method BLASTX
NCBI GI g3540181
BLAST score 303
E value 2.0e-27
Match length 181
% identity 38

NCBI Description (AC004122) Unknown protein [Arabidopsis thaliana]



```
12208
Seq. No.
                  23918 2.R1040
Contig ID
                  LIB3170-060-Q1-K1-H1
5'-most EST
                  12209
Seq. No.
                  23919 1.R1040
Contig ID
                  LIB30\overline{5}1-098-Q1-K1-A7
5'-most EST
                  BLASTX
Method
                   g2204077
NCBI GI
                   193
BLAST score
                   1.0e-14
E value
                   118
Match length
                   38
% identity
NCBI Description (D85623) extracellular insoluble cystatin [Daucus carota]
                   12210
Seq. No.
                   23921 1.R1040
Contig ID
                   hyd70\overline{0}727650.h1
5'-most EST
                   BLASTX
Method
                   g2262105
NCBI GI
                   1121
BLAST score
                   1.0e-123
E value
                   479
Match length
                   47
% identity
                  (AC002343) unknown protein [Arabidopsis thaliana]
NCBI Description
                   12211
Seq. No.
                   23921 2.R1040
Contig ID
                   jC-gm\overline{f}102220054c01a1
5'-most EST
                   12212
Seq. No.
                   23922 1.R1040
Contig ID
                   jC-gmro02800043c03a1
5'-most EST
                   BLASTX
Method
                   g2961352
NCBI GI
                    762
BLAST score
                    9.0e-81
E value
                    380
Match length
                    49
% identity
                   (AL022140) putative protein [Arabidopsis thaliana]
NCBI Description
                    12213
Seq. No.
                   23922 2.R1040
Contig ID
                    LIB3093-042-Q1-K1-E1
5'-most EST
                    12214
Seq. No.
                    23922 3.R1040
Contig ID
                    jC-gmro02800026f07a1
 5'-most EST
                    BLASTX
Method
NCBI GI
                    g2961352
BLAST score
                    448
```

NCBI Description (AL022140) putative protein [Arabidopsis thaliana]

2.0e-44

198

57

E value

Match length

% identity

Seq. No.

Contig ID

12220

23932 1.R1040



```
Seq. No.
                  12215
Contig ID
                  23922 4.R1040
                  LIB30\overline{5}1-068-Q1-K1-G8
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2961352
BLAST score
                  155
E value
                  2.0e-10
Match length
                  66
% identity
                  47
NCBI Description (AL022140) putative protein [Arabidopsis thaliana]
                  12216
Seq. No.
                  23925 1.R1040
Contig ID
                  LIB3051-033-Q1-K1-F10
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3402684
BLAST score
                  421
E value
                  2.0e-41
Match length
                  97
                  77
% identity
NCBI Description (AC004697) hypothetical protein [Arabidopsis thaliana]
                  12217
Seq. No.
Contig ID
                  23925 2.R1040
5'-most EST
                  uxk700669977.h1
                  BLASTX
Method
NCBI GI
                  q3402684
BLAST score
                  256
E value
                  2.0e-22
Match length
                  71
% identity
                  70
NCBI Description (AC004697) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  12218
                  23927 1.R1040
Contig ID
5'-most EST
                  LIB3051-101-Q1-K1-D12
Method
                  BLASTX
NCBI GI
                  g2252847
BLAST score
                   604
E value
                  7.0e-63
Match length
                  134
% identity
                  84
NCBI Description (AF013293) No definition line found [Arabidopsis thaliana]
Seq. No.
                  12219
                  23931 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy214c07b1
Method
                  BLASTX
                  g4105798
NCBI GI
BLAST score
                  572
E value
                  7.0e-59
Match length
                  117
% identity
                  77
NCBI Description (AF049930) PGP237-11 [Petunia x hybrida]
```

NCBI Description



```
pmv700890663.h1
5'-most EST
Method
                  BLASTX
                  q3378491
NCBI GI
                  275
BLAST score
                  3.0e-24
E value
Match length
% identity
                  (AJ007578) pRIB5 protein [Ribes nigrum]
NCBI Description
                  12221
Seq. No.
                  23933 1.R1040
Contig ID
                  q4314031
5'-most EST
                  BLASTX
Method
                  q1168470
NCBI GI
                   321
BLAST score
                  1.0e-29
E value
                   92
Match length
                   70
% identity
                  PROTEIN KINASE APK1A >gi_282877_pir__S28615 protein kinase,
NCBI Description
                   tyrosine/serine/threonine-specific (EC 2.7.1.-) -
                   Arabidopsis thaliana >gi 217829_dbj_BAA02092_ (D12522)
                   protein tyrosine-serine-threonine kinase [Arabidopsis
                   thaliana]
Seq. No.
                   12222
                   23934 1.R1040
Contig ID
                   dpv701097018.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q2055230
BLAST score
                   488
E value
                   9.0e-49
                   172
Match length
                   59
% identity
                   (AB000130) SRC2 [Glycine max]
NCBI Description
                   12223
Seq. No.
                   23951 1.R1040
Contig ID
                   q4294730
5'-most EST
                   BLASTX
Method
                   q4567262
NCBI GI
BLAST score
                   535
                   1.0e-54
E value
Match length
                   121
                   79
% identity
                   (AC006841) putative ubiquitin [Arabidopsis thaliana]
NCBI Description
                   12224
Seq. No.
                   23953 1.R1040
Contig ID
                   uC-gmrominsoy122c01b1
5'-most EST
                   BLASTN
Method
                   q1086988
NCBI GI
                   381
BLAST score
                   0.0e+00
E value
                   942
Match length
                   85
 % identity
                   plasma membrane H(+)-ATPase [Vicia faba, Otafuku, abaxial
```

epidermis, guard cells protoplasts, mRNA, 3319 nt]



12225 Seq. No. 23956 1.R1040 Contig ID  $LIB30\overline{5}1-061-Q1-K1-F1$ 5'-most EST BLASTX Method g4539306 NCBI GI 341 BLAST score 8.0e-32 E value 108 Match length 18 % identity NCBI Description (AL049480) pumilio-like protein [Arabidopsis thaliana] 12226 Seq. No. Contig ID 23983 1.R1040 jex700903803.hl 5'-most EST BLASTX Method g4454039 NCBI GI 361 BLAST score 2.0e-34 E value 152 Match length % identity (AL035394) putative Na+/H+-exchanging protein [Arabidopsis NCBI Description thaliana] Seq. No. 12227 Contig ID 23986 1.R1040 LIB3094-102-Q1-K1-G7 5'-most EST 12228 Seq. No. 23987 1.R1040 Contig ID LIB3094-089-Q1-K1-B6 5'-most EST BLASTX Method q125606 NCBI GI BLAST score 980 1.0e-106 E value Match length 492 % identity 45 PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi 100463\_pir\_\_S12248 NCBI Description pyruvate kinase (EC 2.7.1.40) - potato >qi 22576 emb CAA37727 (X53688) pyruvate kinase [Solanum tuberosum] 12229 Seq. No. 23987 2.R1040 Contig ID 5'-most EST fC-gmse7000755843r1 12230 Seq. No. Contig ID 23987 4.R1040 LIB3139-092-P1-N1-A2 5'-most EST

Seq. No. 12231

Contig ID 23988\_1.R1040 5'-most EST uC-gmropic071c06b1

Method BLASTX
NCBI GI g3548819
BLAST score 233
E value 4.0e-19



Match length 137 % identity 42

NCBI Description (AC005313) putative heterogeneous nuclear ribonucleoprotein

[Arabidopsis thaliana]

Seq. No. 12232

Contig ID 23989\_1.R1040 5'-most EST vwf700676033.h1

Method BLASTX
NCBI GI g2244850
BLAST score 307
E value 6.0e-28
Match length 130
% identity 54

NCBI Description (Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No. 12233

Contig ID 23995 1.R1040

5'-most EST LIB3051-108-Q1-K1-F8

Method BLASTX
NCBI GI g3157949
BLAST score 769
E value 6.0e-82
Match length 234
% identity 62

NCBI Description (AC002131) Similar to glucan endo-1,3-beta-D-glucosidase

precursor gb\_Z28697 from Nicotiana tabacum. ESTs gb\_Z18185 and gb\_AA605362 come from this gene. [Arabidopsis thaliana]

Seq. No. 12234

Contig ID 24008\_1.R1040 5'-most EST asj700967304.h1

Method BLASTX
NCBI GI g3618316
BLAST score 403
E value 3.0e-39
Match length 105
% identity 74

NCBI Description (AB001886) zinc finger protein [Oryza sativa]

Seq. No.

12235

Contig ID 24009\_1.R1040 5'-most EST pmv700891343.h1

Method BLASTX
NCBI GI g2459443
BLAST score 597
E value 6.0e-62
Match length 182
% identity 60

NCBI Description (AC002332) putative NAD(P)-dependent cholesterol

dehydrogenase [Arabidopsis thaliana]

Seq. No.

Contig ID 24013 1.R1040

5'-most EST LIB3051-039-Q1-K1-G6

12236

Method BLASTX NCBI GI g4204295



BLAST score 207
E value 2.0e-16
Match length 81
% identity 54

NCBI Description (AC003027) lcl\_prt\_seq No definition line found

[Arabidopsis thaliana]

Seq. No. 12237

Contig ID 24014\_1.R1040 5'-most EST seb700650637.h1

Method BLASTX
NCBI GI g1339949
BLAST score 466
E value 4.0e-46
Match length 253
% identity 40

NCBI Description (D85230) hypothetical protein [Plectonema boryanum]

Seq. No. 12238

Contig ID 24016\_1.R1040 5'-most EST sat701009759.h1

Method BLASTX
NCBI GI g2760327
BLAST score 669
E value 3.0e-70
Match length 203
% identity 43

NCBI Description (AC002130) F1N21.12 [Arabidopsis thaliana]

Seq. No. 12239

Contig ID 24016\_2.R1040 5'-most EST rlr700901338.h1

Method BLASTX
NCBI GI g4126809
BLAST score 192
E value 8.0e-20
Match length 74
% identity 40

NCBI Description (AB017042) glyoxalase I [Oryza sativa]

Seq. No. 12240

Contig ID 24017\_1.R1040 5'-most EST pmv700891278.h1

Method BLASTX
NCBI GI g2642158
BLAST score 746
E value 5.0e-79
Match length 246
% identity 61

NCBI Description (AC003000) hypothetical protein [Arabidopsis thaliana]

Seq. No. 12241

Contig ID 24018 1.R1040 5'-most EST uC-gmropic091c07b1

Method BLASTX NCBI GI g2911072 BLAST score 306



E value 1.0e-27 Match length 141 % identity 52

NCBI Description (AL021960) putative protein [Arabidopsis thaliana]

Seq. No. 12242

Contig ID 24022 1.R1040

5'-most EST LIB3051-069-Q1-K1-G10

Method BLASTX
NCBI GI g4102839
BLAST score 594
E value 1.0e-61
Match length 148
% identity 78

NCBI Description (AF016713) LeOPT1 [Lycopersicon esculentum]

Seq. No. 12243

Contig ID 24042\_1.R1040 5'-most EST jsh70\overline{1064633.h1}

Method BLASTX
NCBI GI g2791900
BLAST score 574
E value 4.0e-59
Match length 176
% identity 61

NCBI Description (AJ000057) PP7 [Arabidopsis thaliana]

Seq. No. 12244

Contig ID 24042 2.R1040 5'-most EST crh700850920.h1

Seq. No. 12245

Contig ID 24043\_1.R1040

5'-most EST uC-gmrominsoy156d01b1

Method BLASTX
NCBI GI g1076389
BLAST score 482
E value 2.0e-48
Match length 106
% identity 90

NCBI Description protein phosphatase 2A pDF1 - Arabidopsis thaliana

>gi 683502 emb CAA57528 (X82002) protein phosphatase 2A 65

kDa regulatory subunit [Arabidopsis thaliana]

Seq. No. 12246

Contig ID 24043\_2.R1040 5'-most EST dpv701100475.h1

Method BLASTX
NCBI GI g1076389
BLAST score 458
E value 9.0e-46
Match length 103
% identity 53

NCBI Description protein phosphatase 2A pDF1 - Arabidopsis thaliana

>gi\_683502\_emb\_CAA57528\_ (X82002) protein phosphatase 2A 65

kDa regulatory subunit [Arabidopsis thaliana]



Seq. No. Contig ID

5'-most EST

24044 1.R1040 vzv700756622.h1

BLASTX Method q3132470 NCBI GI 559 BLAST score 2.0e-57 E value 204 Match length

% identity NCBI Description (AC003096) unknown protein [Arabidopsis thaliana]

12248 Seq. No.

24060 1.R1040 Contig ID

LIB3051-097-Q1-K1-A11 5'-most EST

54

BLASTX Method q585110 NCBI GI 443 BLAST score 3.0e-75 E value Match length 242 % identity 61

ELECTRON TRANSFER FLAVOPROTEIN BETA-SUBUNIT (BETA-ETF) NCBI Description

>gi\_479194\_pir\_\_S32482 electron transfer flavoprotein beta

chain - human >gi 2781203 pdb 1EFV B Chain B, Three-Dimensional Structure Of Human Electron Transfer Flavoprotein To 2.1 A Resolution >gi\_297902 emb\_CAA50441 (X71129) electron transfer flavoprotein beta subunit [Homo

sapiens] >gi\_4503609\_ref\_NP\_001976.1\_pETFB

electron-transfer-flavoprotein, beta polypeptide

12249 Seq. No.

24064 1.R1040 Contig ID

LIB3051-096-Q1-K1-G4 5'-most EST

BLASTX Method NCBI GI q3150239 223 BLAST score 3.0e-18 E value Match length 126 43 % identity

(AL023635) hypothetical protein MLCB1243.38 [Mycobacterium NCBI Description

leprae]

12250 Seq. No.

24066 1.R1040 Contig ID

LIB3051-103-Q1-K1-G4 5'-most EST

Method BLASTX g3522943 NCBI GI BLAST score 670 2.0e-70 E value 177 Match length 38 % identity

NCBI Description (AC004411) putative p-glycoprotein [Arabidopsis thaliana]

Seq. No. 12251

24067 1.R1040 Contig ID

LIB3051-097-Q1-K1-A7 5'-most EST

BLASTX Method g3608153 NCBI GI



```
BLAST score
                   9.0e-19
E value
                   100
Match length
                   59
% identity
NCBI Description (AC005314) hypothetical protein [Arabidopsis thaliana]
                   12252
Seq. No.
                   24068 1.R1040
Contig ID
                   rlr700900606.hl
5'-most EST
                   BLASTX
Method
                   g2275196
NCBI GI
                   616
BLAST score
                   6.0e-64
E value
                   150
Match length
                   77
% identity
                   (AC002337) water stress-induced protein, WSI76 isolog
NCBI Description
                   [Arabidopsis thaliana]
                   12253
Seq. No.
                   24070 1.R1040
Contig ID
                   seb70\overline{0}649615.h1
5'-most EST
                   12254
Seq. No.
                   24070 2.R1040
Contig ID
                   dpv70\overline{1}100168.h1
5'-most EST
                   12255
Seq. No.
                    24071 1.R1040
Contig ID
                   LIB3138-064-Q1-N1-A7
5'-most EST
                   BLASTX
Method
                    g2160172
NCBI GI
                    396
BLAST score
                    1.0e-62
E value
                    222
Match length
                    52
% identity
                   (AC000132) No definition line found [Arabidopsis thaliana]
NCBI Description
                    12256
Seq. No.
                    24074 1.R1040
Contig ID
                    LIB3051-016-Q1-E1-B1
 5'-most EST
                    BLASTX
Method
                    q3047085
 NCBI GI
 BLAST score
                    770
                    3.0e-82
 E value
                    168
 Match length
                    84
 % identity
                   (AF058914) No definition line found [Arabidopsis thaliana]
 NCBI Description
                    12257
 Seq. No.
                    24077 1.R1040
 Contig ID
                    LIB3109-038-Q1-K1-H11
 5'-most EST
                    BLASTX
 Method
                    q3080426
 NCBI GI
 BLAST score
```

964 1.0e-104

307

62

E value Match length

% identity



NCBI Description (AL022604) putative protein [Arabidopsis thaliana]

Seq. No. 12258

Contig ID 24081\_1.R1040 5'-most EST rlr700895918.h1

Method BLASTX
NCBI GI g2914703
BLAST score 718
E value 5.0e-76
Match length 216
% identity 60

NCBI Description (AC003974) unknown protein [Arabidopsis thaliana]

Seq. No. 12259

Contig ID 24090\_1.R1040

5'-most EST LIB3051-030-Q1-K1-B11

Method BLASTX
NCBI GI g1679803
BLAST score 320
E value 1.0e-29
Match length 125
% identity 52

NCBI Description (D87545) histidine kinase homolog [Arabidopsis thaliana]

>gi 2529684 (AC002535) histidine kinase homolog

[Arabidopsis thaliana]

Seq. No. 12260

Contig ID 24091\_1.R1040 5'-most EST leu701156670.h1

Method BLASTX
NCBI GI g2661412
BLAST score 1288
E value 1.0e-142
Match length 344
% identity 70

NCBI Description (AJ000728) MAP kinase kinase [Lycopersicon esculentum]

Seq. No. 12261

Contig ID 24091\_3.R1040 5'-most EST gsv701049930.h1

Method BLASTX
NCBI GI g2661412
BLAST score 363
E value 2.0e-34
Match length 107
% identity 68

NCBI Description (AJ000728) MAP kinase kinase [Lycopersicon esculentum]

Seq. No. 12262

Contig ID 24091\_4.R1040 5'-most EST epx701105767.h1

Method BLASTX
NCBI GI g2661412
BLAST score 166
E value 8.0e-12
Match length 43
% identity 74

2136

```
(AJ000728) MAP kinase kinase [Lycopersicon esculentum]
NCBI Description
                  12263
Seq. No.
                  24093 1.R1040
Contig ID
                  jsh701064286.h1
5'-most EST
                  BLASTX
Method
                  q4455323
NCBI GI
                  1079
BLAST score
                  1.0e-120
E value
                  324
Match length
% identity
                  (AL035525) aminopeptidase-like protein [Arabidopsis
NCBI Description
                  thaliana]
                  12264
Seq. No.
                  24094 1.R1040
Contig ID
                  crh700856192.h1
5'-most EST
                  BLASTX
Method
                  g3914056
NCBI GI
                   605
BLAST score
                   5.0e-63
E value
                   145
Match length
                   77
% identity
                  DNA MISMATCH REPAIR PROTEIN MSH2 >gi 2522362 (AF002706)
NCBI Description
                   MutS homolog 2 [Arabidopsis thaliana] >gi_2522364
                   (AF003005) MutS homolog 2 [Arabidopsis thaliana]
                   >gi 2547236 (AF026549) DNA mismatch repair protein MSH2
```

[Arabidopsis thaliana]

Seq. No. 12265

24095 1.R1040 Contig ID

LIB3051-117-Q1-K1-G12 5'-most EST

BLASTX Method g2583118 NCBI GI 544 BLAST score 1.0e-55 E value 180 Match length % identity

(AC002387) hypothetical protein [Arabidopsis thaliana] NCBI Description

12266 Seq. No.

24096 1.R1040 Contig ID

jC-gmro02910051a03a1 5'-most EST

BLASTX Method NCBI GI g3172538 737 BLAST score E value 3.0e-78 195 Match length % identity

(AF067789) tSNARE AtTLG2p [Arabidopsis thaliana] NCBI Description

12267 Seq. No.

24096 2.R1040 Contig ID

LIB3051-117-Q1-K1-G8 5'-most EST

BLASTX Method g3172538 NCBI GI 270 BLAST score



E value 6.0e-24 Match length 91 % identity 62

NCBI Description (AF067789) tSNARE AtTLG2p [Arabidopsis thaliana]

Seq. No. 12268

Contig ID 24098\_1.R1040

5'-most EST LIB3051-025-Q1-K1-H10

Method BLASTX
NCBI GI g2642430
BLAST score 410
E value 1.0e-39
Match length 143
% identity 66

NCBI Description (AC002391) putative AP2 domain containing protein

[Arabidopsis thaliana]

Seq. No. 12269

Contig ID 24103\_1.R1040 5'-most EST rlr700902130.h1

Method BLASTX
NCBI GI g4165025
BLAST score 243
E value 7.0e-20
Match length 159
% identity 36

NCBI Description (AF043611) zinc-finger protein MCG4 [Homo sapiens]

Seq. No. 12270

Contig ID 24103\_2.R1040 5'-most EST uC-gmropic034h11b1

Method BLASTX
NCBI GI g4165025
BLAST score 147
E value 3.0e-09
Match length 79
% identity 41

NCBI Description (AF043611) zinc-finger protein MCG4 [Homo sapiens]

Seq. No. 12271

Contig ID 24108\_1.R1040 5'-most EST xpa700796695.h1

Method BLASTX
NCBI GI g3643085
BLAST score 541
E value 4.0e-55
Match length 154
% identity 68

NCBI Description (AF075580) protein phosphatase-2C; PP2C [Mesembryanthemum

crystallinum]

Seq. No. 12272

Contig ID 24110 1.R1040

5'-most EST LIB3051-050-Q1-K1-H10

Method BLASTX
NCBI GI g3805962
BLAST score 445



6.0e-44E value 140 Match length 56 % identity NCBI Description (Y13772) laccase [Populus balsamifera subsp. trichocarpa]

12273 Seq. No.

24122 1.R1040 Contig ID hyd700725182.hl 5'-most EST

BLASTX Method g1806140 NCBI GI 1922 BLAST score 0.0e + 00E value 412 Match length 87 % identity

NCBI Description (X97314) cdc2MsC [Medicago sativa]

12274 Seq. No.

24124 1.R1040 Contig ID ssr700558876.h1 5'-most EST

BLASTX Method g1255951 NCBI GI 749 BLAST score 1.0e-79 E value 161 Match length 81 % identity

NCBI Description (X96932) PS60 [Nicotiana tabacum]

12275 Seq. No.

24125 1.R1040 Contig ID sat701011742.hl 5'-most EST

BLASTX Method g3044214 NCBI GI 1417 BLAST score 1.0e-157 E value 327 Match length

82 % identity

NCBI Description (AF057044) acyl-CoA oxidase [Arabidopsis thaliana]

12276 Seq. No.

24126 1.R1040 Contig ID  $k1170\overline{1}207658.h1$ 5'-most EST

BLASTX Method g3560183 NCBI GI 324 BLAST score E value 6.0e-30 Match length 116 53 % identity

(AL031517) conserved hypothetical protein NCBI Description

[Schizosaccharomyces pombe]

Seq. No. 12277

24126 2.R1040 Contig ID gsv701049179.h1 5'-most EST

12278 Seq. No.

24127 1.R1040 Contig ID hrw701062404.hl 5'-most EST

```
BLASTX
Method
                  q3687223
NCBI GI
                   205
BLAST score
                   7.0e-16
E value
                   112
Match length
                   46
% identity
NCBI Description (AC005169) hypothetical protein [Arabidopsis thaliana]
                   12279
Seq. No.
                   24128 1.R1040
Contig ID
                   wvk700685734.hl
5'-most EST
                   BLASTX
Method
                   q1169544
NCBI GI
                   1138
BLAST score
                   0.0e + 00
E value
                   471
Match length
                   70
% identity
                   ERD1 PROTEIN PRECURSOR >gi 541859_pir__JN0901 ERD1 protein
NCBI Description
                   - Arabidopsis thaliana >gi_497629_dbj_BAA04506_ (D17582)
                   ERD1 protein [Arabidopsis thaliana]
                   12280
Seq. No.
                   24129 1.R1040
Contig ID
5'-most EST
                   tku700646368.h1
Method
                   BLASTX
                   g2190187
NCBI GI
                   371
BLAST score
                   1.0e-35
E value
                   149
Match length
                   54
% identity
                   (D64087) nuclear matrix constituent protein 1 (NMCP1)
NCBI Description
                   [Daucus carota]
                   12281
Seq. No.
                   24180 1.R1040
Contig ID
                   LIB3109-009-Q1-K1-D12
 5'-most EST
Method
                   BLASTX
                                  Ą,
                   q2271477
NCBI GI
                   1475
BLAST score
                   0.0e + 00
E value
                   397
Match length
                   87
 % identity
                   (AF009631) AP47/50p [Arabidopsis thaliana]
 NCBI Description
                    12282
 Seq. No.
                    24180 2.R1040
 Contig ID
                    gsv701043786.hl
 5'-most EST
                    BLASTX
 Method
                    g2271477
 NCBI GI
 BLAST score
                    310
                    1.0e-28
 E value
                    62
 Match length
                    94
 % identity
                   (AF009631) AP47/50p [Arabidopsis thaliana]
 NCBI Description
                    12283
 Seq. No.
```

24197 2.R1040

Contig ID

```
dpv701100585.hl
5'-most EST
                  BLASTX
Method
                   g3176725
NCBI GI
                   157
BLAST score
                   2.0e-10
E value
                   62
Match length
                   47
% identity
                   (AC002392) unknown protein [Arabidopsis thaliana]
NCBI Description
                   12284
Seq. No.
                   24198 1.R1040
Contig ID
                   LIB3051-007-Q1-E1-G7
5'-most EST
                   BLASTX
Method
                   g4510371
NCBI GI
                   315
BLAST score
                   7.0e-29
E value
                   141
Match length
                   48
% identity
                   (AC007017) putative harpin-induced protein [Arabidopsis
NCBI Description
                   thaliana]
                   12285
Seq. No.
                   24198 2.R1040
Contig ID
                   uC-gmropic008c05b1
5'-most EST
                   BLASTX
Method
                   g4510371
NCBI GI
                   331
BLAST score
                   8.0e-31
E value
                   139
Match length
                   50
% identity
                   (AC007017) putative harpin-induced protein [Arabidopsis
NCBI Description
                   thaliana]
                   12286
Seq. No.
                   24228 1.R1040
Contig ID
5'-most EST
                   LIB3051-106-Q1-K1-B1
                   BLASTN
Method
                   q18662
NCBI GI
                    114
BLAST score
E value
                    3.0e-57
                    279
Match length
                    92
 % identity
NCBI Description Glycine max hsp 70 gene
 Seq. No.
                    12287
                    24230 1.R1040
 Contig ID
                    jC-gm\overline{l}e01810053b05a1
 5'-most EST
                    BLASTX
 Method
                    g2827520
 NCBI GI
 BLAST score
                    425
                    2.0e-41
 E value
                    244
 Match length
 % identity
                    40
                    (AL021633) receptor kinase - like protein [Arabidopsis
 NCBI Description
```

12288 Seq. No.

thaliana]



```
24230_2.R1040
Contig ID
                   uC-gmropic102d10b1
5'-most EST
                   BLASTX
Method
                   q2827520
NCBI GI
                   253
BLAST score
                   1.0e-21
E value
                   157
Match length
                   40
% identity
                   (AL021633) receptor kinase - like protein [Arabidopsis
NCBI Description
                   thaliana]
                   12289
Seq. No.
                   24231 1.R1040
Contig ID
                   LIB30\overline{5}1-115-Q1-K1-B1
5'-most EST
Method
                   BLASTX
                   g2626840
NCBI GI
                   383
BLAST score
                   6.0e-37
E value
                   148
Match length
                   49
% identity
                   (D89729) CRM1 protein [Homo sapiens]
NCBI Description
                   >gi 4507943 ref_NP_003391.1_pXP01_ exportin 1 (CRM1, yeast,
                   homolog)
                   12290
Seq. No.
                   24232 1.R1040
Contig ID
                   LIB3093-007-Q1-K1-H12
5'-most EST
                   BLASTX
Method
                   g4204277
NCBI GI
                   441
BLAST score
                   1.0e-43
E value
                   136
Match length
                   60
% identity
                   (AC004146) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   12291
Seq. No.
                   24233 1.R1040
Contig ID
                   LIB3109-001-Q1-K2-B10
5'-most EST
                   BLASTX
Method
                   q3242709
NCBI GI
BLAST score
                   308
                   5.0e-28
E value
                   132
Match length
                   48
% identity
                    (AC003040) putative guanine nucleotide-binding protein
NCBI Description
                    [Arabidopsis thaliana]
                   12292
Seq. No.
                   24234 1.R1040
Contig ID
                   zhf700961926.hl
 5'-most EST
Method
                   BLASTX
                   q3420052
NCBI GI
BLAST score
                   155
                    3.0e-10
E value
Match length
                   75
 % identity
                    49
```

NCBI Description (AC004680) putative ubiqinone reductase [Arabidopsis



## thaliana]

```
12293
Seq. No.
                  24238 1.R1040
Contig ID
                  LIB3051-091-Q1-K1-H4
5'-most EST
                  BLASTX
Method
NCBI GI
                  q3201626
                   656
BLAST score
E value
                  7.0e-70
                   188
Match length
% identity
                   (AC004669) putative protein kinase MAP3K [Arabidopsis
NCBI Description
                   thaliana]
                   12294
Seq. No.
                   24239 1.R1040
Contig ID
                   zsq701124913.hl
5'-most EST
                   BLASTX
Method
                   g1084334
NCBI GI
                   706
BLAST score
                   8.0e-75
E value
                   158
Match length
                   47
% identity
                   calcium-dependent protein kinase (EC 2.7.1.-) 1 -
NCBI Description
                   Arabidopsis thaliana >gi_604880_dbj_BAA04829_ (D21805)
                   calcium-dependent protein kinase [Arabidopsis thaliana]
                   12295
Seq. No.
Contig ID
                   24240 1.R1040
                   bth700845982.h1
5'-most EST
                   BLASTX
Method
                   q3426038
NCBI GI
                   715
BLAST score
E value
                   2.0e-99
                   235
Match length
% identity
                   39
                   (AC005168) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   12296
                   24241 1.R1040
Contig ID
                   dpv701100314.h1
5'-most EST
Method
                   BLASTX
                   g3687245
NCBI GI
BLAST score
                   544
                   2.0e-55
E value
                   129
Match length
% identity
                   (AC005169) putative ribosomal protein [Arabidopsis
NCBI Description
                   thaliana]
                   12297
Seq. No.
                   24243 1.R1040
Contig ID
                   xpa700795709.h1
5'-most EST
                   BLASTX
Method
```

g1685005

1.0e-144

1302

NCBI GI

E value

BLAST score



Match length 476 % identity 52 NCBI Description (U32644) immediate-early salicylate-induced glucosyltransferase [Nicotiana tabacum]

Seq. No. 12298
Contig ID 24249\_1.R1040
5'-most EST uC-gmropic069d11b1
Method BLASTX
NCBI GI g3983665
BLAST score 2043

BLAST score 2043 E value 0.0e+00 Match length 483 % identity 82

NCBI Description (AB011271) importin-beta2 [Oryza sativa]

Seq. No. 12299

Contig ID 24250\_1.R1040

5'-most EST LIB3052-011-Q1-N1-C4

Method BLASTX
NCBI GI g1168446
BLAST score 463
E value 3.0e-46
Match length 162
% identity 53

NCBI Description AMINOPEPTIDASE N (ALPHA-AMINOACYLPEPTIDE HYDROLASE)

>gi\_1073840\_pir\_\_F64132 aminopeptidase N (pepN) homolog Haemophilus influenzae (strain Rd KW20) >gi\_1574460
(U32835) aminopeptidase N (pepN) [Haemophilus influenzae

Rd]

Seq. No. 12300

Contig ID 24251\_1.R1040 5'-most EST zpv700760475.h1

Seq. No. 12301

Contig ID 24252 1.R1040 5'-most EST kl1701213715.h1

Method BLASTX
NCBI GI g1916290
BLAST score 308
E value 1.0e-27
Match length 182
% identity 42

NCBI Description (U89876) ALY [Mus musculus]

12302

Seq. No.

Contig ID 24253\_1.R1040

5'-most EST g4397243
Method BLASTX
NCBI GI g1658504
BLAST score 158
E value 2.0e-18
Match length 104
% identity 51

NCBI Description (U75467) Rga [Drosophila melanogaster]



12303 Seq. No. 24258 1.R1040 Contig ID jC-gmf102220093e02a1 5'-most EST BLASTX Method g2462925 NCBI GI 555 BLAST score 1.0e-56 E value 231 Match length 56 % identity (AJ000053) GTP cyclohydrolase II /NCBI Description 3,4-dihydroxy-2-butanone-4-phoshate synthase [Arabidopsis thaliana] 12304 Seq. No. 24259 1.R1040 Contig ID LIB3139-039-P1-N1-A11 5'-most EST BLASTX Method g2245021 NCBI GI 673 BLAST score 1.0e-70 E value Match length 224 60 % identity (Z97341) heat shock protein 110 homolog [Arabidopsis NCBI Description thaliana] 12305 Seq. No. 24261 1.R1040 Contig ID LIB3051-061-Q1-K1-A9 5'-most EST BLASTX Method g4559380 NCBI GI 1366 BLAST score 1.0e-151 E value 380 Match length 67 % identity (AC006526) putative auxin-responsive GH3 protein NCBI Description [Arabidopsis thaliana] 12306 Seq. No. 24262 1.R1040 Contig ID LIB3109-003-Q1-K1-E6 5'-most EST Method BLASTX q2160156 NCBI GI 1170 BLAST score 1.0e-129 E value 255 Match length % identity (AC000132) Strong similarity to S. pombe leucyl-tRNA NCBI Description synthetase (gb\_Z73100). [Arabidopsis thaliana] 12307 Seq. No. 24266 1.R1040 Contig ID uC-gmropic090e09b1 5'-most EST BLASTN Method

Method BLASTN
NCBI GI g3021356
BLAST score 436
E value 0.0e+00
Match length 904



% identity 87

NCBI Description Cyamopsis tetragonoloba mRNA for UDP-galactose 4-epimerase,

clone GEPI48

Seq. No. 12308

Contig ID 24266\_2.R1040

5'-most EST uC-gmronoir018b10b1

Method BLASTN
NCBI GI g3021356
BLAST score 150
E value 1.0e-78
Match length 378
% identity 85

NCBI Description Cyamopsis tetragonoloba mRNA for UDP-galactose 4-epimerase,

clone GEPI48

Seq. No. 12309

Contig ID 24266 3.R1040 5'-most EST kmv700739674.h1

Method BLASTN
NCBI GI g3021356
BLAST score 132
E value 6.0e-68
Match length 391
% identity 90

NCBI Description Cyamopsis tetragonoloba mRNA for UDP-galactose 4-epimerase,

clone GEPI48

Seq. No. 12310

Contig ID 24266\_4.R1040 5'-most EST cks700764788.h1

Method BLASTX
NCBI GI g3021357
BLAST score 188
E value 5.0e-17
Match length 63
% identity 78

NCBI Description (AJ005082) UDP-galactose 4-epimerase [Cyamopsis

tetragonoloba]

Seq. No. 12311

Contig ID 24273\_1.R1040

5'-most EST LIB3051-039-Q1-K1-H8

Method BLASTX
NCBI GI g3004564
BLAST score 319
E value 4.0e-29
Match length 138
% identity 50

NCBI Description (AC003673) putative receptor Ser/Thr protein kinase

[Arabidopsis thaliana]

Seq. No. 12312

Contig ID 24274\_1.R1040 5'-most EST uxk700668719.h1

Method BLASTX NCBI GI g1172872



BLAST score 3.0e-40E value 115 Match length % identity 70

CYSTEINE PROTEINASE RD19A PRECURSOR >gi\_541856\_pir\_\_JN0718 NCBI Description drought-inducible cysteine proteinase (EC 3.4.22.-) RD19A precursor - Arabidopsis thaliana >gi\_435618\_dbj\_BAA02373\_

(D13042) thiol protease [Arabidopsis thaliana]

>gi\_4539328\_emb\_CAB38829.1\_ (AL035679) drought-inducible cysteine proteinase RD19A precursor [Arabidopsis thaliana]

12313 Seq. No.

24304 1.R1040 Contig ID

uC-gmrominsoy250e08b1 5'-most EST

Seq. No. 12314

24304 2.R1040 Contig ID sat701011186.h1 5'-most EST BLASTX

Method g2501766 NCBI GI BLAST score 328 2.0e-30 E value 96 Match length 74 % identity

(U69174) calmodulin-like domain protein kinase isoenzyme NCBI Description

gamma [Glycine max]

12315 Seq. No.

24305\_1.R1040 Contig ID

LIB3087-003-Q1-K1-E12 5'-most EST

Method BLASTX q4325324 NCBI GI 1156 BLAST score 1.0e-127 E value 254 Match length 84 % identity

(AF125574) lysyl-tRNA synthetase; LysRS [Arabidopsis NCBI Description

thaliana]

12316 Seq. No.

24310 1.R1040 Contig ID

LIB3051-005-Q1-E1-A5 5'-most EST

BLASTX Method q728949 NCBI GI BLAST score 214 E value 7.0e-17 122 Match length % identity

BLUE COPPER PROTEIN PRECURSOR >gi\_99665\_pir\_\_S25555 blue NCBI Description

copper protein - Arabidopsis thaliana >gi\_2147156\_pir\_\_I39698 blue copper-binding protein -Arabidopsis thaliana >gi\_16203\_emb\_CAA78771\_ (Z15058) blue

copper-binding protein [unidentified bacterium]

>gi 739987 prf 2004275A blue copper-binding protein

[Arabidopsis thaliana]

Contig ID

Method

NCBI GI

5'-most EST



```
24366 1.R1040
Contig ID
5'-most EST
                   LIB3106-076-Q1-K1-F4
                   BLASTX
Method
                   g2464855
NCBI GI
                   586
BLAST score
                   1.0e-60
E value
                   150
Match length
                    76
% identity
                   (Z99707) myb-related protein [Arabidopsis thaliana]
NCBI Description
                    12318
Seq. No.
                    24366_2.R1040
Contig ID
5'-most EST
                   uC-gmropic036a11b1
                   BLASTX
Method
                    g2464855
NCBI GI
                    550
BLAST score
                    3.0e-56
E value
                    131
Match length
                    78
% identity
                   (Z99707) myb-related protein [Arabidopsis thaliana]
NCBI Description
                    12319
Seq. No.
                    24368 1.R1040
Contig ID
5'-most EST
                    LIB3170-061-Q1-K2-A3
Method
                    BLASTX
                    q1502430
NCBI GI
                    500
BLAST score
                    1.0e-50
E value
                    147
Match length
                    67
% identity
                    (U62331) phosphate transporter [Arabidopsis thaliana]
NCBI Description
                    >gi 2564661 (AF022872) phosphate transporter [Arabidopsis
                    thaliana] >gi_3869206_dbj_BAA34398_ (AB016166) Phosphate
Transporter 4 [Arabidopsis thaliana] >gi_3928081 (AC005770)
                    phosphate transporter, AtPT2 [Arabidopsis thaliana]
Seq. No.
                    12320
                    24370 1.R1040
Contig ID
5'-most EST
                    uC-qmflminsoy059e04b1
                    12321
Seq. No.
                    24372 1.R1040
Contig ID
                    rlr700898424.h1
5'-most EST
Method
                    BLASTX
                    g2829918
NCBI GI
                    829
BLAST score
E value
                    5.0e-89
Match length
                    229
% identity
                    73
                    (AC002291) similar to "tub" protein gp_U82468_2072162
NCBI Description
                    [Arabidopsis thaliana]
                    12322
Seq. No.
```

2148

24373 1.R1040

BLASTX

g1781279

LIB3051-112-Q1-K1-F7

```
BLAST score
E value
                  9.0e-50
                  157
Match length
% identity
                  62
NCBI Description (Y10455) MtN13 [Medicago truncatula]
                  12323
Seq. No.
                  24375 1.R1040
Contig ID
                  pmv700890120.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q2982243
BLAST score
                  245
E value
                  1.0e-20
Match length
                  111
                  46
% identity
                  (AF051204) hypothetical protein [Picea mariana]
NCBI Description
                  12324
Seq. No.
                  24376 1.R1040
Contig ID
                  LIB3051-061-Q1-K1-G12
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4468991
BLAST score
                  220
E value
                  2.0e-17
Match length
                  77
% identity
                   58
NCBI Description (AL035605) ribosomal-like protein [Arabidopsis thaliana]
                   12325
Seq. No.
                   24377 1.R1040
Contig ID
5'-most EST
                   LIB3051-002-Q1-E1-B7
                   BLASTX
Method
NCBI GI
                   g4467147
BLAST score
                   556
E value
                   3.0e-57
Match length
                   127
% identity
                   87
                  (AL035540) putative protein [Arabidopsis thaliana]
NCBI Description
                   12326
Seq. No.
                   24378 1.R1040
Contig ID
                   LIB3051-004-Q1-E1-B11
5'-most EST
Method
                   BLASTX
```

Method BLASTX
NCBI GI 9730318
BLAST score 197
E value 6.0e-15
Match length 109
% identity 42
NCBI Description POTENT

POTENT HEAT-STABLE PROTEIN PHOSPHATASE 2A INHIBITOR I1PP2A (HLA-DR ASSOCIATED PROTEIN I) (PHAPI) (ACIDIC NUCLEAR PHOSPHOPROTEIN PP32) (CEREBELLAR LEUCINE RICH ACIDIC NUCLEAR PROTEIN) >gi\_631325\_pir\_\_S43309 probable HLA class II-associated protein PHAPI - human

>gi\_403007\_emb\_CAA52981\_ (X75090) PHAPI (Putative HLA DR Associated Protein I) [Homo sapiens] >gi\_1408224 (U60823) potent heat-stable protein phosphatase 2A inhibitor I1PP2A

[Homo sapiens] >gi 1763273 (U73477) acidic nuclear



phosphoprotein pp32 [Homo sapiens] >gi\_2589221 (AF025684) cerebellar leucine rich acidic nuclear protein [Homo sapiens]

Seq. No. 12327

Contig ID 24380 1.R1040

5'-most EST uC-gmrominsoy123c08b1

Method BLASTX
NCBI GI g3522952
BLAST score 569
E value 3.0e-58
Match length 232
% identity 49

NCBI Description (AC004411) putative alcohol dehydrogenase [Arabidopsis

thaliana]

Seq. No. 12328

Contig ID 24381\_1.R1040

5'-most EST LIB3051-050-Q1-K1-H8

Method BLASTX
NCBI GI g113497
BLAST score 1786
E value 0.0e+00
Match length 404
% identity 80

NCBI Description ALPHA-GALACTOSIDASE PRECURSOR (MELIBIASE)

(ALPHA-D-GALACTOSIDE GALACTOHYDROLASE)

>gi 99880 pir S07472 alpha-galactosidase (EC 3.2.1.22)

precursor - guar >gi 18292 emb\_CAA32772\_ (X14619)

alpha-galactosidase preproprotein [Cyamopsis tetragonoloba]

Seq. No. 12329

Contig ID 24381\_2.R1040 5'-most EST ssr700555436.h1

Method BLASTX
NCBI GI g2827655
BLAST score 231
E value 2.0e-25
Match length 96
% identity 41

NCBI Description (AL021637) hypothetical protein [Arabidopsis thaliana]

Seq. No. 12330

Contig ID 24396 1.R1040

5'-most EST LIB3051-015-Q1-E1-A9

Method BLASTX
NCBI GI g3005931
BLAST score 491
E value 2.0e-49
Match length 146
% identity 38

NCBI Description (AJ005016) ABC transporter [Homo sapiens]

Seq. No. 12331

Contig ID 24400\_1.R1040 5'-most EST ncj700980567.h1

Method BLASTX

2150



NCBI GI g231654 BLAST score 223 E value 8.0e-23 Match length 267 % identity 13

NCBI Description BRITTLE-1 PROTEIN PRECURSOR >gi\_82676\_pir\_\_JQ1459 Bt1 protein precursor - maize >gi\_168426 (M79333) brittle-1

protein [Zea mays]

Seq. No. 12332

Contig ID 24401 1.R1040

5'-most EST LIB3093-056-Q1-K1-D5

Method BLASTX
NCBI GI g3608147
BLAST score 315
E value 7.0e-29
Match length 115
% identity 31

NCBI Description (AC005314) putative chloroplast 31 kDa ribonucleoprotein

precursor [Arabidopsis thaliana]

Seq. No. 12333

Contig ID 24402\_1.R1040 5'-most EST gsv701045453.h1

Method BLASTX
NCBI GI g2435519
BLAST score 508
E value 1.0e-51
Match length 112
% identity 85

NCBI Description (AF024504) similar to mouse MEM3 (GB:U47024 and S.

cerevisiae vacuolar sorting protein 35 (SW; P34110)

[Arabidopsis thaliana]

Seq. No. 12334

Contig ID 24402\_2.R1040 5'-most EST xpa700793754.h1

Method BLASTX
NCBI GI g2435519
BLAST score 418
E value 4.0e-41
Match length 98
% identity 81

NCBI Description (AF024504) similar to mouse MEM3 (GB:U47024 and S.

cerevisiae vacuolar sorting protein 35 (SW; P34110)

[Arabidopsis thaliana]

Seq. No. 12335

Contig ID 24433 1.R1040

5'-most EST LIB30 $\overline{5}$ 1-066-Q1-K1-A9

Method BLASTX
NCBI GI g3176684
BLAST score 1053
E value 1.0e-115
Match length 272
% identity 72

NCBI Description (AC003671) Contains similarity to equilibratiave nucleoside



transporter 1 gb\_U81375 from Homo sapiens. ESTs gb\_N65317, gb T20785, gb AA586285 and gb\_AA712578 come from this gene. [Arabidopsis thaliana]

Seq. No. 12336 24454 1.R1040 Contig ID vwf700677862.h1 5'-most EST BLASTN

Method q485950 NCBI GI 288 BLAST score E value 1.0e-160 Match length 877 % identity

NCBI Description N.tabacum NeIF-4A9 mRNA

12337 Seq. No.

24454 2.R1040 Contig ID 5'-most EST uaw700661507.hl

BLASTX Method g2500518 NCBI GI 862 BLAST score E value 7.0e-93 175 Match length % identity 96

EUKARYOTIC INITIATION FACTOR 4A-11 (EIF-4A-11) NCBI Description

>gi\_485987\_emb\_CAA55737\_ (X79136) NeIF-4A11 [Nicotiana

tabacuml

12338 Seq. No.

24455 1.R1040 Contig ID

jC-gmf102220077h02d1 5'-most EST

12339 Seq. No.

24459 1.R1040 Contig ID

uC-gmrominsoy233f06b1 5'-most EST

Method BLASTX NCBI GI q4006875 229 BLAST score 9.0e-19 E value Match length 78 55 % identity

(Z99707) putative protein [Arabidopsis thaliana] NCBI Description

12340 Seq. No.

24461 1.R1040 Contig ID

uC-gmflminsoy063c04b1 5'-most EST

Method BLASTX NCBI GI q4512653 BLAST score 3551 0.0e + 00E value 856 Match length 80 % identity

(AC007048) unknown protein [Arabidopsis thaliana] NCBI Description

Seq. No.

12341 24463 1.R1040 Contig ID leu701151104.h1 5'-most EST

2152



Method BLASTX
NCBI GI g71498
BLAST score 554
E value 6.0e-57
Match length 142
% identity 79

NCBI Description heat shock protein 17.7 - garden pea

Seq. No. 12342

Contig ID 24464\_1.R1040

5'-most EST uC-gmrominsoy212d12b1

Method BLASTX
NCBI GI g3643611
BLAST score 1218
E value 1.0e-134
Match length 297
% identity 74

NCBI Description (AC005395) putative casein kinase [Arabidopsis thaliana]

Seq. No. 12343

Contig ID 24491\_1.R1040

5'-most EST jC-gmro02910010a06a1

Method BLASTX
NCBI GI g3548815
BLAST score 658
E value 5.0e-69
Match length 215
% identity 60

NCBI Description (AC005313) similar to axoneme-associated protein mst101

[Arabidopsis thaliana]

Seq. No. 12344

Contig ID 24492 1.R1040

5'-most EST LIB3051-110-Q1-K1-A3

Method BLASTX
NCBI GI g3249064
BLAST score 658
E value 4.0e-69
Match length 174
% identity 70

NCBI Description (AC004473) Strong similarity to trehalose-6-phosphate

synthase homolog gb\_2245136 from A. thaliana chromosome 4

contig gb Z97344. [Arabidopsis thaliana]

Seq. No. 12345

Contig ID 24494 1.R1040

5'-most EST LIB3051-106-Q1-K1-B8

Method BLASTX
NCBI GI g4539662
BLAST score 162
E value 5.0e-11
Match length 74
% identity 46

NCBI Description (AF061282) polyprotein [Sorghum bicolor]

Seq. No. 12346

Contig ID 24496\_1.R1040

% identity

52



uC-qmrominsoy268d08b1 5'-most EST BLASTX Method q3047077 NCBI GI 190 BLAST score 3.0e-14E value 65 Match length % identity (AF058914) contains similarity to the conserved C-terminal NCBI Description domain of helicases (Pfam: helicase\_C.hmm, score: 90.11), similar to DEAD-box helicases [Arabidopsis thaliana] 12347 Seq. No. 24496 2.R1040 Contig ID  $LIB30\overline{5}1-110-Q1-K1-B7$ 5'-most EST Method BLASTX g3047077 NCBI GI 204 BLAST score 6.0e-16 E value 119 Match length 47 % identity (AF058914) contains similarity to the conserved C-terminal NCBI Description domain of helicases (Pfam: helicase C.hmm, score: 90.11), similar to DEAD-box helicases [Arabidopsis thaliana] 12348 Seq. No. 24502 1.R1040 Contig ID uC-gmflminsoy118g05b1 5'-most EST BLASTX Method g3075398 NCBI GI 1311 BLAST score 1.0e-145 E value 482 Match length 56 % identity (AC004484) unknown protein [Arabidopsis thaliana] NCBI Description 12349 Seq. No. 24504 1.R1040 Contig ID LIB3051-029-Q1-K1-C1 5'-most EST BLASTX Method g2244973 NCBI GI BLAST score 541 5.0e-55 E value 174 Match length 66 % identity (Z97340) similarity to extensin class 1 protein NCBI Description [Arabidopsis thaliana] 12350 Seq. No. 24505 1.R1040 Contig ID zsq701130378.hl 5'-most EST Method BLASTX q3850108 NCBI GI BLAST score 317 6.0e-39 E value 181 Match length

NCBI Description (AL033388) putative calcium-transporting atpase



## [Schizosaccharomyces pombe]

```
12351
Seq. No.
                  24506_1.R1040
Contig ID
                  LIB3094-022-Q1-K1-G7
5'-most EST
                  BLASTX
Method
                  g4309737
NCBI GI
                   478
BLAST score
                   1.0e-47
E value
                   138
Match length
                   71
% identity
                   (AC006439) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   12352
Seq. No.
                   24507 1.R1040
Contig ID
                   LIB3051-036-Q1-K1-A5
5'-most EST
                   12353
Seq. No.
                   24508 1.R1040
Contig ID
                   awf700843155.h1
5'-most EST
Method
                   BLASTX
                   g4336434
NCBI GI
                   223
BLAST score
                   5.0e-18
E value
                   111
Match length
                   48
% identity
                   (AF092431) nodule-enhanced protein phosphatase type 2C
NCBI Description
                   [Lotus japonicus]
                   12354
Seq. No.
                   24508 2.R1040
Contig ID
                   6HA - 01 - Q1 - B1 - F11
5'-most EST
                   BLASTX
Method
                   g499301
NCBI GI
BLAST score
                   150
                   9.0e-10
E value
                   64
Match length
                   52
% identity
                   (X77116) ABI1 [Arabidopsis thaliana] >gi_549981 (U12856)
NCBI Description
                   abscisic acid insensitive protein [Arabidopsis thaliana]
                   >gi 4538937_emb_CAB39673.1_ (AL049483) protein phosphatase
                   ABII [Arabidopsis thaliana]
                   12355
Seq. No.
                   24509 1.R1040
Contig ID
                   seb700648967.h1
5'-most EST
                   12356
Seq. No.
                   24510 2.R1040
Contig ID
                   uC-gmronoir053c08b1
5'-most EST
Method
                   BLASTX
                   a459002
NCBI GI
                   348
BLAST score
                   1.0e-32
E value
                   180
Match length
 % identity
                   37
NCBI Description (U00036) R151.6 gene product [Caenorhabditis elegans]
```



```
12357
Seq. No.
                  24513 1.R1040
Contig ID
                  fC-gmse700654736z1
5'-most EST
                  BLASTX
Method
                  g914915
NCBI GI
                  1008
BLAST score
                  1.0e-110
E value
                  223
Match length
                  85
% identity
NCBI Description (U21745) PEP-carboxykinase [Brassica napus]
                  12358
Seq. No.
                  24513 2.R1040
Contig ID
                  pmv700888213.h1
5'-most EST
                  BLASTN
Method
                  g4490717
NCBI GI
                  140
BLAST score
                  2.0e-72
E value
                  571
Match length
% identity
                  86
                  Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA
NCBI Description
                  project)
                  12359
Seq. No.
                  24513 3.R1040
Contig ID
                  LIB3051-003-Q1-E1-C4
5'-most EST
                  BLASTX
Method
                  g1172571
NCBI GI
                   2069
BLAST score
                   0.0e + 00
E value
                   440
Match length
                   87
% identity
                  PHOSPHOENOLPYRUVATE CARBOXYKINASE (ATP)
NCBI Description
                   >gi_1076277_pir__S52637 phosphoenolpyruvate carboxykinase
                   (ATP) (EC 4.1.1.49) - cucumber >gi_567102 (L31899)
                   phosphoenolpyruvate carboxykinase [Cucumis sativus]
                   12360
Seq. No.
                   24514 1.R1040
Contig ID
                   ssr700558677.hl
5'-most EST
                   BLASTX
Method
                   g2501572
NCBI GI
                   375
BLAST score
E value
                   8.0e-36
                   210
Match length
                   39
% identity
                   LATE EMBRYOGENESIS ABUNDANT PROTEIN EMB8 >gi_1350545
NCBI Description
                   (L47118) EMB8 gene product [Picea glauca]
Seq. No.
                   12361
```

24515 1.R1040 Contig ID

LIB3051-043-Q1-K1-C9 5'-most EST

BLASTX Method g3236255 NCBI GI 400 BLAST score 7.0e-40 E value



```
Match length
                   56
% identity
```

(AC004684) hypothetical protein [Arabidopsis thaliana] NCBI Description

Seq. No. 12362

24516\_1.R1040 Contig ID

uC-qmrominsoy305c12b1 5'-most EST

Method BLASTX q1817544 NCBI GI BLAST score 279 1.0e-24 E value 156 Match length 38 % identity

(D83025) proline oxidase precursor [Arabidopsis thaliana] NCBI Description

Seq. No. 12363

24517 1.R1040 Contig ID

LIB3139-040-P1-N1-G6 5'-most EST

BLASTN Method q4336435 NCBI GI BLAST score 416 0.0e+00E value 909 Match length 88 % identity

Lotus japonicus protein phosphatase type 2C (PP2C2) mRNA, NCBI Description

complete cds

12364 Seq. No.

24519 1.R1040 Contig ID

uC-qmflminsoy023e10b1 5'-most EST

BLASTX Method g2120736 NCBI GI 657 BLAST score 2.0e-68 E value 479 Match length 36 % identity

X-Pro dipeptidyl-peptidase (EC 3.4.14.11) - Xanthomonas maltophilia >gi\_1753197\_dbj\_BAA11872\_ (D83263) dipeptidyl NCBI Description

peptidase IV [Stenotrophomonas maltophilia]

12365 Seq. No.

24520 1.R1040 Contig ID zzp700832489.h1 5'-most EST

BLASTX Method g2655098 NCBI GI BLAST score 842 4.0e-90 E value 445 Match length 40 % identity

(AF023472) peptide transporter [Hordeum vulgare] NCBI Description

Seq. No.

12366

24521 1.R1040 Contig ID

LIB3051-071-Q1-K1-A5 5'-most EST

Seq. No. 12367

24522 1.R1040 Contig ID

2157



seb700652918.hl 5'-most EST BLASTX Method q1076316 NCBI GI 266 BLAST score 7.0e-23 E value 132 Match length 41 % identity drought-induced protein Di19 - Arabidopsis thaliana NCBI Description >gi 469110 emb CAA55321\_ (X78584) Di19 [Arabidopsis thaliana] 12368 Seq. No. 24522 2.R1040 Contig ID  $LIB30\overline{5}1-053-Q1-K2-A10$ 5'-most EST BLASTX g1076316

Method NCBI GI 224 BLAST score 5.0e-18 E value 106 Match length 40 % identity

drought-induced protein Di19 - Arabidopsis thaliana NCBI Description >gi 469110\_emb\_CAA55321\_ (X78584) Di19 [Arabidopsis

thaliana]

12369 Seq. No.

24522 3.R1040 Contig ID

LIB3170-051-Q1-K1-B11 5'-most EST

BLASTX Method q1076316 NCBI GI 217 BLAST score 1.0e-17 E value 73 Match length 47 % identity

drought-induced protein Di19 - Arabidopsis thaliana NCBI Description

>gi 469110\_emb CAA55321\_ (X78584) Di19 [Arabidopsis

thaliana]

12370 Seq. No.

24524 1.R1040 Contig ID 5'-most EST fua701041501.h1

BLASTX Method q3377517 NCBI GI 433 BLAST score 1.0e-42 E value Match length 108 % identity

(AF073361) nitrate transporter NTL1 [Arabidopsis thaliana] NCBI Description

Seq. No. 12371

24552 1.R1040 Contig ID

5'-most EST LIB3051-008-Q1-E1-A3

BLASTX Method NCBI GI g4467139 BLAST score 598 9.0e-62 E value Match length 178 % identity 65



NCBI Description (AL035540) putative protein phosphatase-2c [Arabidopsis thaliana]

Seq. No. 12372

Contig ID 24553\_1.R1040

5'-most EST LIB3170-052-Q1-J1-C2

Method BLASTN
NCBI GI g2921319
BLAST score 680
E value 0.0e+00
Match length 683
% identity 100

NCBI Description Glycine max beta-1,3-glucanase 5 (SGlu5) gene, partial cds

Seq. No. 12373

Contig ID 24559\_1.R1040

5'-most EST uC-gmflminsoy030f10b1

Method BLASTX
NCBI GI g3763932
BLAST score 1475
E value 1.0e-164
Match length 346
% identity 83

NCBI Description (AC004450) putative protein kinase [Arabidopsis thaliana]

Seq. No. 12374

Contig ID 24559 2.R1040 5'-most EST crh700850465.h1

Method BLASTX
NCBI GI g3763932
BLAST score 224
E value 2.0e-18

Match length 71 % identity 62

NCBI Description (AC004450) putative protein kinase [Arabidopsis thaliana]

Seq. No. 12375

Contig ID 24559\_3.R1040 5'-most EST zhf700964361.h1

Method BLASTX
NCBI GI g3763932
BLAST score 216
E value 2.0e-17
Match length 72
% identity 61

NCBI Description (AC004450) putative protein kinase [Arabidopsis thaliana]

Seq. No. 12376

Contig ID 24559\_4.R1040 5'-most EST uC-gmropic029e11b1

Seq. No. 12377

Contig ID 24563\_1.R1040 5'-most EST ssr700558431.h1

Method BLASTX NCBI GI g3643085 BLAST score 304

2159



E value 2.0e-57 Match length 190 % identity 60

NCBI Description (AF075580) protein phosphatase-2C; PP2C [Mesembryanthemum

crystallinum]

Seq. No. 12378

Contig ID 24565\_1.R1040
5'-most EST g4284926
Method BLASTX
NCBI GI g3461836
BLAST score 744
E value 8.0e-79

E value 8.0e Match length 256 % identity 61

NCBI Description (AC005315) putative protein kinase [Arabidopsis thaliana]

>gi\_3927841 (AC005727) putative protein kinase [Arabidopsis

thaliana]

Seq. No. 12379

Contig ID 24569\_1.R1040 5'-most EST eep700866464.h1

Method BLASTX
NCBI GI g2558660
BLAST score 584
E value 6.0e-60
Match length 256
% identity 47

NCBI Description (AC002354) No definition line found [Arabidopsis thaliana]

Seq. No. 12380

Contig ID 24570\_1.R1040 5'-most EST leu701147641.h1

Seq. No.

12381

Contig ID 24570\_2.R1040

5'-most EST LIB3072-021-Q1-E1-D10

Seq. No. 12382

Contig ID 24571\_1.R1040 5'-most EST zhf700964476.h1

Method BLASTX
NCBI GI g3551425
BLAST score 210
E value 4.0e-16
Match length 182
% identity 34

NCBI Description (AB015291) pyrrolidone carboxyl peptidase [Pyrococcus

furiosus]

Seq. No. 12383

Contig ID 24571\_2.R1040 5'-most EST leu701155918.h1

Method BLASTX
NCBI GI g3551425
BLAST score 183
E value 5.0e-13



Match length 185 % identity 32

NCBI Description (AB015291) pyrrolidone carboxyl peptidase [Pyrococcus

furiosus]

Seq. No. 12384

Contig ID 24571 3.R1040

5'-most EST LIB3138-052-Q1-N1-F9

Seq. No. 12385

Contig ID 24571\_4.R1040

5'-most EST ASG3244V4L-01-Q1-E1-A3

Seq. No. 12386

Contig ID 24571\_6.R1040 5'-most EST hrw701061183.h1

Seq. No. 12387

Contig ID 24572 1.R1040

5'-most EST uC-gmrominsoy032b06b1

Method BLASTX
NCBI GI g3334323
BLAST score 392
E value 5.0e-38
Match length 83
% identity 90

NCBI Description GTP-BINDING PROTEIN SAR1A >gi\_1314860 (U56929) Sar1 homolog

[Arabidopsis thaliana] >gi\_2104532\_gb\_AAC78700.1

(AF001308) SAR1/GTP-binding secretory factor [Arabidopsis

thaliana] >gi\_2104550 (AF001535) AGAA.4 [Arabidopsis

thaliana]

Seq. No. 12388

Contig ID 24573\_1.R1040

5'-most EST jC-gmf102220108g01a1

Method BLASTX
NCBI GI g3033400
BLAST score 1429
E value 1.0e-158
Match length 564
% identity 55

NCBI Description (AC004238) putative Ser/Thr protein kinase [Arabidopsis

thaliana]

Seq. No. 12389

Contig ID 24573\_2.R1040 5'-most EST fC-gmro7000749669r1

Method BLASTX
NCBI GI g3033400
BLAST score 497
E value 4.0e-50
Match length 109
% identity 83

NCBI Description (AC004238) putative Ser/Thr protein kinase [Arabidopsis

thaliana]



Contig ID 24573\_3.R1040 5'-most EST wrg700789968.h2

Method BLASTX
NCBI GI g3033400
BLAST score 595
E value 2.0e-61
Match length 154
% identity 81

NCBI Description (AC004238) putative Ser/Thr protein kinase [Arabidopsis

thaliana]

Seq. No. 12391

Contig ID 24574\_1.R1040

5'-most EST uC-gmflminsoy001b08b1

Method BLASTX
NCBI GI g3445416
BLAST score 602
E value 3.0e-62
Match length 202
% identity 68

NCBI Description (Y11154) DEAD box-like RNA helicase [Arabidopsis thaliana]

Seq. No. 12392

Contig ID 24576\_1.R1040 5'-most EST txt700733942.h1

Method BLASTX
NCBI GI g2244749
BLAST score 765
E value 2.0e-81
Match length 209
% identity 68

NCBI Description (Z97335) hydroxymethyltransferase [Arabidopsis thaliana]

Seq. No. 12393

Contig ID 24577\_1.R1040

5'-most EST jC-gm $\overline{f}$ 102220101f09a1

Method BLASTX
NCBI GI g3894158
BLAST score 378
E value 2.0e-36
Match length 146
% identity 46

NCBI Description (AC005312) similar to phloem-specific lectin [Arabidopsis

thaliana]

Seq. No. 12394

Contig ID 24578\_1.R1040

5'-most EST LIB3170-065-Q1-K1-D7

Method BLASTX
NCBI GI g2558938
BLAST score 172
E value 7.0e-12
Match length 71
% identity 48

NCBI Description (AF024625) arm repeat containing protein [Brassica napus]



```
24581 1.R1040
Contig ID
5'-most EST
                  LIB3051-004-Q1-E1-D11
Method
                  BLASTX
                  q4204095
NCBI GI
                  288
BLAST score
                  8.0e-26
E value
                  91
Match length
                   62
% identity
                  (AF030260) CYP94A1 [Vicia sativa]
NCBI Description
                   12396
Seq. No.
                   24581 2.R1040
Contig ID
5'-most EST
                  xpa700794890.h1
Method
                  BLASTX
                   g4204095
NCBI GI
                   141
BLAST score
                   8.0e-09
E value
                   43
Match length
                   65
% identity
                  (AF030260) CYP94A1 [Vicia sativa]
NCBI Description
                   12397
Seq. No.
                   24582 1.R1040
Contig ID
                   LIB3170-058-Q1-K1-E6
5'-most EST
Method
                   BLASTX
                   g3169091
NCBI GI
                   502
BLAST score
                   2.0e-50
E value
                   284
Match length
                   37
% identity
                   (AL023706) hypothetical protein [Schizosaccharomyces pombe]
NCBI Description
                   12398
Seq. No.
                   24583 1.R1040
Contig ID
                   LIB3051-060-Q1-K1-A2
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3249064
                   583
BLAST score
                   2.0e-60
E value
Match length
                   153
                   71
% identity
                   (AC004473) Strong similarity to trehalose-6-phosphate
NCBI Description
                   synthase homolog gb_2245136 from A. thaliana chromosome 4
                   contig gb_Z97344. [Arabidopsis thaliana]
                   12399
Seq. No.
                   24584 1.R1040
Contig ID
5'-most EST
                   asn701137006.hl
                   BLASTX
Method
                   q2665536
NCBI GI
                   326
BLAST score
                   4.0e-30
E value
                   82
Match length
                   87
```

% identity

(AF027808) HCF106 precursor protein [Zea mays] NCBI Description



```
24586 1.R1040
Contia ID
                  LIB3051-034-Q1-K1-E5
5'-most EST
                  BLASTX
Method
                  g3258576
NCBI GI
BLAST score
                   198
                   6.0e-15
E value
Match length
                  82
                   48
% identity
                   (U89959) Unknown protein [Arabidopsis thaliana]
NCBI Description
                   12401
Seq. No.
                   24586 2.R1040
Contig ID
5'-most EST
                   epx701107634.hl
                   BLASTX
Method
                   q3258576
NCBI GI
                   779
BLAST score
                   6.0e-83
E value
Match length
                   220
% identity
                   (U89959) Unknown protein [Arabidopsis thaliana]
NCBI Description
                   12402
Seq. No.
                   24587 1.R1040
Contig ID
                   pcp700995628.h1
5'-most EST
                   BLASTX
Method
                   q833835
NCBI GI
                   886
BLAST score
                   1.0e-95
E value
Match length
                   252
                   63
% identity
                   (U26025) amygdalin hydrolase isoform AH I precursor [Prunus
NCBI Description
                   serotina]
                   12403
Seq. No.
                   24593 1.R1040
Contig ID
                   LIB3051-058-Q1-K2-D9
5'-most EST
Method
                   BLASTN
NCBI GI
                   q495
                   599
BLAST score
                   0.0e+00
E value
                   642
Match length
                   98
 % identity
                   Bos taurus mRNA coding for pre-prolactin. This messenger
NCBI Description
                   RNA was isolated from bovine anterior pituitary glands
                   12404
Seq. No.
                   24624 1.R1040
 Contig ID
                   fua701041289.h1
 5'-most EST
                   BLASTX
 Method
                   q1353516
 NCBI GI
```

Method BLASTX
NCBI GI g135351
BLAST score 356
E value 1.0e-33
Match length 131
% identity 56

NCBI Description (U38651) sugar transporter [Medicago truncatula]



Contig ID 24625\_1.R1040 5'-most EST dpv701099360.h1

Method BLASTX
NCBI GI g1703394
BLAST score 528
E value 1.0e-53
Match length 177
% identity 55

NCBI Description ADP-RIBOSYLATION FACTOR-LIKE PROTEIN 5

>gi\_1150556\_emb\_CAA55338\_ (X78604) ARF-like protein 5

[Rattus norvegicus]

Seq. No. 12406

Contig ID 24625\_2.R1040

5'-most EST LIB3107-079-Q1-K1-A3

Method BLASTX
NCBI GI g114121
BLAST score 215
E value 3.0e-17
Match length 73
% identity 59

NCBI Description ADP-RIBOSYLATION FACTOR 1 >gi\_101185\_pir\_\_B36167

ADP-ribosylation factor 1 - yeast (Saccharomyces

cerevisiae) >gi\_171073 (J03276) ADP-ribosylation factor [Saccharomyces cerevisiae] >gi\_1004303\_emb\_CAA58255\_ (X83276) ADP-ribosylationfactor 2 [Saccharomyces

cerevisiae] >gi\_1431314\_emb\_CAA98769\_ (Z74240) ORF YDL192w

[Saccharomyces cerevisiae]

Seq. No. 12407

Contig ID 24625\_3.R1040 5'-most EST uaw700661926.h1

Method BLASTX
NCBI GI g1703394
BLAST score 236
E value 6.0e-20
Match length 90
% identity 50

NCBI Description ADP-RIBOSYLATION FACTOR-LIKE PROTEIN 5

>gi\_1150556\_emb\_CAA55338\_ (X78604) ARF-like protein 5

[Rattus norvegicus]

Seq. No. 12408

Contig ID 24626\_1.R1040 5'-most EST uxk700673168.h1

Method BLASTN
NCBI GI g3399678
BLAST score 74
E value 3.0e-33
Match length 340
% identity 84

NCBI Description Arabidopsis thaliana chromosome 1 BAC F13M7 sequence,

complete sequence [Arabidopsis thaliana]

Seq. No. 12409

Contig ID 24639\_1.R1040

5'-most EST uC-gmrominsoy052f12b1



Method BLASTN

NCBI GI g499059

BLAST score 63

E value 2.0e-26

Match length 384

% identity 85

NCBI Description C.arietinum mRNA for open reading frame

Seq. No. 12410 Contig ID 24642\_1.R1040 5'-most EST uaw700662744.h1

Method BLASTX
NCBI GI g127112
BLAST score 433
E value 1.0e-42
Match length 129
% identity 60

NCBI Description MAK16 PROTEIN >gi\_73269\_pir\_\_BVBYK6 MAK16 protein - yeast

(Saccharomyces cerevisiae) >gi\_171880 (J03852) MAK16 protein [Saccharomyces cerevisiae] >gi\_595561 (U12980) Mak16p: putative nuclear protein [Saccharomyces cerevisiae]

Seq. No. 12411

Contig ID 24648\_1.R1040 5'-most EST jsh701066794.h1

Method BLASTX
NCBI GI g2252472
BLAST score 675
E value 6.0e-71
Match length 161
% identity 80

NCBI Description (Z97558) argininosuccinate lyase [Arabidopsis thaliana]

Seq. No. 12412

Contig ID 24648\_2.R1040 5'-most EST hyd700725818.h1

Seq. No. 12413

Contig ID 24650 1.R1040 5'-most EST txt700731433.h1

Method BLASTX
NCBI GI g3935151
BLAST score 719
E value 4.0e-76
Match length 198
% identity 64

NCBI Description (AC005106) T25N20.15 [Arabidopsis thaliana]

Seq. No. 12414

Contig ID 24653\_1.R1040

5'-most EST LIB3107-074-Q1-K1-E4

Method BLASTN
NCBI GI g510545
BLAST score 79
E value 2.0e-36
Match length 163
% identity 93



```
NCBI Description P.sativum mRNA for starch branching enzyme I
                  12415
Seq. No.
Contig ID
                  24656 1.R1040
5'-most EST
                  jC-qmle01810082b02a1
Method
                  BLASTX
NCBI GI
                  q2651305
BLAST score
                  231
E value
                  6.0e-19
Match length
                  108
% identity
                  51
                  (AC002336) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  12416
Seq. No.
Contig ID
                  24658 1.R1040
5'-most EST
                  LIB3051-058-Q1-K2-C8
                  BLASTX
Method
                  g2244919
NCBI GI
BLAST score
                  337
                  4.0e-31
E value
Match length
                  171
                  42
% identity
                  (Z97339) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  12417
                  24664 1.R1040
Contig ID
5'-most EST
                  jC-qmf102220128f09a1
Method
                  BLASTX
NCBI GI
                  g2842490
BLAST score
                  316
                  6.0e-29
E value
Match length
                  79
% identity
                  76
                  (AL021749) heat-shock protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  12418
                  24664 2.R1040
Contig ID
                  zhf700958488.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g2842490
BLAST score
                  353
E value
                  2.0e-33
Match length
                  108
% identity
                  64
NCBI Description (ALO21749) heat-shock protein [Arabidopsis thaliana]
Seq. No.
                  12419
                  24667 1.R1040
Contig ID
                  bth700845438.h1
5'-most EST
```

BLASTX Method g1653625 NCBI GI BLAST score 304 2.0e-27 E value 155 Match length 42 % identity

NCBI Description (D90915) hypothetical protein [Synechocystis sp.]



```
12420
Seq. No.
Contig ID
                   24668 1.R1040
                   kl1701212767.hl
5'-most EST
                   BLASTX
Method
                   q2253582
NCBI GI
                   211
BLAST score
                   9.0e-17
E value
                   60
Match length
                   65
% identity
                   (U78721) Serine proteinase (stubble) isolog [Arabidopsis
NCBI Description
                   thaliana]
                   12421
Seq. No.
                   24673 1.R1040
Contig ID
                   zsg701125613.hl
5'-most EST
                   BLASTX
Method
                   q7288
NCBI GI
                   686
BLAST score
                   3.0e-72
E value
                   212
Match length
                   60
% identity
                   (X62142) glycogen phosphorylase 1 [Dictyostelium
NCBI Description
                   discoideum]
                   12422
Seq. No.
                   24676 1.R1040
Contig ID
                   smc700747338.h1
5'-most EST
                   BLASTX
Method
                   g1175381
NCBI GI
                   266
BLAST score
                    4.0e-23
E value
                   127
Match length
                    41
% identity
                   HYPOTHETICAL 44.9 KD PROTEIN C18B11.02C IN CHROMOSOME I
NCBI Description
                   >gi_2130286_pir__S58301 hypothetical protein SPAC18B11.02c
- fission yeast (Schizosaccharomyces pombe)
                    >gi_929888_emb_CAA90587_ (Z50728) hypothetical protein
                    [Schizosaccharomyces pombe]
                    12423
Seq. No.
                    24677 1.R1040
Contig ID
                    LIB3138-045-Q1-N1-D4
5'-most EST
                    BLASTX
Method
                    q2702270
NCBI GI
BLAST score
                    457
                    4.0e-56
E value
                    194
Match length
                    54
 % identity
NCBI Description (AC003033) unknown protein [Arabidopsis thaliana]
 Seq. No.
                    12424
                    24680 1.R1040
```

Contig ID

5'-most EST

LIB3170-033-Q1-K1-F7

Seq. No.

12425

Contig ID 5'-most EST 24683 1.R1040

LIB3051-071-Q1-K1-C6

NCBI Description



```
BLASTX
Method
                   q3941736
NCBI GI
                   187
BLAST score
                   1.0e-13
E value
                   141
Match length
                   37
% identity
NCBI Description (AF109719) BAT3 [Mus musculus]
                   12426
Seq. No.
                   24684 1.R1040
Contig ID
                   LIB30\overline{5}1-016-Q1-E1-B4
5'-most EST
                   BLASTX
Method
                   g2982434
NCBI GI
                   392
BLAST score
E value
                   7.0e-38
Match length
                   158
                   51
% identity
                   (AL022224) putative protein [Arabidopsis thaliana]
NCBI Description
                   12427
Seq. No.
                   24685 1.R1040
Contig ID
                   wrg700790286.h2
5'-most EST
                   BLASTX
Method
                   g3776559
NCBI GI
                   232
BLAST score
                   6.0e-19
E value
                   94
Match length
                   52
% identity
                   (AC005388) Strong similarity to gene F14J9.26 gi_3482933
NCBI Description
                   cdc2 protein kinase homolog from A. thaliana BAC
                   gb AC003970. ESTs gb_Z35332 and gb_F19907 come from this
                   gene. [Arabidopsis thaliana]
                   12428
Seq. No.
                   24689 1.R1040
Contig ID
                   leu701147359.h1
5'-most EST
                   BLASTX
Method
                   q2981475
NCBI GI
                   623
BLAST score
                   1.0e-64
E value
Match length
                   154
                   73
% identity
                    (AF053084) putative cinnamyl alcohol dehydrogenase [Malus
NCBI Description
                   domestica]
                    12429
 Seq. No.
                    24690 1.R1040
 Contig ID
                   uC-qmrominsoy175h02b1
 5'-most EST
 Method
                    BLASTX
                    q3702321
 NCBI GI
 BLAST score
                    986
                    1.0e-107
 E value
                    235
 Match length
                    48
 % identity
```

[Arabidopsis thaliana]

(AC005397) putative TGF-beta receptor interacting protein



Seq. No. 12430
Contig ID 24690
5'-most EST zhf700

24690\_2.R1040 zhf700959686.h1

Method BLASTX
NCBI GI g2494896
BLAST score 465
E value 2.0e-46
Match length 92
% identity 51

NCBI Description EUKARYOTIC TRANSLATION INITIATION FACTOR 3 DELTA SUBUNIT (EIF-3 DELTA) (EIF3 P36) (TGF-BETA RECEPTOR INTERACTING

PROTEIN 1) (TRIP-1) >gi\_2129749\_pir\_\_S60256 TGF-beta receptor interacting protein 1 homolog - Arabidopsis

thaliana >gi\_1036803 (U36765) TGF-beta receptor interacting

protein 1 homolog [Arabidopsis thaliana]

Seq. No. 12431

Contig ID 24690\_3.R1040 5'-most EST hrw701059464.h1

Method BLASTX
NCBI GI g2494896
BLAST score 366
E value 3.0e-35
Match length 71
% identity 92

NCBI Description EUKARYOTIC TRANSLATION INITIATION FACTOR 3 DELTA SUBUNIT

(EIF-3 DELTA) (EIF3 P36) (TGF-BETA RECEPTOR INTERACTING PROTEIN 1) (TRIP-1) >gi\_2129749\_pir\_\_S60256 TGF-beta receptor interacting protein 1 homolog - Arabidopsis

thaliana >gi\_1036803 (U36765) TGF-beta receptor interacting

protein 1 homolog [Arabidopsis thaliana]

Seq. No. 12432

Contig ID 24704\_1.R1040

5'-most EST LIB3051-006-Q1-E1-C3

Method BLASTX
NCBI GI g4335729
BLAST score 212
E value 5.0e-17
Match length 121
% identity 5

NCBI Description (AC006248) putative salt-inducible protein [Arabidopsis

thaliana]

Seq. No. 12433

Contig ID 24706\_1.R1040 5'-most EST seb700653306.h1

Method BLASTX
NCBI GI g4512685
BLAST score 509
E value 5.0e-51
Match length 237
% identity 46

NCBI Description (AC006931) hypothetical protein [Arabidopsis thaliana]

>gi\_4559325\_gb\_AAD22987.1\_AC007087\_6 (AC007087)

hypothetical protein [Arabidopsis thaliana]

NCBI Description



```
Seq. No.
                  12434
Contig ID
                  24708 1.R1040
5'-most EST
                  LIB3051-044-Q1-K1-A7
                  BLASTX
Method
                  q3894159
NCBI GI
                  222
BLAST score
E value
                  4.0e-18
Match length
                  101
% identity
                  (AC005312) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  12435
Seq. No.
Contig ID
                  24709 1.R1040
                  LIB3051-045-Q1-K1-A7
5'-most EST
                  BLASTX
Method
                  g2914703
NCBI GI
BLAST score
                   498
                  2.0e-50
E value
Match length
                  160
                   64
% identity
NCBI Description (AC003974) unknown protein [Arabidopsis thaliana]
                  12436
Seq. No.
Contig ID
                  24711_1.R1040
5'-most EST
                  LIB3051-053-Q1-K2-A7
Method
                  BLASTX
                   g1617274
NCBI GI
BLAST score
                   968
E value
                   1.0e-105
                   239
Match length
% identity
                   75
NCBI Description (Z72152) AMP-binding protein [Brassica napus]
Seq. No.
                   12437
                   24714 1.R1040
Contig ID
5'-most EST
                   kl1701213815.h1
Method
                   BLASTX
NCBI GI
                   q3128215
BLAST score
                   161
E value
                   7.0e-11
Match length
                   135
% identity
                   35
NCBI Description (AC004077) hypothetical protein [Arabidopsis thaliana]
                   12438
Seq. No.
                   24717 1.R1040
Contig ID
                   kl1701213116.h1
5'-most EST
Method
                   BLASTX
                   q3193293
NCBI GI
BLAST score
                   463
                   4.0e-46
E value
                   151
Match length
% identity
                   66
```

[Arabidopsis thaliana]

(AF069298) contains a short region of similarity to another Arabidopsis hypothetical protein F19K23.8 (GB:AC000375)



Seq. No. 12439 Contig ID 24720

Contig ID 24720\_1.R1040 5'-most EST sat701007170.h1

Method BLASTX
NCBI GI g1175408
BLAST score 154
E value 6.0e-10
Match length 99
% identity 27

NCBI Description HYPOTHETICAL 107.3 KD TRP-ASP REPEATS CONTAINING PROTEIN

C31A2.14 IN CHROMOSOME I >gi 2130425\_pir \_\_S58107 hypothetical protein SPAC31A2.14 - fission yeast (Schizosaccharomyces pombe) >gi 914892\_emb\_CAA90472\_

(Z50113) unknown [Schizosaccharomyces pombe]

Seq. No. 12440

Contig ID 24722 1.R1040

5'-most EST LIB3051-014-Q1-E1-E10

Method BLASTX
NCBI GI g400384
BLAST score 164
E value 5.0e-11
Match length 125
% identity 34

NCBI Description NADH-UBIQUINONE OXIDOREDUCTASE B14 SUBUNIT (COMPLEX I-B14)

(CI-B14) >gi\_346536\_pir\_\_S28245 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain CI-B14 - bovine

>gi 240 emb CAA44896 (X63211) NADH dehydrogenase [Bos

taurus]

Seq. No. 12441

Contig ID 24722 2.R1040 5'-most EST kl1701208517.h1

Seq. No. 12442

Contig ID 24724\_1.R1040 5'-most EST uC-gmropic070e08b1

Method BLASTX
NCBI GI 94200044
BLAST score 520
E value 9.0e-53
Match length 152
% identity 64

NCBI Description (AB022732) cytochrome P450 [Glycyrrhiza echinata]

Seq. No. 12443

Contig ID 24724\_2.R1040 5'-most EST uC-gmropic059e01b1

Method BLASTX
NCBI GI g3850630
BLAST score 259
E value 2.0e-22
Match length 113
% identity 44

NCBI Description (AJ012581) cytochrome P450 [Cicer arietinum]



Contig ID 24736\_1.R1040 5'-most EST LIB3107-015-Q1-K1-F11

Seq. No. 12445

Contig ID 24736\_2.R1040

5'-most EST LIB3051-107-Q1-K1-H2

Method BLASTX
NCBI GI g4538993
BLAST score 166
E value 3.0e-11
Match length 48
% identity 62

NCBI Description (AL049481) putative host response protein [Arabidopsis

thaliana]

Seq. No. 12446

Contig ID 24742\_1.R1040

5'-most EST LIB3051-015-Q1-E1-H1

Method BLASTX
NCBI GI g2088652
BLAST score 428
E value 6.0e-42
Match length 146
% identity 60

NCBI Description (AF002109) 26S proteasome regulatory subunit S12 isolog

[Arabidopsis thaliana] >gi\_2351376 (U54561) translation initiation factor eIF2 p47 subunit homolog [Arabidopsis

thaliana]

Seq. No. 12447

Contig ID 24743\_1.R1040 5'-most EST rry700808313.h1

Method BLASTX
NCBI GI g626598
BLAST score 406
E value 4.0e-39
Match length 210
% identity 45

NCBI Description hypothetical protein YHR016c - yeast (Saccharomyces

cerevisiae) >gi 500710 (U10400) Ysc84p [Saccharomyces

cerevisiae]

Seq. No. 12448

Contig ID 24744\_1.R1040

5'-most EST LIB3138-091-Q1-N1-G8

Method BLASTX
NCBI GI g3337352
BLAST score 786
E value 2.0e-83
Match length 412
% identity 46

NCBI Description (AC004481) putative chromatin structural protein Supt5hp

[Arabidopsis thaliana]

Seq. No. 12449

Contig ID 24747 1.R1040

5'-most EST LIB3051-095-Q1-K1-H4

NCBI Description

12454

24784\_1.R1040

Seq. No.

Contig ID



```
Method
                   BLASTX
NCBI GI
                   q4185599
BLAST score
                   225
E value
                   2.0e-18
Match length
                   125
% identity
                   39
NCBI Description
                   (AB010708) Anthocyanin 5-aromatic acyltransferase [Gentiana
Seq. No.
                   12450
                   24750 1.R1040
Contig ID
5'-most EST
                   jex700907353.h1
Method
                   BLASTX
NCBI GI
                   q4510376
BLAST score
                   212
E value
                   7.0e-17
Match length
                   69
% identity
                   57
NCBI Description
                   (AC007017) unknown protein [Arabidopsis thaliana]
                   12451
Seq. No.
Contig ID
                   24753 1.R1040
5'-most EST
                   taw700660235.h1
Method
                   BLASTN
NCBI GI
                   q1256829
BLAST score
                   279
E value
                   1.0e-155
Match length
                   857
% identity
                   86
NCBI Description
                   Phaseolus vulgaris cysteine endopeptidase 1 (PvCEP-1) mRNA,
                   complete cds >gi_2959417_emb_AJ224766_PVA224766 Phaseolus
                   vulgaris mRNA cotyledon cysteine protease
                   12452
Seq. No.
Contig ID
                   24770 1.R1040
5'-most EST
                   LIB3051-091-Q1-K1-F3
Method
                   BLASTX
NCBI GI
                   g3402691
BLAST score
                   314
E value
                   1.0e-28
Match length
                   82
                   72
% identity
                   (AC004697) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   12453
Contig ID
                   24772 1.R1040
5'-most EST
                   LIB3051-094-Q1-K1-D3
Method
                   BLASTX
NCBI GI
                   q2829927
BLAST score
                   673
E value
                   3.0e-70
                   388
Match length
% identity
                   45
```

(AC002291) Unknown protein [Arabidopsis thaliana]

% identity

NCBI Description

51



```
5'-most EST
                  LIB3051-116-Q1-K1-E1
Method
                  BLASTX
                  q4038594
NCBI GI
                  357
BLAST score
                  6.0e-41
E value
Match length
                  102
                  72
% identity
                  (AJ222798) tDET1 protein [Lycopersicon esculentum]
NCBI Description
                  >gi_4454332_emb_CAA11914_ (AJ224356) tDET1 protein
                  [Lycopersicon esculentum]
                  12455
Seq. No.
                  24786 1.R1040
Contig ID
                  LIB3051-095-Q1-K1-B3
5'-most EST
Method
                  BLASTX
                  q3540180
NCBI GI
BLAST score
                  724
E value
                  1.0e-76
Match length
                  212
% identity
                  68
NCBI Description (AC004122) Unknown protein [Arabidopsis thaliana]
                  12456
Seq. No.
Contig ID
                  24819 1.R1040
                  LIB3051-110-Q1-K1-F7
5'-most EST
Method
                  BLASTX
NCBI GI
                  q2505878
BLAST score
                  513
E value
                  4.0e-52
Match length
                  114
% identity
                  82
                  (Y12776) gene5; most likely [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   12457
Contig ID
                   24820 1.R1040
5'-most EST
                  LIB3087-011-Q1-K1-E10
Method
                  BLASTX
NCBI GI
                   q4115936
BLAST score
                   1102
E value
                   1.0e-120
Match length
                   244
                   85
% identity
                  (AF118223) No definition line found [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   12458
                   24822 1.R1040
Contig ID
5'-most EST
                   txt700731413.h1
Method
                   BLASTX
NCBI GI
                   q3548801
BLAST score
                   524
E value
                   6.0e-53
Match length
                   193
```

2175

(ACO05313) putative transmembrane protein [Arabidopsis

thaliana] >gi\_4335768\_gb\_AAD17445\_ (AC006284) putative

integral membrane protein [Arabidopsis thaliana]



```
Seq. No.
                  24842 1.R1040
Contig ID
5'-most EST
                  uC-gmflminsoy056e11b1
                  12460
Seq. No.
Contig ID
                  24850 1.R1040
5'-most EST
                  jC-gmro02910017e04a1
Seq. No.
                  12461
                  24851 1.R1040
Contig ID
5'-most EST
                  leu701148732.h1
Method
                  BLASTX
NCBI GI
                  q2735550
                  222
BLAST score
                  6.0e-18
E value
Match length
                  98
% identity
                  43
NCBI Description (U96638) unc-50 related protein; URP [Rattus norvegicus]
                  12462
Seq. No.
                  24851 2.R1040
Contig ID
                  LIB3109-002-Q1-K2-F4
5'-most EST
Seq. No.
                  12463
                  24853 1.R1040
Contig ID
                  seb700648224.h1
5'-most EST
                  BLASTX
Method
                  q4105697
NCBI GI
BLAST score
                   428
                   3.0e-69
E value
                   165
Match length
% identity
                   78
NCBI Description (AF049870) thaumatin-like protein [Arabidopsis thaliana]
                   12464
Seq. No.
Contig ID
                   24858 1.R1040
5'-most EST
                   eep700869607.h1
Method
                   BLASTX
NCBI GI
                   q1657621
BLAST score
                   1112
E value
                   1.0e-167
Match length
                   373
                   78
% identity
                   (U72505) G6p [Arabidopsis thaliana] >gi 3068711 (AF049236)
NCBI Description
                   putative acyl-coA dehydrogenase [Arabidopsis thaliana]
Seq. No.
                   12465
Contig ID
                   24862 1.R1040
                   LIB3051-102-Q1-K1-B4
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3192881
                   859
BLAST score
```

NCBI GI g3192881
BLAST score 859
E value 2.0e-92
Match length 186
% identity 84

NCBI Description (AF068834) starch synthase [Ipomoea batatas]

% identity



```
Seq. No.
                   24863 1.R1040
Contig ID
                   jex70\overline{0}905092.h1
5'-most EST
Method
                   BLASTX
                   q3402679
NCBI GI
                   468
BLAST score
E value
                   1.0e-46
                   227
Match length
% identity
NCBI Description (AC004697) unknown protein [Arabidopsis thaliana]
Seq. No.
                   12467
Contig ID
                   24864 1.R1040
                   LIB3051-049-Q1-K1-H11
5'-most EST
Method
                   BLASTX
                   a3413707
NCBI GI
BLAST score
                   366
E value
                   2.0e-37
Match length
                   116
% identity
NCBI Description (AC004747) hypothetical protein [Arabidopsis thaliana]
                   12468
Seq. No.
Contig ID
                   24865 1.R1040
                   LIB3051-112-Q1-K1-E10
5'-most EST
Method
                   BLASTX
                   g1865677
NCBI GI
                   832
BLAST score
E value
                   2.0e-89
Match length
                   208
% identity
                   76
                   (Y08568) trehalose-6-phosphate synthase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   12469
Contig ID
                   24867 1.R1040
5'-most EST
                   epx701105710.hl
Method
                   BLASTX
NCBI GI
                   q1764100
BLAST score
                   997
                   1.0e-108
E value
Match length
                   231
% identity
                   83
NCBI Description
                   (U81805) GDP-D-mannose-4,6-dehydratase [Arabidopsis
                   thaliana]
Seq. No.
                   12470
                   24868 1.R1040
Contig ID
                   g5606730
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2282473
                   945
BLAST score
E value
                   1.0e-102
Match length
                   347
                   52
```

NCBI Description (AB005911) xanthine dehydrogenase [Bombyx mori]



```
.12471
Seq. No.
Contig ID
                  24870 1.R1040
5'-most EST
                  LIB3107-057-Q1-K1-C3
Method
                  BLASTX
NCBI GI
                   q3036796
BLAST score
                   545
E value
                   1.0e-55
                   167
Match length
% identity
                   66
                   (AL022373) putative protein [Arabidopsis thaliana]
NCBI Description
                   >gi 3805858 emb CAA21478 (AL031986) putative protein
                   [Arabidopsis thaliana]
                   12472
Seq. No.
                   24876 3.R1040
Contig ID
                   trc700563537.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                   g3461828
                   237
BLAST score
                   1.0e-19
E value
Match length
                   136
% identity
                   38
NCBI Description (AC004138) unknown protein [Arabidopsis thaliana]
Seq. No.
                   12473
Contig ID
                   24878 1.R1040
                   r1r700901507.h1
5'-most EST
Method
                   BLASTX
                   g4154352
NCBI GI
BLAST score
                   264
                   5.0e-23
E value
Match length
                   141
% identity
                   41
NCBI Description
                  (AF110333) PrMC3 [Pinus radiata]
                   12474
Seq. No.
                   24880 1.R1040
Contig ID
5'-most EST
                   uaw700660891.hl
Method
                   BLASTX
NCBI GI
                   q3080417
BLAST score
                   285
E value
                   2.0e-25
Match length
                   74
% identity
                   78
NCBI Description (AL022604) putative protein [Arabidopsis thaliana]
Seq. No.
                   12475
                   24880 3.R1040
Contig ID
5'-most EST
                   zzp700835211.h1
                   12476
Seq. No.
```

24881 1.R1040 Contig ID

5'-most EST LIB3106-085-Q1-K1-E6

Method BLASTX g3005069 NCBI GI BLAST score 710 E value 7.0e-75



Match length 252 % identity 52

NCBI Description (AF043327) N-myristoyltransferase 2 [Mus musculus]

Seq. No. 12477

Contig ID 24885\_1.R1040

5'-most EST LIB3092-008-Q1-K1-D5

Method BLASTX
NCBI GI g2501599
BLAST score 357
E value 2.0e-33
Match length 220
% identity 38

NCBI Description HYPOTHETICAL 29.1 KD PROTEIN W06E11.4 IN CHROMOSOME III

>gi 669022 (U20862) W06E11.4 gene product [Caenorhabditis

elegans]

Seq. No. 12478

Contig ID 24886\_1.R1040 5'-most EST eep700863708.h1

Method BLASTX
NCBI GI g2980795
BLAST score 469
E value 2.0e-46
Match length 166
% identity 54

NCBI Description (AL022197) putative protein [Arabidopsis thaliana]

Seq. No. 12479

Contig ID 24887\_1.R1040 5'-most EST zsg701118390.h1

Method BLASTX
NCBI GI g3603353
BLAST score 384
E value 7.0e-37
Match length 167
% identity 50

NCBI Description (AF074843) peroxisomal targeting signal type 1 receptor

[Arabidopsis thaliana]

Seq. No. 12480

Contig ID 24889\_1.R1040

5'-most EST jC-gmle01810026a02a1

Method BLASTX
NCBI GI g3269292
BLAST score 292
E value 1.0e-25
Match length 71
% identity 72

NCBI Description (AL030978) putative protein [Arabidopsis thaliana]

Seq. No. 12481

Contig ID 24890\_1.R1040 5'-most EST uC-gmropic108e11b1 Method RLASTX

Method BLASTX
NCBI GI g3056593
BLAST score 174



E value 2.0e-12 Match length 67 % identity 51

NCBI Description (AC004255) T1F9.14 [Arabidopsis thaliana]

Seq. No. 12482

Contig ID 24891\_1.R1040 5'-most EST gsv701045404.h1

Method BLASTX
NCBI GI g2293568
BLAST score 289
E value 8.0e-26
Match length 82
% identity 62

NCBI Description (AF012897) HvB12D homolog [Oryza sativa]

Seq. No. 12483

Contig ID 24895\_1.R1040 5'-most EST zhf700952218.h1

Method BLASTX
NCBI GI g1483218
BLAST score 866
E value 4.0e-93
Match length 308
% identity 55

NCBI Description (X99793) induced upon wounding stress [Arabidopsis

thaliana]

Seq. No. 12484

Contig ID 24896\_1.R1040 5'-most EST fde700873028.h1

Method BLASTX
NCBI GI g1762933
BLAST score 156
E value 4.0e-10
Match length 171
% identity 31

NCBI Description (U66263) tumor-related protein [Nicotiana tabacum]

Seq. No. 12485

Contig ID 24896 2.R1040

5'-most EST LIB3051-109-Q1-K1-G1

Method BLASTX
NCBI GI g266323
BLAST score 205
E value 8.0e-16
Match length 123
% identity 37

NCBI Description ALPHA-AMYLASE/SUBTILISIN INHIBITOR (RASI)

>gi\_100651\_pir\_\_S24131 subtilisin/alpha-amylase inhibitor, 20K - rice >gi\_254616\_bbs\_112376 bifunctional

20K - rice >gi\_254616\_bbs\_112376 bifunctional subtilisin/alpha-amylase inhibitor, RASI [Oryza sativa=rice, seeds, bran, Peptide, 176 aa]

Seq. No. 12486

Contig ID 24899\_1.R1040

5'-most EST jC-gmro02910022e12a1



```
Method
                  BLASTX
                  q4455340
NCBI GI
                  307
BLAST score
                  8.0e-30
E value
                  105
Match length
                   64
% identity
                  (AL035522) putative protein [Arabidopsis thaliana]
NCBI Description
                  12487
Seq. No.
                  24899 2.R1040
Contig ID
                   jC-gmle01810094c03a1
5'-most EST
                  BLASTX
Method
                   g4455340
NCBI GI
BLAST score
                   241
                   8.0e-21
E value
                   95
Match length
                   55
% identity
                  (AL035522) putative protein [Arabidopsis thaliana]
NCBI Description
                   12488
Seq. No.
                   24900 1.R1040
Contig ID
                   jC-gmf102220081h08d1
5'-most EST
                   BLASTX
Method
                   g2462745
NCBI GI
BLAST score
                   312
                   2.0e-28
E value
                   118
Match length
                   48
% identity
                  (AC002292) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   12489
Seq. No.
                   24901 1.R1040
Contig ID
                   LIB3170-040-Q1-K1-E9
5'-most EST
Method
                   BLASTX
                   q2246442
NCBI GI
BLAST score
                   211
E value
                   9.0e-17
                   82
Match length
% identity
                   55
                  (U63298) farnesyltransferase alpha subunit [Pisum sativum]
NCBI Description
                   12490
Seq. No.
                   24902 1.R1040
Contig ID
                   fC-qmst700666881a3
5'-most EST
Method
                   BLASTX
                   q541816
NCBI GI
BLAST score
                   983
                   1.0e-107
E value
Match length
                   227
                   81
% identity
                   protein kinase - common ice plant >gi 457689_emb_CAA82990_
NCBI Description
                   (Z30329) protein kinase [Mesembryanthemum crystallinum]
                   12491
Seq. No.
                   24902 2.R1040
Contig ID
```

BLASTX

5'-most EST

Method

LIB3051-108-Q1-K1-G1

Seq. No.

Contig ID



```
a1076632
NCBI GI
BLAST score
                  1181
E value
                  1.0e-164
Match length
                  359
                  82
% identity
                  protein kinase - common tobacco >gi_506534_emb_CAA50374_
NCBI Description
                  (X71057) protein kinase [Nicotiana tabacum]
                  12492
Seq. No.
                  24904 1.R1040
Contig ID
5'-most EST
                  LIB3106-076-Q1-K1-F6
Method
                  BLASTX
NCBI GI
                  g4309734
BLAST score
                  196
                  5.0e-15
E value
Match length
                  81
                  54
% identity
                  (AC006439) putative 26S proteosome regulatory subunit 8
NCBI Description
                  [Arabidopsis thaliana]
                  12493
Seq. No.
                  24918_1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy173h06b1
                  BLASTX
Method
NCBI GI
                  g1945611
BLAST score
                  293
                  2.0e-26
E value
Match length
                  128
                  47
% identity
                  (AB003103) 26S proteasome subunit p55 [Homo sapiens]
NCBI Description
                  >qi 4506221 ref NP 002807.1 pPSMD12 proteasome (prosome,
                  macropain) 26S subunit, non-ATPase,
                  12494
Seq. No.
Contig ID
                  24919 1.R1040
5'-most EST
                  LIB3051-102-Q1-K1-H3
Method
                  BLASTX
                  g4490729
NCBI GI
BLAST score
                  173
E value
                  5.0e-12
                  108
Match length
% identity
NCBI Description (AL035709) hexokinase-like protein [Arabidopsis thaliana]
Seq. No.
                  12495
                  24920 1.R1040
Contig ID
5'-most EST
                  LIB3170-057-Q1-K1-H11
                  BLASTX
Method
NCBI GI
                  q4262241
BLAST score
                   278
E value
                   2.0e-24
Match length
                  113
% identity
                  (AC006200) unknown protein [Arabidopsis thaliana]
NCBI Description
                   12496
```

24922 1.R1040



```
LIB3051-111-Q1-K1-G1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2398533
BLAST score
                  441
                  1.0e-43
E value
                  97
Match length
                  82
% identity
NCBI Description (Y13725) Transcription factor [Arabidopsis thaliana]
                  12497
Seq. No.
                  24923 1.R1040
Contig ID
5'-most EST
                  uC-gmflminsoy084g09b1
Method
                  BLASTX
NCBI GI
                  g4454010
BLAST score
                  1370
                  1.0e-152
E value
                  423
Match length
% identity
                  60
NCBI Description (AL035396) putative protein [Arabidopsis thaliana]
                  12498
Seq. No.
                  24926 1.R1040
Contig ID
5'-most EST
                  LIB3051-010-Q1-E1-H11
Seq. No.
                  12499
                  24931 1.R1040
Contig ID
5'-most EST
                  jC-gmf102220073d03a1
                  BLASTX
Method
                  g2911049
NCBI GI
BLAST score
                  909
                  4.0e-98
E value
Match length
                  300
                  61
% identity
NCBI Description
                  (AL021961) glucosyltransferase -like protein [Arabidopsis
                  thaliana]
                  12500
Seq. No.
                  24932 1.R1040
Contig ID
5'-most EST
                  uaw700664294.hl
Method
                  BLASTX
                  q4406770
NCBI GI
                  1243
BLAST score
                  1.0e-137
E value
                  309
Match length
% identity
                  73
NCBI Description
                  (AC006836) unknown protein [Arabidopsis thaliana]
                   12501
Seq. No.
                  24932 3.R1040
Contig ID
5'-most EST
                  fde700876173.h1
Method
                  BLASTX
NCBI GI
                  q4406770
BLAST score
                   189
E value
                  1.0e-14
Match length
                  71
                  58
% identity
```

NCBI Description (AC006836) unknown protein [Arabidopsis thaliana]

NCBI Description



```
12502
Seq. No.
                   24936 1.R1040
Contig ID
                   LIB3051-032-Q1-K1-G9
5'-most EST
Method
                   BLASTX
                   g1346396
NCBI GI
BLAST score
                   193
E value
                   1.0e-14
                   104
Match length
                   43
% identity
                   PUTATIVE RECEPTOR PROTEIN KINASE ZMPK1 PRECURSOR
NCBI Description
                   >gi 100913 pir S10930 probable receptor protein kinase (EC
                   2.7.1.-) precursor - maize >gi 22432_emb_CAA36611_ (X52384)
                   precursor protein (AA -26 to 791) [Zea mays]
                   >gi_22436_emb_CAA47962_ (X67733) receptor-like protein
kinase [Zea mays] >gi_226927_prf__1611404A receptor protein
                   kinase [Zea mays]
                   12503
Seq. No.
                   24937 1.R1040
Contig ID
                   uaw700666782.h1
5'-most EST
                   BLASTX
Method
                   g2244827
NCBI GI
BLAST score
                   225
E value
                   2.0e-18
Match length
                   69
                   74
% identity
                   (Z97336) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   12504
                   24938 1.R1040
Contig ID
5'-most EST
                   LIB3051-034-Q1-K1-G5
Method
                   BLASTX
NCBI GI
                   g3242708
BLAST score
                   244
                   2.0e-20
E value
Match length
                   113
% identity
                   45
                   (AC003040) putative serine/threonine protein kinase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   12505
                   24938 2.R1040
Contig ID
5'-most EST
                   uC-gmropic071g05b1
Seq. No.
                   12506
                   24939 1.R1040
Contig ID
5'-most EST
                   wvk700686226.h1
Method
                   BLASTX
NCBI GI
                   q627468
                   308
BLAST score
                   3.0e-28
E value
                   141
Match length
                   47
% identity
```

(D13635) KIAA0010 [Homo sapiens]

hypothetical protein 1 - human >gi\_285983\_dbj\_BAA02799\_

NCBI Description



```
Seq. No.
                  12507
                  24940 1.R1040
Contig ID
                  crh700850996.h1
5'-most EST
                  BLASTX
Method
                  q2983690
NCBI GI
                  187
BLAST score
E value
                  5.0e-14
Match length
                  121
% identity
NCBI Description (AE000730) hypothetical protein [Aquifex aeolicus]
                  12508
Seq. No.
                  24941 1.R1040
Contig ID
                  LIB3051-111-Q1-K1-E3
5'-most EST
                  BLASTX
Method
                  g452593
NCBI GI
BLAST score
                   213
                   5.0e-17
E value
Match length
                   67
                   52
% identity
NCBI Description (D21814) ORF [Lilium longiflorum]
                   12509
Seq. No.
                   24944 1.R1040
Contig ID
5'-most EST
                  LIB3051-050-Q1-K1-G8
                  BLASTX
Method
                   g2224927
NCBI GI
BLAST score
                   271
                   7.0e-24
E value
Match length
                   79
                   65
% identity
                   (AF004213) ethylene-insensitive3-like1 [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   12510
                   24945 1.R1040
Contig ID
                   jC-gmle01810012b06a1
5'-most EST
                   BLASTX
Method
                   q3540198
NCBI GI
BLAST score
                   636
                   2.0e-66
E value
                   180
Match length
% identity
                   71
                  (AC004260) Unknown protein [Arabidopsis thaliana]
NCBI Description
                   12511
Seq. No.
                   24949 1.R1040
Contig ID
                   uC-gmflminsoy065c11b1
5'-most EST
Method
                   BLASTN
NCBI GI
                   g2970651
BLAST score
                   376
                   0.0e + 00
E value
Match length
                   696
                   90
% identity
```

Vigna unguiculata ferritin subunit cowpea3 precursor, mRNA,

nuclear gene encoding chloroplast protein, complete cds



```
12512
Seq. No.
Contig ID
                  24951 1.R1040
5'-most EST
                  LIB3051-037-Q1-K1-E7
Method
                  BLASTX
                  g1707015
NCBI GI
                  234
BLAST score
                  2.0e-19
E value
                  134
Match length
                  37
% identity
                  (U78721) protein phosphatase 2C isolog [Arabidopsis
NCBI Description
                  thaliana]
                  12513
Seq. No.
                  24952 1.R1040
Contig ID
5'-most EST
                  uC-gmflminsoy078f12b1
Method
                  BLASTX
                  q100293
NCBI GI
                  688
BLAST score
                   4.0e-72
E value
                  250
Match length
% identity
                   61
                  ribonucleoprotein A, 29K - wood tobacco
NCBI Description
                   >gi 19754 emb CAA43427 (X61113) 29kD A ribonucleoprotein
                   [Nicotiana sylvestris]
Seq. No.
                   12514
                   24952 2.R1040
Contig ID
5'-most EST
                  hyd700731196.h1
Method
                  BLASTX
                   q4056477
NCBI GI
BLAST score
                   421
                   3.0e-41
E value
Match length
                   142
                   37
% identity
                   (AC005896) putative RNA binding protein [Arabidopsis
NCBI Description
                   thaliana]
                   12515
Seq. No.
                   24952 3.R1040
Contig ID
                   jC-gm\overline{l}e01810031e09d1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q1350820
BLAST score
                   204
                   8.0e-16
E value
Match length
                   51
% identity
                   40
                   CHLOROPLAST 30 KD RIBONUCLEOPROTEIN PRECURSOR
NCBI Description
                   >gi_280402_pir__S26203 RNA-binding protein 30 -
                   curled-leaved tobacco >gi_19708_emb_CAA46234_ (X65118) RNA
                   binding protein 30 [Nicotiana plumbaginifolia]
                   12516
Seq. No.
```

Contig ID 24953\_1.R1040 5'-most EST sat701010511.h1

Method BLASTX NCBI GI g2606077 BLAST score 1110



E value 1.0e-122
Match length 264
% identity 78

NCBI Description (AF030301) auxin-induced protein [Helianthus annuus]

Seq. No. 12517

Contig ID 24953 2.R1040 5'-most EST leu701152306.h1

Method BLASTX
NCBI GI g1352461
BLAST score 597
E value 5.0e-62
Match length 136
% identity 81

NCBI Description IN2-2 PROTEIN

Seq. No. 12518

Contig ID 24956\_1.R1040 5'-most EST uC-gmropic047a08b1

Method BLASTX
NCBI GI g3122572
BLAST score 357
E value 6.0e-34
Match length 121
% identity 63

NCBI Description NADH-UBIQUINONE OXIDOREDUCTASE 75 KD SUBUNIT PRECURSOR

(COMPLEX I-75KD) (CI-75KD) (76 KD MITOCHONDRIAL COMPLEX I SUBUNIT) >gi\_1084434\_pir\_\_S52737 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 76K chain precursor - potato >gi\_758340\_emb\_CAA59818\_ (X85808) 76 kDa mitochondrial

complex I subunit [Solanum tuberosum]

Seq. No. 12519

Contig ID 24957 1.R1040

5'-most EST LIB3139-040-P1-N1-A2

Method BLASTX
NCBI GI g3894170
BLAST score 597
E value 7.0e-62
Match length 177
% identity 63

NCBI Description (AC005312) putative glutathione s-transferase [Arabidopsis

thaliana]

Seq. No. 12520

Contig ID 24959\_1.R1040 5'-most EST V4R-01-Q1-B1-G4

Method BLASTX
NCBI GI g1009232
BLAST score 1922
E value 0.0e+00
Match length 484
% identity 79

NCBI Description (L38828) EF-1-alpha-related GTP-binding protein [Nicotiana

tabacum]

Seq. No. 12521



Contig ID 24961\_1.R1040 5'-most EST kmv700739190.h1

Method BLASTX
NCBI GI g2191184
BLAST score 369
E value 2.0e-35
Match length 133
% identity 61

NCBI Description (AF007271) Similar to sodium/hydrogen exchanger; coded for

by A. thaliana cDNA T75860 [Arabidopsis thaliana]

Seq. No. 12522

Contig ID 24962\_1.R1040 5'-most EST epx701104540.h1

Method BLASTX
NCBI GI g3292849
BLAST score 340
E value 2.0e-31
Match length 160
% identity 45

NCBI Description (AJ007582) arginine methyltransferase [Arabidopsis

thaliana]

Seq. No. 12523

Contig ID 24965\_1.R1040 5'-most EST trc700566576.h1

Method BLASTX
NCBI GI g4508076
BLAST score 216
E value 2.0e-17
Match length 97
% identity 42

NCBI Description (AC005882) 55659 [Arabidopsis thaliana]

Seq. No. 12524

Contig ID 25015\_1.R1040 5'-most EST zhf700953214.h1

Method BLASTX
NCBI GI g461753
BLAST score 1829
E value 0.0e+00
Match length 394
% identity 91

NCBI Description ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA HOMOLOG

PRECURSOR >gi 419773 pir S31164 ATP-dependent ClpB

proteinase regulatory chain homolog precursor, chloroplast - garden pea >gi\_169128 (L09547) nuclear encoded precursor

to chloroplast protein [Pisum sativum]

Seq. No. 12525

Contig ID 25067\_2.R1040 5'-most EST eep700869985.h1

Method BLASTX
NCBI GI g3953470
BLAST score 236
E value 9.0e-20
Match length 64



% identity (AC002328) F20N2.15 [Arabidopsis thaliana] NCBI Description

12526 Seq. No.

25067 3.R1040 Contig ID

5'-most EST LIB3107-010-Q1-K1-G8

12527 Seq. No.

25096 1.R1040 Contig ID kl1701211709.h1 5'-most EST

Method BLASTN NCBI GI g170775 BLAST score 409 0.0e + 00E value Match length 805 88 % identity

Wheat translation elongation factor 1 alpha-subunit (TEF1) NCBI Description

mRNA, complete cds

12528 Seq. No.

25234 1.R1040 Contig ID hyd700725459.h1 5'-most EST

Method BLASTX g3355474 NCBI GI BLAST score 1040 E value 1.0e-113 Match length 267 77 % identity

NCBI Description (AC004218) unknown protein [Arabidopsis thaliana]

Seq. No.

25297 1.R1040 Contig ID 5'-most EST kmv700744005.h1

12529

Method BLASTN NCBI GI q169127 BLAST score 600 E value 0.0e+00Match length 872 92 % identity

Pisum sativum (clone pCLp) nuclear encoded precursor to NCBI Description

chloroplast protein mRNA, complete cds

12530 Seq. No.

25297 2.R1040 Contig ID

jC-gmle01810070f02d1 5'-most EST

Method BLASTN NCBI GI g169127 BLAST score 114 E value 4.0e-57 Match length 194 90 % identity

Pisum sativum (clone pCLp) nuclear encoded precursor to NCBI Description

chloroplast protein mRNA, complete cds

12531 Seq. No.

25334 1.R1040 Contig ID 5'-most EST  $g4396\overline{5}98$ 

Match length

% identity

70

73



```
Method
                   BLASTN
NCBI GI
                   g452768
BLAST score
                   541
E value
                   0.0e+00
Match length
                   762
% identity
NCBI Description P.acutifolius alcohol dehydrogenase-1F mRNA, complete CDS
Seq. No.
                   12532
Contig ID
                   25334 2.R1040
5'-most EST
                   bth700849406.h1
Seq. No.
                   12533
                   25388 1.R1040
Contia ID
                   kl1701206427.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3875246
BLAST score
                   413
E value
                   1.0e-40
Match length
                   124
% identity
                   47
                   (Z81490) similar to WD domain, G-beta repeats (2 domains);
NCBI Description
                   cDNA EST EMBL: T00482 comes from this gene; cDNA EST
                   EMBL:T00923 comes from this gene; cDNA EST yk449d4.3 comes
                   from this gene; cDNA EST yk449d4.5 comes from this gene;
Seq. No.
                   12534
Contig ID
                   25421_1.R1040
5'-most EST
                   uC-gmrominsoy312q12b1
Method
                   BLASTX
NCBI GI
                   g2832642
BLAST score
                   337
E value
                   2.0e-31
Match length
                   158
% identity
                  (AL021710) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   12535
Contig ID
                   25421 2.R1040
5'-most EST
                   LIB3051-018-01-E1-B2
Method
                   BLASTX
NCBI GI
                   g2832642
BLAST score
                   140
E value
                   1.0e-08
Match length
                   62
% identity
                   47
NCBI Description (AL021710) putative protein [Arabidopsis thaliana]
Seq. No.
                   12536
Contig ID
                   25430 1.R1040
5'-most EST
                  LIB30\overline{5}1-010-Q1-E1-B9
Method
                  BLASTX
NCBI GI
                  g3790585
BLAST score
                  298
E value
                  5.0e-27
```



NCBI Description (AF079181) RING-H2 finger protein RHFla [Arabidopsis thaliana]

Seq. No. 12537

Contig ID 25436 1.R1040

5'-most EST LIB3138-031-Q1-N1-H4

Method BLASTX
NCBI GI g2842482
BLAST score 246
E value 1.0e-20
Match length 73
% identity 62

NCBI Description (AL021749) protein phosphatase 2C-like protein [Arabidopsis

thaliana]

Seq. No. 12538

Contig ID 25442 1.R1040

5'-most EST LIB3051-013-Q1-E1-A2

Method BLASTX
NCBI GI g2623295
BLAST score 573
E value 5.0e-59
Match length 134
% identity 79

NCBI Description (AC002409) hypothetical protein [Arabidopsis thaliana]

Seq. No. 12539

Contig ID 25444 2.R1040

5'-most EST LIB3139-021-P1-N1-G6

Method BLASTX
NCBI GI g4539453
BLAST score 249
E value 2.0e-21
Match length 63
% identity 68

NCBI Description (AL049500) putative protein [Arabidopsis thaliana]

Seq. No. 12540

Contig ID 25453\_1.R1040

5'-most EST LIB3051-019-Q1-E1-H8

Method BLASTX
NCBI GI g2191150
BLAST score 431
E value 1.0e-42
Match length 105
% identity 32

NCBI Description (AF007269) similar to mitochondrial carrier family

[Arabidopsis thaliana]

Seq. No. 12541

Contig ID 25468\_1.R1040 5'-most EST asn701139947.h1

Method BLASTX
NCBI GI g1103318
BLAST score 828
E value 1.0e-88
Match length 282



Seq. No. 12542

Contig ID 25472\_1.R1040 5'-most EST uC-gmropic057h07b1

Method BLASTX
NCBI GI g2244965
BLAST score 242
E value 3.0e-20
Match length 96
% identity 53

NCBI Description (Z97340) unnamed protein product [Arabidopsis thaliana]

Seq. No. 12543

Contig ID 25474 1.R1040 5'-most EST seb700651227.h1

Method BLASTX
NCBI GI g140496
BLAST score 174
E value 4.0e-12
Match length 176
% identity 32

NCBI Description HYPOTHETICAL 42.5 KD PROTEIN IN TSM1-ARE1 INTERGENIC REGION

>gi\_83226\_pir\_\_S19457 probable membrane protein YCR044c yeast (Saccharomyces cerevisiae) >gi\_1907186\_emb\_CAA42292\_

(X59720) YCR044c, len:357 [Saccharomyces cerevisiae]

Seq. No. 12544

Contig ID 25474 2.R1040

5'-most EST LIB3170-030-Q1-K1-E6

Method BLASTX
NCBI GI g3168910
BLAST score 172
E value 1.0e-11
Match length 202
% identity 29

NCBI Description (AF068718) No definition line found [Caenorhabditis

elegans]

Seq. No. 12545

Contig ID 25474\_3.R1040 5'-most EST awf700837978.h1

Seq. No. 12546

Contig ID 25482 1.R1040

5'-most EST uC-qmrominsoy123a01b1

Method BLASTX
NCBI GI g2828294
BLAST score 507
E value 2.0e-51
Match length 144
% identity 45

NCBI Description (AL021687) putatative protein [Arabidopsis thaliana]

NCBI Description

aestivum]



- 12547 Seq. No. 25484 1.R1040 Contig ID LIB3138-103-Q1-N1-C8 5'-most EST BLASTX Method g3212866 NCBI GI 260 BLAST score 4.0e-22 E value 177 Match length % identity 37 (AC004005) unknown protein [Arabidopsis thaliana] NCBI Description 12548 Seq. No. 25484 2.R1040 Contig ID 5'-most EST g4290659 Method BLASTX g4544369 NCBI GI 175 BLAST score 2.0e-12 E value 91 Match length 43 % identity (AC006920) hypothetical protein [Arabidopsis thaliana] NCBI Description 12549 Seq. No. 25484 3.R1040 Contig ID 5'-most EST awf700837450.h1 BLASTX Method g3212866 NCBI GI 128 BLAST score 2.0e-11 E value 65 Match length 65 % identity (AC004005) unknown protein [Arabidopsis thaliana] NCBI Description 12550 Seq. No. 25486 1.R1040 Contig ID 5'-most EST uaw700661911.hl Method BLASTX q2146740 NCBI GI 331 BLAST score E value 4.0e-39 179 Match length 47 % identity inner mitochondrial membrane protein - Arabidopsis thaliana NCBI Description >qi 603056 (U18126) inner mitochondrial membrane protein [Arabidopsis thaliana] 12551 Seq. No. 25490 1.R1040 Contig ID 5'-most EST trc700563891.hl BLASTX Method NCBI GI q951453 BLAST score 234 2.0e-19 E value Match length 85 % identity 55

2193

(M95746) initiation factor (iso)4f p82 subunit [Triticum



12552 Seq. No. 25492 2.R1040 Contig ID rca700997231.hl 5'-most EST BLASTX Method q4006876 NCBI GI 114 BLAST score 5.0e-10 E value 106 Match length 42 % identity (Z99707) hypothetical protein [Arabidopsis thaliana] NCBI Description

Seq. No. 12553

Contig ID 25494\_1.R1040

5'-most EST LIB3106-094-Q1-K1-H11

Method BLASTX
NCBI GI g2498981
BLAST score 322
E value 1.0e-29
Match length 125
% identity 47

NCBI Description TRANSCRIPTION INITIATION FACTOR TFIID 31 KD SUBUNIT

(TAFII-31) (TAFII-32) (TAFII32) >gi\_2136305\_pir\_\_I39141 transcription factor TFIID 32K chain TAFII32 - human >gi\_841308 (U21858) TAFII32 precursor [Homo sapiens] >gi\_882393 (U25112) TBP-associated factor TAFII31 [Homo sapiens] >gi\_940151 (U30504) TAFII31 [Homo sapiens]

>gi 1098347 prf 2115400A transcription factor

IID:SUBUNIT=32kD [Homo sapiens]

>gi\_4507351\_ref\_NP\_003178.1\_pTAF2G\_ TATA box binding

protein (TBP)-associated factor, RNA polymerase II, G, 32kD

Seq. No. 12554

Contig ID 25497\_1.R1040 5'-most EST rlr700898749.h1

Method BLASTX
NCBI GI g4432849
BLAST score 475
E value 2.0e-47
Match length 201
% identity 47

NCBI Description (AC006300) hypothetical protein [Arabidopsis thaliana]

>gi\_4567241\_gb\_AAD23655.1\_AC007070\_4 (AC007070)

hypothetical protein [Arabidopsis thaliana]

Seq. No. 12555

Contig ID 25515\_1.R1040 5'-most EST rca700998009.h1

Method BLASTX
NCBI GI g3413719
BLAST score 259
E value 2.0e-22
Match length 150
% identity 45

NCBI Description (AC004747) unknown protein [Arabidopsis thaliana]

>gi\_3643592 (AC005395) unknown protein [Arabidopsis

thaliana]



Seq. No. 12556 25524 1.R1040 Contig ID  $LIB30\overline{5}1-038-Q1-K1-D5$ 5'-most EST Method BLASTX NCBI GI g1149595 BLAST score 168 E value 1.0e-11 Match length 51

65

% identity NCBI Description (Z49860) 1-acyl-sn-glycerol-3-phosphate acyltransferase

[Brassica napus]

12557 Seq. No.

25528 1.R1040 Contig ID 5'-most EST nci700975691.hl

Method BLASTN NCBI GI q732904 BLAST score 300 E value 1.0e-168 Match length 712 % identity 86

NCBI Description P.sativum mRNA for pollen allergen-like protein

Seq. No. 12558

Contig ID 25530 1.R1040

5'-most EST LIB3139-060-P1-N1-A3

Method BLASTX NCBI GI q4567197 BLAST score 400 E value 8.0e-39 Match length 192 % identity 47

NCBI Description (AC007168) unknown protein [Arabidopsis thaliana]

Seq. No. 12559

Contig ID 25534 1.R1040

5'-most EST LIB3051-045-Q1-K1-G3

Method BLASTX NCBI GI q3249070 BLAST score 304 E value 1.0e-27 Match length 151 % identity 49

(AC004473) Contains similarity to siah binding protein 1 NCBI Description (SiahBP1) gb U51586 from Homo sapiens. ESTs gb T43314,

gb\_T43315 and gb\_R90521, gb\_T75905 [Arabidopsis thaliana]

Seq. No. 12560

25534 2.R1040 Contig ID 5'-most EST  $wvk70\overline{0}682717.h1$ 

Seq. No. 12561

Contig ID 25536 1.R1040

5'-most EST jC-gmst02400073a04a1

Method BLASTX NCBI GI q3763921



BLAST score 1.0e-100 E value 291 Match length 66 % identity (AC004450) putative pirin protein [Arabidopsis thaliana] NCBI Description Seq. No. 12562 25536 3.R1040 Contig ID 5'-most EST LIB3106-037-Q1-K1-E3 BLASTX Method NCBI GI g3763921 BLAST score 221 E value 4.0e-18 65 Match length % identity (AC004450) putative pirin protein [Arabidopsis thaliana] NCBI Description Seq. No. 12563 25538 5.R1040 Contig ID LIB3170-080-Q1-K1-G11 5'-most EST BLASTX Method NCBI GI g2911067 BLAST score 221 E value 4.0e-18 54 Match length 78 % identity (AL021960) UV-damaged DNA-binding protein- like NCBI Description [Arabidopsis thaliana] Seq. No. 12564 Contig ID 25539 1.R1040 5'-most EST uC-gmflminsoy049f01b1 BLASTX Method NCBI GI g3142300 BLAST score 241 E value 5.0e-20 Match length 63 % identity 73 NCBI Description (AC002411) Contains similarity to pre-mRNA processing protein PRP39 gb L29224 from S. cerevisiae. ESTs gb R64908 and gb T88158, gb N38703 and gb AA651043 come from this gene. [Arabidopsis thaliana] Seq. No. 12565 25539 2.R1040 Contig ID LIB3139-052-P1-N1-A2 5'-most EST Method BLASTX NCBI GI q3142300 BLAST score 457

3.0e-76 E value Match length 216 70 % identity

(AC002411) Contains similarity to pre-mRNA processing NCBI Description protein PRP39 gb L29224 from S. cerevisiae. ESTs gb\_R64908 and gb T88158, gb N38703 and gb AA651043 come from this

gene. [Arabidopsis thaliana]



12566 Seq. No.

25539 4.R1040

Contig ID 5'-most EST q5606000 Method BLASTX g3142300 NCBI GI BLAST score 466

E value 9.0e-47 Match length 110 % identity 77

(AC002411) Contains similarity to pre-mRNA processing NCBI Description

protein PRP39 gb\_L29224 from S. cerevisiae. ESTs gb\_R64908 and gb\_T88158, gb\_N38703 and gb\_AA651043 come from this

gene. [Arabidopsis thaliana]

12567 Seq. No.

Contig ID 25539 6.R1040 5'-most EST kl1701207729.h1

Method BLASTX NCBI GI g3142300 BLAST score 233 E value 1.0e-25 Match length 68 85 % identity

NCBI Description (AC002411) Contains similarity to pre-mRNA processing

protein PRP39 gb L29224 from S. cerevisiae. ESTs gb\_R64908 and gb T88158, gb N38703 and gb AA651043 come from this

gene. [Arabidopsis thaliana]

12568 Seq. No.

Contig ID 25539 8.R1040 kl1701209461.hl 5'-most EST

Method BLASTX q3142300 NCBI GI BLAST score 256 E value 5.0e-22 Match length 96 % identity 70

(AC002411) Contains similarity to pre-mRNA processing NCBI Description

protein PRP39 gb L29224 from S. cerevisiae. ESTs gb\_R64908 and gb\_T88158, gb\_N38703 and gb\_AA651043 come from this

gene. [Arabidopsis thaliana]

12569 Seq. No.

Contig ID 25541 1.R1040

LIB3138-015-Q1-N2-G4 5'-most EST

Method BLASTX NCBI GI q2598589 BLAST score 821 E value 8.0e-88 Match length 220 % identity

(Y15367) MtN19 [Medicago truncatula] NCBI Description

12570 Seq. No.

25541 2.R1040 Contig ID

5'-most EST  $LIB30\overline{5}1-046-Q1-K1-G6$ 

Method BLASTX

Method

NCBI GI

BLASTX g1495366



```
g2598589
NCBI GI
                  192
BLAST score
                  2.0e-14
E value
Match length
                  49
                  73
% identity
NCBI Description (Y15367) MtN19 [Medicago truncatula]
                  12571
Seq. No.
                   25549 1.R1040
Contig ID
                  LIB3051-048-Q1-K1-B2
5'-most EST
                  BLASTN
Method
                   g169980
NCBI GI
BLAST score
                   41
                   7.0e-14
E value
Match length
                   169
% identity
                   86
NCBI Description Soybean heat-shock protein (Gmhsp26-A) gene, complete cds
                   12572
Seq. No.
                   25550 1.R1040
Contia ID
                   LIB3170-038-Q1-K1-F6
5'-most EST
                   12573
Seq. No.
                   25551 1.R1040
Contig ID
                   asn70\overline{1}134637.h2
5'-most EST
Method
                   BLASTX
                   g2982459
NCBI GI
BLAST score
                   528
                   1.0e-53
E value
                   144
Match length
                   69
% identity
                   (AL022223) putative protein [Arabidopsis thaliana]
NCBI Description
                   12574
Seq. No.
                   25551 2.R1040
Contig ID
                   rca701002626.hl
5'-most EST
                   12575
Seq. No.
                   25551 3.R1040
Contig ID
                   LIB30\overline{5}1-048-Q1-K1-F5
5'-most EST
                   BLASTX
Method
                   q2982459
NCBI GI
                   144
BLAST score
                   5.0e-09
E value
                   48
Match length
                   60
% identity
NCBI Description (AL022223) putative protein [Arabidopsis thaliana]
                   12576
Seq. No.
 Contig ID
                    25551 4.R1040
 5'-most EST
                   ncj700983487.hl
                    12577
 Seq. No.
 Contig ID
                    25555 1.R1040
                    q5606685
 5'-most EST
```



```
BLAST score
                  517
E value
                  4.0e-52
Match length
                  298
                  35
% identity
NCBI Description (Z69370) nitrite transporter [Cucumis sativus]
Seq. No.
                  12578
Contig ID
                  25555 2.R1040
5'-most EST
                  jex700903661.h1
Method
                  BLASTX
NCBI GI
                  g2213590
BLAST score
                  236
E value
                  9.0e-20
Match length
                  139
% identity
                  37
NCBI Description (AC000348) T7N9.10 [Arabidopsis thaliana]
                  12579
Seq. No.
                  25556 1.R1040
Contig ID
5'-most EST
                  LIB3139-063-P1-N1-H10
Method
                  BLASTX
NCBI GI
                  g2760321
BLAST score
                  1177
E value
                  1.0e-129
Match length
                  301
% identity
                  73
NCBI Description (AC002130) F1N21.6 [Arabidopsis thaliana]
Seq. No.
                  12580
Contig ID
                  25556 2.R1040
5'-most EST
                  kl1701212822.h1
Seq. No.
                  12581
Contig ID
                  25558 1.R1040
5'-most EST
                  LIB3051-049-Q1-K1-D3
                  12582
Seq. No.
Contig ID
                  25560 1.R1040
5'-most EST
                  g5753634
                  BLASTX
Method
NCBI GI
                  g2369690
BLAST score
                  351
E value
                  5.0e-33
                  99
Match length
% identity
                  70
NCBI Description (Y11988) FPF1 protein [Arabidopsis thaliana]
Seq. No.
                  12583
Contig ID
                  25560 2.R1040
5'-most EST
                  LIB3170-039-Q1-K1-E7
Method
                  BLASTX
NCBI GI
                  g2370459
```

Method BLASTX
NCBI GI g2370459
BLAST score 337
E value 3.0e-31
Match length 108
% identity 64

NCBI Description (Y11987) FPF1 protein [Sinapis alba]



```
12584
Seq. No.
                  25560 3.R1040
Contig ID
5'-most EST
                  dpv701101140.h1
Seq. No.
                  12585
                  25560 4.R1040
Contig ID
5'-most EST
                  kl1701214626.h1
Method
                  BLASTX
NCBI GI
                  g2369690
BLAST score
                  347
E value
                  1.0e-32
Match length
                  99
                  72
% identity
NCBI Description (Y11988) FPF1 protein [Arabidopsis thaliana]
                  12586
Seq. No.
Contig ID
                  25562 1.R1040
5'-most EST
                  uaw700663123.h1
Method
                  BLASTX
NCBI GI
                  g2191154
BLAST score
                  821
                  1.0e-143
E value
Match length
                  404
% identity
                   65
NCBI Description
                  (AF007269) A IG002N01.11 gene product [Arabidopsis
                  thaliana]
Seq. No.
                  12587
                  25562 2.R1040
Contig ID
                  rlr700895650.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3702323
BLAST score
                  1190
                  0.0e + 00
E value
Match length
                   424
                  79
% identity
NCBI Description (AC005397) unknown protein [Arabidopsis thaliana]
                  12588
Seq. No.
Contig ID
                  25567 1.R1040
                  LIB3051-050-Q1-K1-C11
5'-most EST
Method
                  BLASTX
NCBI GI
                  q3080420
BLAST score
                   345
E value
                   5.0e-54
Match length
                  245
% identity
                  52
                  (AL022604) putative sugar transporter protein [Arabidopsis
NCBI Description
                  thaliana]
                  12589
```

Seq. No.

Contig ID

25578 1.R1040

5'-most EST

LIB3170-044-Q1-K1-C6

Seq. No.

12590

Contig ID

25585 1.R1040



```
jC-qmf102220094e04a1
5'-most EST
Method
                  BLASTX
                  a3115374
NCBI GI
                  680
BLAST score
                  3.0e-71
E value
                  354
Match length
                  43
% identity
NCBI Description (AF002016) acyl CoA oxidase homolog [Cucurbita sp.]
                  12591
Seq. No.
                  25588_1.R1040
Contig ID
                  uC-gmrominsoy186g07b1
5'-most EST
                  BLASTX
Method
NCBI GI
                   q4200165
                   648
BLAST score
                   1.0e-177
E value
                   500
Match length
                   66
% identity
NCBI Description (Y16262) neutral invertase [Daucus carota]
                   12592
Seq. No.
                   25588_3.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy153e06b1
Seq. No.
                   12593
                   25590 1.R1040
Contig ID
                   LIB3051-061-Q1-K1-G11
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3128194
BLAST score
                   390
                   6.0e-38
E value
                   117
Match length
% identity
                  (AC004521) putative heme A: farnesyltransferase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   12594
                   25597 1.R1040
Contig ID
5'-most EST
                   LIB3170-026-Q1-K1-D7
Method
                   BLASTX
NCBI GI
                   q166878
BLAST score
                   447
E value
                   5.0e-44
Match length
                   171
% identity
NCBI Description (M95796) St12p protein [Arabidopsis thaliana]
Seq. No.
                   12595
                   25597 2.R1040
Contig ID
                   LIB30\overline{5}1-062-Q1-K1-G7
5'-most EST
Method
                   BLASTX
                   q166878
NCBI GI
                   210
BLAST score
                   1.0e-16
E value
                   98
Match length
                   49
% identity
```

NCBI Description (M95796) St12p protein [Arabidopsis thaliana]



```
Seq. No.
                   12596
                   25598 1.R1040
Contig ID
                  uxk70\overline{0}668850.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                   g1707015
BLAST score
                   273
                   2.0e-47
E value
Match length
                   157
% identity
                   63
NCBI Description
                  (U78721) protein phosphatase 2C isolog [Arabidopsis
                  thaliana]
                   12597
Seq. No.
                   25601 1.R1040
Contig ID
5'-most EST
                   LIB3051-063-Q1-K1-B4
Method
                   BLASTX
NCBI GI
                   q3450842
BLAST score
                   320
E value
                   1.0e-29
Match length
                   122
% identity
                   51
                  (AF080436) mitogen activated protein kinase kinase [Oryza
NCBI Description
                   12598
Seq. No.
Contig ID
                   25604 1.R1040
                  LIB30\overline{5}1-063-Q1-K1-D1
5'-most EST
Seq. No.
                   12599
Contig ID
                   25605 1.R1040
                   LIB3170-046-Q1-K1-B12
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4206209
BLAST score
                   414
                   1.0e-40
E value
                   89
Match length
                   90
% identity
NCBI Description
                   (AF071527) putative glucan synthase component [Arabidopsis
                   thaliana] >gi 4263042 gb AAD15311 (AC005142) putative
                   glucan synthase component [Arabidopsis thaliana]
                   12600
Seq. No.
Contig ID
                   25606 1.R1040
5'-most EST
                   LIB3170-046-Q1-K1-A12
Method
                   BLASTX
NCBI GI
                   q136636
BLAST score
                   283
E value
                   3.0e-25
Match length
                   70
```

% identity 74

NCBI Description

UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1 (UBIQUITIN-PROTEIN

LIGASE 1) (UBIQUITIN CARRIER PROTEIN 1)

>gi\_1076424\_pir\_\_S43781 ubiquitin-conjugating enzyme UBC1 -Arabidopsis thaliana >gi\_442594\_pdb\_1AAK\_ Ubiquitin Conjugating Enzyme (E.C.6.3.2.19) >gi 2981894 pdb 2AAK Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana



>gi\_166924 (M62721) ubiquitin carrier protein [Arabidopsis
thaliana] >gi\_431260 (L19351) ubiquitin conjugating enzyme
[Arabidopsis thaliana]

Seq. No. 12601 Contig ID 25612 1.R1040 LIB3170-050-Q1-K1-D6 5'-most EST BLASTX Method NCBI GI q3954807 BLAST score 349 E value 2.0e-38 Match length 143 % identity NCBI Description (AJ011862) flavonoid 3',5'-hydroxylase [Catharanthus roseus] 12602 Seq. No. Contig ID 25615 1.R1040 5'-most EST LIB3170-062-Q1-J1-A12 Method BLASTX g3377517 NCBI GI BLAST score 376 E value 4.0e-36 Match length 101 % identity 67 NCBI Description (AF073361) nitrate transporter NTL1 [Arabidopsis thaliana] Seq. No. 12603 25616 1.R1040 Contig ID 5'-most EST jC-gmro02910025g07d1 Seq. No. 12604 Contig ID 25618 1.R1040 5'-most EST LIB3051-070-Q1-K1-A8 Method BLASTX NCBI GI q629669 BLAST score 175 E value 2.0e-12 Match length 88 % identity 44 NCBI Description hypothetical protein - tomato 12605 Seq. No. 25620 1.R1040 Contig ID 5'-most EST LIB3051-070-Q1-K1-F2 Method BLASTN NCBI GI g3869071 BLAST score 50 E value 5.0e-19

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MIL23, complete sequence [Arabidopsis thaliana]

Seq. No. 12606

Match length

% identity

Contig ID 25630 1.R1040 5'-most EST LIB3051-071-Q1-K1-G7



```
12607
Seq. No.
                  25635 1.R1040
Contig ID
                  LIB3051-073-Q1-K1-H9
5'-most EST
Seq. No.
                  12608
                  25644 1.R1040
Contig ID
                  LIB3170-056-Q1-K1-H2
5'-most EST
                   BLASTX
Method
                   g2244763
NCBI GI
BLAST score
                   683
                   8.0e-72
E value
                   211
Match length
                   65
% identity
                   (Z97335) A6 anther-specific protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   12609
                   25649 1.R1040
Contig ID
                   LIB3051-084-Q1-K1-E4
5'-most EST
                   12610
Seq. No.
                   25649 2.R1040
Contig ID
                   V4R-02-Q1-B1-A2
5'-most EST
                   BLASTN
Method
                   g2924733
NCBI GI
                   34
BLAST score
                   2.0e-09
E value
                   94
Match length
% identity
                   89
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MUF9, complete sequence [Arabidopsis thaliana]
Seq. No.
                   12611
                   25649_3.R1040
Contig ID
                   uC-gmropic113c10b1
 5'-most EST
                   BLASTN
Method
                   g2924733
NCBI GI
                   34
 BLAST score
                   1.0e-09
 E value
                   94
 Match length
                   89
 % identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
 NCBI Description
                   MUF9, complete sequence [Arabidopsis thaliana]
                   12612
 Seq. No.
                   25650_1.R1040
 Contig ID
                   LIB3051-084-Q1-K1-F8
 5'-most EST
                   BLASTX
 Method
                   q2827714
 NCBI GI
                    298
 BLAST score
                    6.0e-27
```

E value 6.0eMatch length 136
% identity 46

NCBI Description (AL021684) receptor protein kinase - like protein

[Arabidopsis thaliana]

Seq. No. 12613

Match length

% identity

117

56



```
25651 1.R1040
.. Contig ID
                   LIB3170-056-Q1-K1-B10
5'-most EST
                   BLASTX
Method
                   g3176715
NCBI GI
                   611
BLAST score
                   2.0e-63
E value
                   166
Match length
                   73
 % identity
                    (AC002392) putative receptor-like protein kinase
NCBI Description
                    [Arabidopsis thaliana]
                    12614
 Seq. No.
                    25652 1.R1040
 Contig ID
                   LIB3170-053-Q1-K1-C10
 5'-most EST
 Method
                    BLASTX
                    g2244899
 NCBI GI
                    324
 BLAST score
                    5.0e-30
 E value
                    71
 Match length
                    82
 % identity
                   (Z97338) similar to UFD1 protein [Arabidopsis thaliana]
 NCBI Description
                    12615
 Seq. No.
                    25658 1.R1040
 Contig ID
                    LIB3170-056-Q1-K1-A11
 5'-most EST
 Method
                    BLASTX
                    g1778101
 NCBI GI
                    470
 BLAST score
                    1.0e-46
 E value
                    100
 Match length
 % identity
                    84
                   (U64891) expansin [Pinus taeda]
 NCBI Description
                    12616
 Seq. No.
                    25658_2.R1040
 Contig ID
                    LIB3051-082-Q1-K1-A5
 5'-most EST
                    12617
 Seq. No.
                    25659 1.R1040
 Contig ID
 5'-most EST
                    yza700763932.hl
                    BLASTX
 Method
                    q1652104
 NCBI GI
 BLAST score
                    568
                    2.0e-58
 E value
                    220
 Match length
                    49
 % identity
                   (D90902) hypothetical protein [Synechocystis sp.]
 NCBI Description
                    12618
  Seq. No.
                    25660 1.R1040
  Contig ID
                    LIB3170-055-Q1-K1-H10
  5'-most EST
                    BLASTX
 Method
  NCBI GI
                    g1680686
  BLAST score
                    337
                    2.0e-31
  E value
```

```
(U51330) rust resistance kinase Lr10 [Triticum aestivum]
NCBI Description
                  12619
Seq. No.
Contig ID
                  25662 1.R1040
5'-most EST
                  LIB3170-040-Q1-K1-G10
Method
                  BLASTX
NCBI GI
                  q3395441
BLAST score
                  514
E value
                  3.0e-52
Match length
                  139
% identity
                  71
NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]
                  12620
Seq. No.
Contig ID
                  25662 2.R1040
5'-most EST
                  zzp700835721.h1
                  BLASTX
Method
                  g3395441
NCBI GI
BLAST score
                  321
                  8.0e-30
E value
Match length
                  86
                  73
% identity
NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]
Seq. No.
                  12621
                  25665 2.R1040
Contig ID
5'-most EST
                  fua701041605.h1
Seq. No.
                   12622
Contig ID
                  25667 1.R1040
5'-most EST
                  uC-gmropic074f12b1
Method
                  BLASTX
NCBI GI
                  g4138209
BLAST score
                  301
```

4.0e-27

E value 138 Match length 37 % identity

(AJ223071) serine/threonine kinase protein MSTK2L,long-form NCBI Description [Mus musculus]

12623

Seq. No. Contig ID 25670 1.R1040

5'-most EST LIB3170-056-Q1-K1-H12

BLASTX Method NCBI GI q3548803 BLAST score 885 1.0e-95 E value Match length 231 % identity 76

NCBI Description (AC005313) putative DNA-binding protein [Arabidopsis thaliana] >gi\_4335770\_gb\_AAD17447\_ (AC006284) putative SMUBP-2 [mouse] DNA-binding protein [Arabidopsis thaliana]

Seq. No. 12624

Contig ID 25675 1.R1040

LIB3051-087-Q1-K1-F10 5'-most EST

Method BLASTN



NCBI GI g3821780
BLAST score 33
E value 7.0e-09
Match length 33
% identity 58

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 12625

Contig ID 25680\_1.R1040

5'-most EST LIB3051-087-Q1-K1-H10

Method BLASTX
NCBI GI g1142619
BLAST score 237
E value 7.0e-20
Match length 102
% identity 53

NCBI Description (U18348) phaseolin G-box binding protein PG1 [Phaseolus

vulgaris]

Seq. No. 12626

Contig ID 25682\_1.R1040 5'-most EST ssr700555610.h1

Method BLASTX
NCBI GI g2252830
BLAST score 893
E value 4.0e-96
Match length 296
% identity 60

NCBI Description (AF013293) weak similarity to receptor protein kinase

[Arabidopsis thaliana]

Seq. No. 12627

Contig ID 25683 1.R1040

5'-most EST LIB3051-088-Q1-K1-A12

Seq. No. 12628

Contig ID 25688\_1.R1040

5'-most EST uC-gmrominsoy115b12b1

Seq. No. 12629

Contig ID 25698\_1.R1040

5'-most EST LIB3051-095-Q1-K1-E3

Method BLASTX
NCBI GI 94559367
BLAST score 235
E value 1.0e-19
Match length 138
% identity 38

NCBI Description (AC006585) putative MADS-box protein [Arabidopsis thaliana]

Seq. No. 12630

Contig ID 25698\_2.R1040

5'-most EST LIB3051-100-Q1-K1-F9

Seq. No. 12631

Contig ID 25699\_1.R1040 5'-most EST g4296838



```
BLASTX
Method
                  q3367521
NCBI GI
                  759
BLAST score
                  1.0e-80
E value
                  250
Match length
                  57
% identity
                  (AC004392) Similar to gb_U08285 membrane-associated
NCBI Description
                  salt-inducible protein from Nicotiana tabacum. ESTs
                  gb T44131 and gb_T04378 come from this gene. [Arabidopsis
                  thaliana]
                  12632
Seq. No.
                  25700 1.R1040
Contig ID
                  LIB3051-095-Q1-K1-F5
5'-most EST
Method
                  BLASTX
                  g4490319
NCBI GI
                  235
BLAST score
                  3.0e-39
E value
                  142
Match length
                   64
% identity
                   (AL035678) metal-transporting P-type ATPase [Arabidopsis
NCBI Description
                  thaliana]
                   12633
Seq. No.
                   25704 1.R1040
Contig ID
                   uC-gmropic064a01b1
5'-most EST
                   BLASTX
Method
                   g3193234
NCBI GI
                   586
BLAST score
                   9.0e-61
E value
                   146
Match length
                   51
% identity
                   (AF068690) peroxisomal targeting signal-1 receptor
NCBI Description
                   [Citrullus lanatus]
                   12634
Seq. No.
                   25708 1.R1040
Contig ID
                   LIB3170-057-Q1-K1-E10
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3482974
                   744
BLAST score
E value
                   4.0e-79
                   184
Match length
                   79
% identity
                   (AL031369) ATP-dependent Clp proteinase-like protein
NCBI Description
                   [Arabidopsis thaliana]
                   12635
Seq. No.
                   25712 1.R1040
Contiq ID
                   LIB3170-058-Q1-K1-A10
 5'-most EST
                   BLASTX
Method
                   q2764574
NCBI GI
                   654
BLAST score
                   2.0e-68
 E value
Match length
                   185
```

NCBI Description (AJ001009) pore protein of 24 kD (OEP24) [Pisum sativum]

74

% identity



Seq. No. 12636

Contig ID 25712\_2.R1040 5'-most EST fC-gmf1700908266a1

Method BLASTX
NCBI GI g2764574
BLAST score 627
E value 2.0e-65
Match length 161
% identity 72

NCBI Description (AJ001009) pore protein of 24 kD (OEP24) [Pisum sativum]

Seq. No. 12637

Contig ID 25730 1.R1040 5'-most EST jex700905783.h1

Method BLASTN
NCBI GI g3510345
BLAST score 57
E value 9.0e-23
Match length 305
% identity 82

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MNJ8, complete sequence [Arabidopsis thaliana]

Seq. No. 12638

Contig ID 25730\_2.R1040

5'-most EST LIB3170-061-Q1-K2-D2

Seq. No. 12639

Contig ID 25730\_3.R1040

5'-most EST jC-gmle01810047b09a1

Seq. No. 12640

Contig ID 25736\_1.R1040 5'-most EST uaw700664311.h1

Method BLASTX
NCBI GI g4454056
BLAST score 582
E value 5.0e-60
Match length 133
% identity 89

NCBI Description (AJ000930) ClpP [Arabidopsis thaliana]

Seq. No. 12641

Contig ID 25738\_1.R1040

5'-most EST LIB3170-064-Q1-K1-B8

Seq. No. 12642

Contig ID 25740\_1.R1040

5'-most EST LIB3051-107-Q1-K1-B10

Method BLASTX
NCBI GI g3461846
BLAST score 516
E value 1.0e-52
Match length 147
% identity 32

NCBI Description (AC005315) putative zinc-finger protein [Arabidopsis



## thaliana]

Seq. No. 12643 Contig ID 25744\_1.R1040 5'-most EST uaw700666130.h1

Method BLASTX
NCBI GI g3193324
BLAST score 661
E value 1.0e-135
Match length 312

% identity 68
NCBI Description (AF069299) contains similarity to WD domains, G-beta

repeats (Pfam: G-beta.hmm, score: 22.80 and 35.84)

[Arabidopsis thaliana]

Seq. No. 12644

Contig ID 25746\_1.R1040

5'-most EST LIB3138-125-Q1-N1-H8

Method BLASTX
NCBI GI g1707998
BLAST score 548
E value 2.0e-82
Match length 196
% identity 81

NCBI Description SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL PRECURSOR

(SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE)

(SHMT) >gi\_481944\_pir\_\_S40218 glycine

hydroxymethyltransferase (EC 2.1.2.1) - potato >gi\_438247\_emb\_CAA81082\_ (Z25863) glycine hydroxymethyltransferase [Solanum tuberosum]

Seq. No. 12645

Contig ID 25746 3.R1040

5'-most EST LIB3051-107-Q1-K1-G9

Method BLASTX
NCBI GI g1707998
BLAST score 303
E value 2.0e-27
Match length 105
% identity 67

NCBI Description SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL PRECURSOR

(SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE)

(SHMT) >gi\_481944\_pir\_\_S40218 glycine

hydroxymethyltransferase (EC 2.1.2.1) - potato >gi\_438247\_emb\_CAA81082\_ (Z25863) glycine hydroxymethyltransferase [Solanum tuberosum]

Seq. No. 12646

Contig ID 25748\_1.R1040

5'-most EST LIB3051-108-Q1-K1-A5

Method BLASTX
NCBI GI g1346113
BLAST score 280
E value 9.0e-25
Match length 70
% identity 71

NCBI Description GTP CYCLOHYDROLASE II >gi\_1084339 pir\_\_JC4209 GTP



cyclohydrolase II (EC 3.5.4.25) - Arabidopsis thaliana >gi\_940383\_dbj\_BAA08113\_ (D45165) GTP cyclohydrolase II [Arabidopsis thaliana]

```
12647
Seq. No.
                  25757 1.R1040
Contig ID
5'-most EST
                  LIB3138-035-Q1-N1-B10
Method
                  BLASTX
NCBI GI
                  g3298544
BLAST score
                  459
                  2.0e-45
E value
Match length
                  225
% identity
                  48
NCBI Description (AC004681) unknown protein [Arabidopsis thaliana]
Seq. No.
                  12648
Contig ID
                  25758 1.R1040
5'-most EST
                  LIB3107-075-Q1-K1-D6
Method
                  BLASTX
NCBI GI
                  q1724114
BLAST score
                  494
E value
                  2.0e-67
Match length
                  229
% identity
                  58
NCBI Description (U80041) Af10-protein [Avena fatua]
Seq. No.
                  12649
                  25758_2.R1040
Contig ID
5'-most EST
                  zpv700760792.h1
Method
                  BLASTX
NCBI GI
                  g1724114
BLAST score
                  358
E value
                   6.0e-34
Match length
                  86
% identity
                  73
NCBI Description (U80041) Af10-protein [Avena fatua]
Seq. No.
                  12650
Contig ID
                  25764 1.R1040
                  LIB3170-061-Q1-K2-H11
5'-most EST
                  BLASTX
Method
NCBI GI
                  g2598603
BLAST score
                  235
E value
                  1.0e-19
                  96
Match length
                  55
% identity
NCBI Description (AJ002315) shaggy-like kinase 59 [Nicotiana tabacum]
```

Seq. No. 12651

Contig ID 25766 1.R1040

5'-most EST LIB3051-110-Q1-K1-C10

Method BLASTX
NCBI GI g3377517
BLAST score 398
E value 1.0e-38
Match length 144
% identity 57



NCBI Description (AF073361) nitrate transporter NTL1 [Arabidopsis thaliana]

Seq. No. 12652

Contig ID 25777\_1.R1040

5'-most EST LIB30 $\overline{5}1$ -111-Q1-K1-F4

Method BLASTX
NCBI GI 94204303
BLAST score 237
E value 1.0e-28
Match length 79
% identity 78

NCBI Description (AC003027) lcl prt seq No definition line found

[Arabidopsis thaliana]

Seq. No. 12653

Contig ID 25778\_1.R1040

5'-most EST LIB3170-068-Q1-K1-E8

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 1.0e-10
Match length 36
% identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 12654

Contig ID 25782 1.R1040

5'-most EST LIB3170-066-Q1-K1-C8

Method BLASTX
NCBI GI g166949
BLAST score 595
E value 1.0e-61
Match length 180
% identity 59

NCBI Description (M32885) cytochrome P-450LXXIA1 (cyp71A1) [Persea

americana]

Seq. No. 12655

Contig ID 25783 1.R1040

5'-most EST LIB3170-066-Q1-K1-G9

Method BLASTN
NCBI GI g4309719
BLAST score 64
E value 3.0e-27
Match length 148
% identity 86

NCBI Description Arabidopsis thaliana chromosome II BAC T30D6 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 12656

Contig ID 25786 1.R1040

5'-most EST LIB3051-012-Q1-E1-H7

Method BLASTX
NCBI GI g3047125
BLAST score 154
E value 2.0e-16
Match length 58



```
% identity
                  (AF058919) No definition line found [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  12657
                  25796 1.R1040
Contig ID
                  uC-gmropic014h05b1
5'-most EST
                  BLASTX
Method
                  q3559816
NCBI GI
BLAST score
                  877
E value
                  1.0e-94
Match length
                  205
                  83
% identity
                  (Y15782) transketolase 2 [Capsicum annuum]
NCBI Description
                   12658
Seq. No.
                   25796 2.R1040
Contig ID
                   jC-gmf102220115a09a1
5'-most EST
Method
                   BLASTX
                   a3559816
NCBI GI
BLAST score
                   486
                   5.0e-73
E value
Match length
                   226
                   71
% identity
                  (Y15782) transketolase 2 [Capsicum annuum]
NCBI Description
                   12659
Seq. No.
                   25796_4.R1040
Contig ID
                   uC-qmronoir042d09b1
5'-most EST
Method
                   BLASTX
                   q3559816
NCBI GI
                   610
BLAST score
                   2.0e-63
E value
                   141
Match length
                   82
% identity
NCBI Description (Y15782) transketolase 2 [Capsicum annuum]
                   12660
Seq. No.
                   25799 1.R1040
Contig ID
                   LIB3051-093-Q1-K1-B1
5'-most EST
                   BLASTN
Method
                   g3152879
NCBI GI
                   148
BLAST score
                   2.0e-77
E value
                   357
Match length
                   87
% identity
NCBI Description Pisum sativum cell wall invertase (bfruct1) mRNA, complete
                   cds
                   12661
Seq. No.
                   25802 1.R1040
Contig ID
 5'-most EST
                   LIB3170-084-Q1-K1-D1
Method
                   BLASTX
                   q3915037
NCBI GI
                   3750
BLAST score
                   0.0e + 00
 E value
Match length
                   808
```

88

% identity



NCBI Description SUCROSE SYNTHASE 2 (SUCROSE-UDP GLUCOSYLTRANSFERASE 2)

>gi 2570067\_emb\_CAA04512\_ (AJ001071) second sucrose

synthase [Pisum sativum]

Seq. No. 12662

Contig ID 25802\_2.R1040 5'-most EST uC-gmropic030f11b1

Method BLASTN
NCBI GI g2570066
BLAST score 159
E value 5.0e-84
Match length 231
% identity 92

NCBI Description Pisum sativum mRNA for second sucrose synthase

Seq. No. 12663

Contig ID 25806 1.R1040

5'-most EST jC-gmro02910031d09a1

Method BLASTX
NCBI GI g136739
BLAST score 908
E value 8.0e-98
Match length 389
% identity 51

NCBI Description UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (UDP-GLUCOSE

PYROPHOSPHORYLASE) (UDPGP) >gi 67061 pir XNPOU

UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) -

potato >qi 218001 dbj BAA00570 (D00667) UDP-glucose

pyrophosphorylase precursor [Solanum tuberosum]

Seq. No. 12664

Contig ID 25806 2.R1040 5'-most EST fC-gmro700864991x3

Method BLASTX
NCBI GI g136739
BLAST score 408
E value 2.0e-39
Match length 273
% identity 52

NCBI Description UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (UDP-GLUCOSE

PYROPHOSPHORYLASE) (UDPGP) >gi\_67061\_pir\_ XNPOU

UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) -

potato >gi 218001 dbj BAA00570 (D00667) UDP-glucose

pyrophosphorylase precursor [Solanum tuberosum]

Seq. No. 12665

Contig ID 25806 3.R1040

5'-most EST LIB3138-024-Q1-N1-B11

Seq. No. 12666

Contig ID 25809\_1.R1040 5'-most EST ssr700554018.h1

Method BLASTX
NCBI GI g4490732
BLAST score 447
E value 3.0e-44
Match length 147



```
% identity
                  (AL035709) phosphoenolpyruvate carboxykinase (ATP)-like
NCBI Description
                  protein [Arabidopsis thaliana]
                  12667
Seq. No.
                  25815 1.R1040
Contig ID
5'-most EST
                  fC-gmst700663176f2
Method
                  BLASTX
                  g3925363
NCBI GI
                  1206
BLAST score
                  1.0e-133
E value
                  267
Match length
                  85
% identity
                  (AF067961) homeodomain protein [Malus domestica]
NCBI Description
Seq. No.
                  12668
                  25825 1.R1040
Contig ID
                  pxt700943207.hl
5'-most EST
                  BLASTX
Method
                  q4455283
NCBI GI
                  925
BLAST score
                  1.0e-110
E value
                  258
Match length
                  76
% identity
                   (AL035527) L1 specific homeobox gene ATML1/ovule-specific
NCBI Description
                  homeobox protein A20 [Arabidopsis thaliana]
                  12669
Seq. No.
                   25838 1.R1040
Contig ID
5'-most EST
                  LIB3170-056-Q1-K1-G4
                  BLASTX
Method
                   q3522939
NCBI GI
                   443
BLAST score
                   6.0e-44
E value
Match length
                   123
                   70
% identity
                  (AC004411) putative squamosa-promoter binding protein
NCBI Description
                   [Arabidopsis thaliana]
                   12670
Seq. No.
                   25839 1.R1040
Contig ID
                   jC-qmro02910012a06a1
5'-most EST
                   BLASTX
Method
                   q729775
NCBI GI
BLAST score
                   609
                   6.0e-63
E value
                   254
Match length
                   54
% identity
                   HEAT SHOCK FACTOR PROTEIN HSF8 (HEAT SHOCK TRANSCRIPTION
NCBI Description
```

FACTOR 8) (HSTF 8) (HEAT STRESS TRANSCRIPTION FACTOR)

>gi\_100264\_pir\_\_S25481 heat shock transcription factor 8 Peruvian tomato >gi\_19492\_emb\_CAA47869\_ (X67600) heat shock

transcription factor 8 [Lycopersicon peruvianum]

12671 Seq. No.

25841 1.R1040 Contig ID

LIB3139-002-Q1-N1-D8 5'-most EST



Method BLASTN
NCBI GI g2995454
BLAST score 208
E value 1.0e-113
Match length 442
% identity 87

NCBI Description L.luteus mRNA for tRNA-glutamine synthetase

Seq. No. 12672

Contig ID 25849\_1.R1040

5'-most EST LIB3051-002-Q1-E1-A12

Seq. No. 12673

Contig ID 25850 1.R1040

5'-most EST LIB3051-002-Q1-E1-A2

Seq. No. 12674

Contig ID 25857 1.R1040

Method BLASTX
NCBI GI g3024894
BLAST score 432
E value 5.0e-42
Match length 307
% identity 35

NCBI Description HYPOTHETICAL 54.8 KD PROTEIN CY20H10.28C

Seq. No. 12675

Contig ID 25857 2.R1040

5'-most EST jC-gmf102220080c05d1

Seq. No. 12676

Contig ID 25858 1.R1040

5'-most EST LIB3051-004-Q1-E1-C1

Seq. No. 12677

Contig ID 25859\_1.R1040

5'-most EST LIB3051-044-Q1-K1-H4

Seq. No. 12678

Contig ID 25867\_1.R1040 5'-most EST vzy700754360.h1

Seq. No. 12679

Contig ID 25869 1.R1040

5'-most EST LIB3051-016-Q1-E1-C8

Method BLASTN
NCBI GI g2062705
BLAST score 34
E value 3.0e-09
Match length 34
% identity 61

NCBI Description Human butyrophilin (BTF5) mRNA, complete cds

Seq. No. 12680

Contig ID 25869 2.R1040

5'-most EST LIB3170-043-Q1-J1-C3



Contig ID 25869\_3.R1040 5'-most EST LIB3051-046-Q1-K1-D8

Seq. No. 12682

Contig ID 25869\_4.R1040

5'-most EST LIB3170-055-Q1-K1-B2

Seq. No. 12683

Contig ID 25870\_1.R1040

5'-most EST LIB3051-006-Q1-E1-B4

Seq. No. 12684

Contig ID 25872\_1.R1040

5'-most EST LIB3051-006-Q1-K1-D2

Seq. No. 12685

Contig ID 25877\_1.R1040

5'-most EST LIB3051-006-Q1-E1-F1

Seq. No. 12686

Contig ID 25884\_1.R1040

5'-most EST LIB $30\overline{5}1$ -007-Q1-E1-E1

Method BLASTX
NCBI GI g4105633
BLAST score 318
E value 3.0e-29
Match length 128
% identity 55

NCBI Description (AF048982) putative ethylene receptor [Arabidopsis

thaliana]

Seq. No. 12687

Contig ID 25885\_1.R1040

5'-most EST jC-gmro02910023c06d1

Method BLASTX
NCBI GI 94371285
BLAST score 245
E value 1.0e-20
Match length 101
% identity 51

NCBI Description (AC006260) hypothetical protein [Arabidopsis thaliana]

Seq. No. 12688

Contig ID 25898\_1.R1040

5'-most EST LIB3139-004-P1-N1-F5

Seq. No. 12689

Contig ID 25908\_1.R1040

5'-most EST LIB3051-009-Q1-E1-D2

Method BLASTX
NCBI GI g3608154
BLAST score 264
E value 7.0e-23
Match length 101
% identity 52

```
(AC005314) unknown protein [Arabidopsis thaliana]
NCBI Description
                  12690
Seq. No.
                  25912 1.R1040
Contig ID
                  LIB3109-048-Q1-K1-F6
5'-most EST
                  BLASTX
Method
                  g2239236
NCBI GI
                  382
BLAST score
                  3.0e-46
E value
                  357
Match length
                  35
% identity
                  (Z97211) probable involvement in ergosterol synthesis
NCBI Description
                  [Schizosaccharomyces pombe]
```

12691 Seq. No. 25912 2.R1040 Contig ID LIB3170-064-Q1-K1-C10 5'-most EST BLASTX Method a548437 NCBI GI BLAST score 162

5.0e-11 E value 128 Match length 35 % identity

OSH1 PROTEIN >gi\_1078479\_pir\_\_S53463 SWH1 protein (version NCBI Description

1) - yeast (Saccharomyces cerevisiae) >gi\_456143 (L28920)

Osh1p [Saccharomyces cerevisiae]

Seq. No. 12692

25916 1.R1040 Contig ID

LIB3051-010-Q1-E1-A7 5'-most EST

12693 Seq. No.

25922 1.R1040 Contig ID wrg700786913.h2 5'-most EST

BLASTX Method g2739378 NCBI GI 284 BLAST score 4.0e-25 E value 225 Match length % identity 43

NCBI Description (AC002505) AR781 [Arabidopsis thaliana]

12694 Seq. No.

25926 1.R1040 Contig ID 5'-most EST gsv701049309.hl

12695 Seq. No.

25931\_1.R1040 Contig ID

5'-most EST uC-qmrominsoy039g03b1

Method BLASTX NCBI GI q2384916 BLAST score 160 1.0e-10 E value Match length 128 35 % identity

(AF022982) contains similarity to a DNAJ-like domain NCBI Description

[Caenorhabditis elegans]



```
12696
Seq. No.
Contig ID
                  25938 1.R1040
                  LIB3051-011-Q1-E1-E11
5'-most EST
                  12697
Seq. No.
                  25938 2.R1040
Contig ID
5'-most EST
                  g5677361
                  BLASTX
Method
NCBI GI
                  g231654
BLAST score
                  160
                  1.0e-10
E value
Match length
                  82
% identity
                  15
NCBI Description BRITTLE-1 PROTEIN PRECURSOR >gi_82676_pir__JQ1459 Bt1
                  protein precursor - maize >gi_168426 (M79333) brittle-1
                  protein [Zea mays]
                  12698
Seq. No.
                  25938 4.R1040
Contig ID
5'-most EST
                  jC-gmst02400013g01d1
                  12699
Seq. No.
Contig ID
                  25938 5.R1040
5'-most EST
                  pxt700944615.h1
Seq. No.
                  12700
                  25943 1.R1040
Contig ID
5'-most EST
                  jC-gmle01810060g03a1
Method
                  BLASTX
NCBI GI
                  g1947137
BLAST score
                  187
                  1.0e-33
E value
Match length
                  374
% identity
                  32
NCBI Description
                  (AF000264) similar to the ATP-binding transport protein
                  family (ABC transporters). [Caenorhabditis elegans]
                  12701
Seq. No.
Contig ID
                  25945 1.R1040
5'-most EST
                  LIB3051-011-Q1-E1-G5
                  BLASTX
Method
                  q3434975
NCBI GI
BLAST score
                  267
E value
                  3.0e-23
                  166
Match length
% identity
                  46
                  (AB008107) ethylene responsive element binding factor 5
NCBI Description
                   [Arabidopsis thaliana]
```

Seq. No. Contig ID

12702

Contig ID 25949 1.R1040

5'-most EST LIB3051-011-Q1-E1-H6

Seq. No.

12703

Contig ID 25955\_1.R1040

5'-most EST LIB3051-012-Q1-E1-F11



Contig ID 25957\_1.R1040

5'-most EST LIB3051-012-Q1-E1-F7

Seq. No. 12705

Contig ID 25959 1.R1040

5'-most EST LIB3051-012-Q1-E1-G3

Seq. No. 12706

Contig ID 25964 1.R1040

5'-most EST LIB3051-013-Q1-E1-C6

Method BLASTN
NCBI GI g2924653
BLAST score 76
E value 2.0e-34
Match length 232
% identity 83

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MDA7, complete sequence [Arabidopsis thaliana]

Seq. No. 12707

Contig ID 25968 1.R1040

5'-most EST jC-gmle01810077d04d1

Method BLASTX
NCBI GI g2501555
BLAST score 413
E value 4.0e-40
Match length 104
% identity 67

NCBI Description POSSIBLE APOSPORY-ASSOCIATED PROTEIN C >gi\_549984 (U13148)

possible apospory-associated protein [Pennisetum ciliare]

Seq. No. 12708

Contig ID 25969\_1.R1040

5'-most EST uC-gmrominsoy224c01b1

Method BLASTX
NCBI GI g2961383
BLAST score 326
E value 1.0e-29
Match length 190
% identity 55

NCBI Description (AL022141) putative protein [Arabidopsis thaliana]

Seq. No. 12709

Contig ID 25969 2.R1040

5'-most EST LIB3092-003-Q1-K1-A10

Method BLASTN
NCBI GI 9479145
BLAST score 86
E value 3.0e-40
Match length 126
% identity 92

NCBI Description G.max gene for ATP synthase subunit

Seq. No. 12710

Contig ID 25969\_3.R1040



```
5'-most EST
                   LIB3051-047-Q1-K1-G9
Method
                   BLASTN
                   a3821780
NCBI GI
                   36
BLAST score
                   1.0e-10
E value
                   38
Match length
                   61
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                   12711
Seq. No.
Contig ID
                   25969 6.R1040
5'-most EST
                   sat701012518.hl
Seq. No.
                   12712
                   25971 1.R1040
Contig ID
                   LIB3051-014-Q1-E1-A11
5'-most EST
                   12713
Seq. No.
                   25979 1.R1040
Contig ID
                   uxk70\overline{0}667138.h1
5'-most EST
                   BLASTX
Method
                   g4220518
NCBI GI
BLAST score
                   443
E value
                   1.0e-43
Match length
                   195
                   48
% identity
NCBI Description (AL035356) hypothetical protein [Arabidopsis thaliana]
                   12714
Seq. No.
Contig ID
                   25981 1.R1040
                   LIB3051-014-Q1-E1-E1
5'-most EST
                   12715
Seq. No.
Contig ID
                   25984 1.R1040
5'-most EST
                   LIB30\overline{5}1-014-Q1-E1-F1
Method
                   BLASTX
NCBI GI
                   q3184283
BLAST score
                   748
E value
                   2.0e-79
Match length
                   306
% identity
                   (AC004136) putative TBP-binding protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   12716
                   25987 1.R1040
Contig ID
5'-most EST
                   zhf700956302.h1
Method
                   BLASTX
NCBI GI
                   q3702340
BLAST score
                   413
E value
                   2.0e-40
Match length
                   102
% identity
                   75
NCBI Description (AC005397) hypothetical protein [Arabidopsis thaliana]
```

Contig ID 25988 1.R1040



5'-most EST fC-gmf1700905074g1

Seq. No. 12718

Contig ID 25992 1.R1040 5'-most EST rlr700897444.h1

Seq. No. 12719

Contig ID 25993\_1.R1040 5'-most EST kl1701213410.h1

Seq. No. 12720

Contig ID 26002\_1.R1040

5'-most EST LIB3051-084-Q1-K1-G4

Seq. No. 12721

Contig ID 26003\_1.R1040

5'-most EST uC-gmronoir073b09b1

Method BLASTX
NCBI GI g3786014
BLAST score 364
E value 2.0e-34
Match length 191
% identity 43

NCBI Description (AC005499) hypothetical protein [Arabidopsis thaliana]

Seq. No. 12722

Contig ID 26009 1.R1040

5'-most EST uC-gmrominsoy207h08b1

Seq. No. 12723

Contig ID 26010 1.R1040 5'-most EST gsv701052080.h1

Seq. No. 12724

Contig ID 26011\_1.R1040

5'-most EST LIB3051-016-Q1-E1-B6

Method BLASTX
NCBI GI g1086900
BLAST score 410
E value 8.0e-40
Match length 202
% identity 41

NCBI Description (U41278) contains similarity to G beta repeats

(PROSITE: PS00670) of the beta-transducin family

[Caenorhabditis elegans]

Seq. No. 12725

Contig ID 26011 2.R1040

5'-most EST LIB3109-053-Q1-K1-B9

Seq. No. 12726

Contig ID 26012 1.R1040

5'-most EST LIB3051-016-Q1-E1-B8

Seq. No. 12727

Contig ID 26013 1.R1040

5'-most EST LIB3051-016-Q1-E1-B9



Method BLASTX
NCBI GI g3128234
BLAST score 384
E value 1.0e-36
Match length 75
% identity 92

NCBI Description (AC004077) hypothetical protein [Arabidopsis thaliana]

Seq. No. 12728

Contig ID 26018\_1.R1040 5'-most EST leu701147551.h1

Seq. No. 12729

Contig ID 26020\_1.R1040

5'-most EST jC-gmfl02220103d03a1

Seq. No. 12730

Contig ID 26022\_1.R1040

5'-most EST LIB3093-022-Q1-K1-H4

Seq. No. 12731

Contig ID 26024\_1.R1040

5'-most EST LIB3093-018-Q1-K1-C7

Seq. No. 12732

Contig ID 26025\_1.R1040 5'-most EST kl1701204963.h1

Seq. No. 12733

Contig ID 26030\_1.R1040

5'-most EST LIB3051-017-Q1-E1-A5

Seq. No. 12734

Contig ID 26041\_1.R1040

5'-most EST LIB3051-017-Q1-E1-E5

Seq. No. 12735

Contig ID 26051\_1.R1040 5'-most EST kmv700738607.h1

Seq. No. 12736

Contig ID 26053\_1.R1040

5'-most EST jC-gmf102220051g01d1

Seq. No. 12737

Contig ID 26054 1.R1040

5'-most EST LIB3051-018-Q1-E1-D7

Method BLASTX
NCBI GI g4469014
BLAST score 256
E value 6.0e-22
Match length 77
% identity 68

NCBI Description (AL035602) putative protein [Arabidopsis thaliana]

Seq. No. 12738

Contig ID 26058 1.R1040



```
5'-most EST
                  sat701011106.h1
Method
                  BLASTX
NCBI GI
                  a3834302
                  390
BLAST score
                  1.0e-37
E value
                  112
Match length
                  66
% identity
                  (AC005679) Similar to gb D45384 vacuolar H+-pyrophosphatase
NCBI Description
                  from Oryza sativa. ESTs gb F14272 and gb_F14273 come from
                  this gene. [Arabidopsis thaliana]
                  12739
Seq. No.
Contig ID
                  26062 1.R1040
                  LIB3051-018-Q1-E1-G3
5'-most EST
                  BLASTN
Method
                  a1403521
NCBI GI
                  91
BLAST score
E value
                  1.0e-43
Match length
                  159
```

89 % identity NCBI Description P.vulgaris mRNA for chitinase

12740 Seq. No. Contig ID 26063 1.R1040 LIB3051-018-Q1-E1-G4 5'-most EST Method BLASTN g3821780 NCBI GI BLAST score 36 1.0e-10

E value 49 Match length % identity 66

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 12741

26068 1.R1040 Contig ID

jC-gmro02910010h01a1 5'-most EST

Method BLASTX NCBI GI q2129604 BLAST score 154 E value 5.0e-10 65 Match length 57 % identity

GTP-binding protein 1 - Arabidopsis thaliana NCBI Description

>gi\_2129607\_pir\_\_S71584 GTP-binding protein ATBG1 -Arabidopsis thaliana >gi 1184981 (U46924) ATGB1

[Arabidopsis thaliana]

12742 Seq. No.

26069 1.R1040 Contig ID 5'-most EST cle700967883.h1

12743 Seq. No.

26073 1.R1040 Contig ID 5'-most EST uC-gmropic091c12b1

12744 Seq. No.

26074\_1.R1040 Contig ID



5'-most EST LIB3051-019-Q1-K1-G11

12745 Seq. No.

26083 1.R1040 Contig ID 5'-most EST fua701038382.h1

Seq. No. 12746

26085 1.R1040 Contig ID 5'-most EST gsv701051204.h1

Seq. No. 12747

Contig ID 26087 1.R1040

5'-most EST LIB3051-020-Q1-E1-H2

12748 Seq. No.

26094 1.R1040 Contig ID

5'-most EST jC-gmst02400058e02a1

12749 Seq. No.

26095 1.R1040 Contig ID 5'-most EST ncj700985743.hl

BLASTX Method NCBI GI g3776005 BLAST score 1011 1.0e-110 E value 207 Match length 91

% identity

NCBI Description (AJ010466) RNA helicase [Arabidopsis thaliana]

12750 Seq. No.

26095 2.R1040 Contig ID 5'-most EST  $smc70\overline{0}746810.h1$ 

BLASTX Method NCBI GI q3776005 BLAST score 483 E value 1.0e-48 Match length 128 % identity 76

NCBI Description (AJ010466) RNA helicase [Arabidopsis thaliana]

Seq. No.

12751

26098 1.R1040 Contig ID

5'-most EST uC-gmflminsoy091a04b1

12752 Seq. No.

26098 2.R1040 Contig ID

5'-most EST uC-gmflminsoy018b12b1

Seq. No. 12753

26101 1.R1040 Contig ID trc700566779.h1 5'-most EST

12754 Seq. No.

26104 1.R1040 Contig ID 5'-most EST uC-gmropic100a06b1

Method BLASTX NCBI GI g4572674



```
BLAST score
                  382
                  2.0e-36
E value
                  228
Match length
% identity
                  44
                  (AC006954) unknown protein [Arabidopsis thaliana]
NCBI Description
                  12755
Seq. No.
                  26104 2.R1040
Contig ID
                  sat701014102.h1
5'-most EST
                  BLASTX
Method
                  g4572674
NCBI GI
BLAST score
                  524
                   4.0e-53
E value
                  269
Match length
% identity
                  46
```

(AC006954) unknown protein [Arabidopsis thaliana] NCBI Description

12756 Seq. No. 26106 1.R1040 Contig ID 5'-most EST fua701041985.hl Method BLASTX g1076603 NCBI GI

201 BLAST score 5.0e-15 E value 133 Match length % identity 39

NCBI Description vsf-1 protein - tomato

Seq. No. 12757

26108 1.R1040 Contig ID

5'-most EST LIB3051-024-Q1-K1-B9

Method BLASTX g4490735 NCBI GI 291 BLAST score 4.0e-26 E value 118 Match length 51 % identity

(AL035708) putative protein [Arabidopsis thaliana] NCBI Description

12758 Seq. No.

Contig ID 26109 1.R1040

5'-most EST LIB3093-016-Q1-K1-G11

12759 Seq. No.

26114 1.R1040 Contig ID 2DC-01-Q1-B1-F1 5'-most EST

Method BLASTX g1405438 NCBI GI BLAST score 145 3.0e-13 E value Match length 131 % identity 36

(X98575) DNA-dependent DNA polymerase [Anaerocellum NCBI Description

thermophilum]

Seq. No. 12760

26125\_1.R1040 Contig ID



5'-most EST LIB3051-025-Q1-K1-H12

Seq. No. 12761

Contig ID 26126 1.R1040

5'-most EST LIB3051-026-Q1-K1-A3

Method BLASTX
NCBI GI g2494910
BLAST score 714
E value 1.0e-131
Match length 608
% identity 42

NCBI Description HYPOTHETICAL 91.7 KD TRP-ASP REPEATS CONTAINING PROTEIN IN

NUP116-FAR3 INTERGENIC REGION >gi\_1077983\_pir\_\_S54549 probable membrane protein YMR049c - yeast (Saccharomyces cerevisiae) >gi\_817882\_emb\_CAA89759\_ (Z49703) unknown

[Saccharomyces cerevisiae]

Seq. No. 12762

Contig ID 26126 2.R1040

5'-most EST LIB3072-010-Q1-E1-G6

Seq. No. 12763

Contig ID 26132\_1.R1040

5'-most EST LIB3051-030-Q1-K1-D4

Seq. No. 12764

Contig ID 26139\_1.R1040

5'-most EST LIB3051-031-Q1-K1-F9

Method BLASTX
NCBI GI g2129578
BLAST score 734
E value 1.0e-77
Match length 156
% identity 87

NCBI Description dTDP-glucose 4-6-dehydratases homolog - Arabidopsis

thaliana >gi\_928932\_emb\_CAA89205\_ (Z49239) homolog of dTDP-glucose 4-6-dehydratases [Arabidopsis thaliana] >gi\_1585435\_prf\_\_2124427B diamide resistance gene

[Arabidopsis thaliana]

Seq. No. 12765

Contig ID 26139 2.R1040 5'-most EST zhf700961911.h1

Method BLASTX
NCBI GI g2129578
BLAST score 954
E value 1.0e-103
Match length 247
% identity 78

NCBI Description dTDP-glucose 4-6-dehydratases homolog - Arabidopsis

thaliana >gi\_928932\_emb\_CAA89205\_ (Z49239) homolog of dTDP-glucose 4-6-dehydratases [Arabidopsis thaliana] >gi\_1585435\_prf\_\_2124427B diamide resistance gene

[Arabidopsis thaliana]

Seq. No. 12766

Contig ID 26139 3.R1040

NCBI Description



```
vzy700751523.hl
5'-most EST
                  BLASTX
Method
NCBI GI
                  q2129578
BLAST score
                  220
                  5.0e-18
E value
                  64
Match length
                  70
% identity
                  dTDP-glucose 4-6-dehydratases homolog - Arabidopsis
NCBI Description
                  thaliana >gi_928932_emb_CAA89205_ (Z49239) homolog of
                  dTDP-glucose 4-6-dehydratases [Arabidopsis thaliana]
                  >gi 1585435_prf__2124427B diamide resistance gene
                  [Arabidopsis thaliana]
                  12767
Seq. No.
                  26139 5.R1040
Contig ID
                  rca700997744.hl
5'-most EST
                  BLASTN
Method
                  g928931
NCBI GI
                  151
BLAST score
                  2.0e-79
E value
                  323
Match length
                  87
% identity
NCBI Description A.thaliana mRNA for putative dTDP-glucose 4-6-dehydratases
                  12768
Seq. No.
                  26147 1.R1040
Contig ID
                  LIB3093-024-Q1-K1-H12
5'-most EST
                  12769
Seq. No.
                  26153 1.R1040
Contig ID
                  jC-gmro02910074c09a1
5'-most EST
                   12770
Seq. No.
                   26165 1.R1040
Contig ID
                   jC-gmle01810090f05d1
5'-most EST
                   BLASTX
Method
                   q3193292
NCBI GI
BLAST score
                   173
                   3.0e-12
E value
Match length
                   39
                   79
% identity
                  (AF069298) similar to ATPases associated with various
NCBI Description
                   cellular activites (Pfam: AAA.hmm, score: 230.91)
                   [Arabidopsis thaliana]
Seq. No.
                   12771
                   26165 2.R1040
Contig ID
                   awf700839238.hl
5'-most EST
Method
                   BLASTX
                   q3193292
NCBI GI
BLAST score
                   164
                   3.0e-11
E value
                   37
Match length
% identity
                   84
```

2228

[Arabidopsis thaliana]

(AF069298) similar to ATPases associated with various

cellular activites (Pfam: AAA.hmm, score: 230.91)



Contig ID 26167\_1.R1040 5'-most EST tku700646349.h1

Seq. No. 12773

Contig ID 26167\_3.R1040 5'-most EST bth700846196.h1

Seq. No. 12774

Contig ID 26176\_1.R1040 5'-most EST pmv700891970.h1

Method BLASTX
NCBI GI g3522943
BLAST score 337
E value 1.0e-31
Match length 101
% identity 35

NCBI Description (AC004411) putative p-glycoprotein [Arabidopsis thaliana]

Seq. No. 12775

Contig ID 26179\_1.R1040 5'-most EST uC-gmropic047c07b1

Method BLASTX
NCBI GI g1711572
BLAST score 932
E value 1.0e-101
Match length 217
% identity 82

NCBI Description SUCCINYL-COA LIGASE (GDP-FORMING), ALPHA-CHAIN PRECURSOR

(SUCCINYL-COA SYNTHETASE, ALPHA CHAIN) (SCS-ALPHA)

>gi\_1076415\_pir\_\_S30579 succinate--CoA ligase (GDP-forming)
(EC 6.2.1.4) alpha chain - Arabidopsis thaliana (fragment)
>gi\_16510\_emb\_CAA48891\_ (X69138) succinate--CoA ligase

(GDP-forming) [Arabidopsis thaliana]

Seq. No. 12776

Contig ID 26183\_1.R1040

5'-most EST LIB3051-047-Q1-K1-E1

Method BLASTX
NCBI GI g2252843
BLAST score 346
E value 3.0e-32
Match length 195
% identity 44

NCBI Description (AF013293) No definition line found [Arabidopsis thaliana]

Seq. No. 12777

Contig ID 26187 1.R1040

5'-most EST LIB3170-040-Q1-K1-D7

Seq. No. 12778

Contig ID 26189 1.R1040 5'-most EST smc700750422.h1

Seq. No. 12779

Contig ID 26189 2.R1040



```
kl1701214477.h1
5'-most EST
                   12780
Seq. No.
                   26190 1.R1040
Contig ID
5'-most EST
                   LIB3170-040-Q1-K1-B8
Seq. No.
                   12781
                   26192 1.R1040
Contig ID
                   zhf70\overline{0}951796.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3785983
BLAST score
                   334
E value
                   4.0e-31
Match length
                   109
% identity
                   58
                   (AC005560) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   12782
                   26194 1.R1040
Contig ID
5'-most EST
                   LIB3170-040-Q1-J1-A8
                   BLASTN
Method
NCBI GI
                   q1431738
BLAST score
                   104
E value
                   3.0e-51
Match length
                   173
% identity
                   90
                  Soybean (Glycine max) low MW heat shock protein gene
NCBI Description
                   (Gmhsp17.5-M)
                   12783
Seq. No.
                   26207 1.R1040
Contig ID
5'-most EST
                   LIB3051-055-Q1-K1-C6
                   12784
Seq. No.
                   26220 1.R1040
Contig ID
5'-most EST
                   LIB3109-009-Q1-K1-F12
Seq. No.
                   12785
                   26221 1.R1040
Contig ID
                   LIB3051-058-Q1-K2-B10
5'-most EST
Method
                   BLASTN
                   g665587
NCBI GI
BLAST score
                   208
E value
                   1.0e-113
                   314
Match length
% identity
                   94
NCBI Description Human mRNA for calmodulin, complete cds
                   12786
Seq. No.
                   26227 1.R1040
Contig ID
5'-most EST
                   LIB3051-059-Q1-K2-E6
                   12787
Seq. No.
```

26230 2.R1040 Contig ID

5'-most EST LIB3051-048-Q1-K1-E2

Seq. No. 12788



Contig ID 26230 3.R1040

5'-most EST LIB3051-059-Q1-K2-H10

Seq. No. 12789

Contig ID 26234\_1.R1040 5'-most EST seb700650936.h1

Seq. No. 12790

Contig ID 26234\_2.R1040 5'-most EST gsv701045249.h1

Seq. No. 12791

Contig ID 26236\_1.R1040 5'-most EST ssr700553512.h1

Method BLASTX
NCBI GI g3461835
BLAST score 1048
E value 1.0e-114
Match length 315
% identity 63

NCBI Description (AC005315) putative protein kinase [Arabidopsis thaliana]

>gi 3927840 (AC005727) putative protein kinase [Arabidopsis

thaliana]

Seq. No. 12792

Contig ID 26236 2.R1040

5'-most EST LIB3051-061-Q1-K1-C1

Seq. No. 12793

Contig ID 26236\_3.R1040 5'-most EST epx701105519.h1

Seq. No. 12794

Contig ID 26238\_1.R1040

5'-most EST LIB3107-001-Q1-K1-E7

Seq. No. 12795

Contig ID 26239 1.R1040

5'-most EST LIB30 $\overline{5}1-103-Q1-K1-G12$ 

Method BLASTX
NCBI GI g2664210
BLAST score 751
E value 2.0e-79
Match length 399
% identity 43

NCBI Description (AJ222644) asparaginyl-tRNA synthetase [Arabidopsis

thaliana]

Seq. No. 12796

Contig ID 26241\_1.R1040 5'-most EST zhf700964851.h1

Seq. No.

12797 26247 1.R1040

Contig ID 26247\_1.R1040 5'-most EST LIB3051-061-Q1-K1-H6

Seq. No. 12798



```
26247 2.R1040
Contig ID
5'-most EST
                  LIB3106-110-Q1-K1-E11
                  BLASTX
Method
                  q3935175
NCBI GI
                  503
BLAST score
                  1.0e-50
E value
Match length
                  137
% identity
                  74
NCBI Description (AC004557) F17L21.18 [Arabidopsis thaliana]
                  12799
Seq. No.
                  26254 1.R1040
Contig ID
5'-most EST
                  LIB3106-091-Q1-K1-G10
Method
                  BLASTX
                  g1764100
NCBI GI
                  209
BLAST score
                  2.0e-17
E value
Match length
                  64
% identity
                  68
                  (U81805) GDP-D-mannose-4,6-dehydratase [Arabidopsis
NCBI Description
                  thaliana]
                  12800
Seq. No.
Contig ID
                  26254 2.R1040
5'-most EST
                  dpv701103466.hl
Method
                  BLASTX
NCBI GI
                  g1764100
BLAST score
                  453
E value
                  5.0e-45
Match length
                  110
% identity
                  76
                  (U81805) GDP-D-mannose-4,6-dehydratase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  12801
Contig ID
                  26255 1.R1040
5'-most EST
                  LIB3051-064-Q1-K1-A1
Seq. No.
                  12802
Contig ID
                  26256 1.R1040
5'-most EST
                  LIB3051-064-Q1-K1-C1
                  12803
Seq. No.
Contig ID
                  26265 1.R1040
5'-most EST
                  LIB3170-052-Q1-K1-D3
Seq. No.
                  12804
Contig ID
                  26270 1.R1040
5'-most EST
                  LIB3051-066-Q1-K1-H2
Seq. No.
                  12805
```

26271 1.R1040 Contig ID

5'-most EST LIB3051-075-Q1-K1-H6

Seq. No.

12806

26271 2.R1040 Contig ID

LIB3170-052-Q1-K1-F4 5'-most EST



Contig ID 26275\_1.R1040 5'-most EST sat701012251.h1

Seq. No. 12808

Contig ID 26277\_1.R1040

5'-most EST LIB3051-069-Q1-K1-A7

Method BLASTX
NCBI GI 94455245
BLAST score 185
E value 2.0e-13
Match length 147
% identity 33

NCBI Description (AL035523) hypothetical protein [Arabidopsis thaliana]

Seq. No. 12809

Contig ID 26278\_1.R1040

5'-most EST LIB3170-051-Q1-K1-H6

Seq. No. 12810

Contig ID 26280\_1.R1040

5'-most EST LIB3051-070-Q1-K1-A9

Seq. No. 12811

Contig ID 26286\_1.R1040 5'-most EST uxk700673345.h1

Method BLASTX
NCBI GI g3482977
BLAST score 279
E value 1.0e-24
Match length 171
% identity 41

NCBI Description (AL031369) putative protein [Arabidopsis thaliana]

Seq. No. 12812

Contig ID 26287\_1.R1040

5'-most EST LIB3170-052-Q1-K1-F9

Seq. No. 12813

Contig ID 26290 1.R1040

5'-most EST LIB3138-128-Q1-N1-B9

Method BLASTX
NCBI GI g3873707
BLAST score 285
E value 5.0e-25
Match length 246
% identity 33

NCBI Description (Z73102) Similarity to B. subtilis DNAJ protein

(SW:DNAJ BACSU); cDNA EST yk437a1.5 comes from this gene

[Caenorhabditis elegans]

Seq. No. 12814

Contig ID 26291\_1.R1040 5'-most EST sat701005893.h1

Method BLASTX NCBI GI g4033467



BLAST score 380 E value 1.0e-36 Match length 103 % identity 71

NCBI Description ARGININE/SERINE-RICH SPLICING FACTOR RSP31

>gi 1707366 emb\_CAA67798\_ (X99435) splicing factor

[Arabidopsis thaliana]

Seq. No. 12815

Contig ID 26291\_2.R1040 5'-most EST uxk700671765.h1

Method BLASTX
NCBI GI g4033467
BLAST score 154
E value 5.0e-10
Match length 34
% identity 79

NCBI Description ARGININE/SERINE-RICH SPLICING FACTOR RSP31

>gi 1707366\_emb\_CAA67798\_ (X99435) splicing factor

[Arabidopsis thaliana]

Seq. No. 12816

Contig ID 26300\_1.R1040

5'-most EST jC-gmle01810062f11a1

Method BLASTX
NCBI GI g4455350
BLAST score 296
E value 3.0e-49
Match length 201
% identity 55

NCBI Description (AL035524) putative protein [Arabidopsis thaliana]

Seq. No. 12817

Contig ID 26302\_1.R1040

5'-most EST LIB3051-076-B1-K1-E10

Seq. No. 12818

Contig ID 26311\_1.R1040

5'-most EST LIB3170-041-Q1-K1-G2

Seq. No. 12819

Contig ID 26317\_1.R1040

5'-most EST LIB3051-081-Q1-K1-A3

Method BLASTX
NCBI GI g4417293
BLAST score 267
E value 3.0e-23
Match length 52
% identity 87

NCBI Description (AC007019) unknown protein [Arabidopsis thaliana]

Seq. No. 12820

Contig ID 26318\_1.R1040 5'-most EST zhf700956754.h1

Method BLASTX NCBI GI g3882211 BLAST score 367



E value 1.0e-34 Match length 176 % identity 39

NCBI Description (AB018288) KIAA0745 protein [Homo sapiens]

Seq. No. 12821

Contig ID 26320 1.R1040

5'-most EST LIB3051-082-Q1-K1-A9

Seq. No. 12822

Contig ID 26332 1.R1040 5'-most EST jex700908922.h1

Seq. No. 12823

Contig ID 26337 1.R1040

5'-most EST jC-qmro02910047f01a1

Method BLASTX
NCBI GI g4455192
BLAST score 1407
E value 1.0e-156
Match length 487
% identity 35

NCBI Description (AL035440) putative protein [Arabidopsis thaliana]

Seq. No. 12824

Contig ID 26337 2.R1040

5'-most EST jC-qmst02400048h10a1

Method BLASTX
NCBI GI g4455192
BLAST score 505
E value 7.0e-51
Match length 164
% identity 44

NCBI Description (AL035440) putative protein [Arabidopsis thaliana]

Seq. No. 12825

Contig ID 26339 1.R1040

5'-most EST LIB3051-090-Q1-K1-A1

Seq. No. 12826

Contig ID 26356 1.R1040

5'-most EST LIB3139-104-P1-N1-E7

Method BLASTX
NCBI GI g3600049
BLAST score 465
E value 1.0e-46
Match length 121
% identity 77

NCBI Description (AF080120) similar to initiation factor IF2-beta (Pfam:

GTP EFTU.hmm, score: 226.67) [Arabidopsis thaliana]

Seq. No. 12827

Contig ID 26356\_2.R1040

5'-most EST LIB3170-059-Q1-K1-F1

Method BLASTX NCBI GI g3600049 BLAST score 187



4.0e-14 E value 40 Match length % identity 90 (AF080120) similar to initiation factor IF2-beta (Pfam: NCBI Description GTP EFTU.hmm, score: 226.67) [Arabidopsis thaliana] 12828 Seq. No. 26360 1.R1040 Contig ID LIB3051-094-Q1-K1-G5 5'-most EST 12829 Seq. No. 26363 1.R1040 Contig ID 5'-most EST sat701011253.h1 12830 Seq. No.

26367 1.R1040 Contig ID

5'-most EST LIB3051-095-Q1-K1-H9

12831 Seq. No.

26370 1.R1040 Contig ID

 $LIB30\overline{5}1-096-Q1-K1-E11$ 5'-most EST

12832 Seq. No.

Contig ID 26371 1.R1040

5'-most EST LIB3051-096-Q1-K1-G9

Method BLASTX g4204314 NCBI GI 353 BLAST score 5.0e-33 E value Match length 305

29 % identity

NCBI Description (AC003027) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 12833

26372 1.R1040 Contig ID pmv700890438.h1 5'-most EST

Method BLASTX q3123908 NCBI GI 159 BLAST score E value 2.0e-10 92 Match length 36 % identity

NCBI Description (AF038392) pre-mRNA splicing factor [Homo sapiens]

Seq. No. 12834

26373 1.R1040 Contig ID

5'-most EST LIB3051-097-Q1-K1-A9

Method BLASTX NCBI GI g3877252 BLAST score 355 E value 4.0e - 34Match length 150 % identity 53

(Z93382) F45G2.10 [Caenorhabditis elegans] NCBI Description

12835 Seq. No.

26376\_1.R1040 Contig ID



5'-most EST LIB3051-097-Q1-K1-B2

Seq. No. 12836

Contig ID 26379\_1.R1040 5'-most EST ssr700559644.h1

Method BLASTX
NCBI GI g1077581
BLAST score 189
E value 8.0e-14
Match length 55
% identity 55

NCBI Description probable membrane protein YDR126w - yeast (Saccharomyces

cerevisiae)

Seq. No. 12837

Contig ID 26380 1.R1040

5'-most EST LIB3092-047-Q1-K1-C9

Seq. No. 12838

Contig ID 26380\_2.R1040 5'-most EST wvk700683092.h1

Seq. No. 12839

Contig ID 26381\_1.R1040 5'-most EST pmv700893124.h1

Seq. No. 12840

Contig ID 26390 1.R1040

5'-most EST LIB30 $\overline{5}1$ -097-Q1-K1-H5

Seq. No. 12841

Contig ID 26395\_1.R1040

5'-most EST LIB30 $\overline{5}1$ -098-Q1-K1-C3

Seq. No. 12842

Contig ID 26396\_1.R1040 5'-most EST leu701153389.h1

Method BLASTX
NCBI GI g3738297
BLAST score 930
E value 1.0e-100
Match length 349
% identity 44

NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]

Seq. No. 12843

Contig ID 26396\_2.R1040 5'-most EST has700548269.h1

Method BLASTX
NCBI GI g3738297
BLAST score 340
E value 8.0e-32
Match length 100
% identity 25

NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]

Seq. No. 12844



Contig ID 26397 1.R1040 5'-most EST LIB3051-098-Q1-K1-C8 Method BLASTX NCBI GI q3702335 BLAST score 322 2.0e-29 E value Match length 93 % identity 59 NCBI Description (AC005397) putative DNA binding protein [Arabidopsis thaliana] Seq. No. 12845 Contig ID 26404 1.R1040 5'-most EST LIB3051-098-Q1-K1-G7 12846 Seq. No. Contig ID 26404 2.R1040 5'-most EST LIB3107-008-Q1-K1-A9 12847 Seq. No. Contig ID 26411 1.R1040 5'-most EST LIB3051-096-Q1-K1-B11 Method BLASTX NCBI GI g4468814 BLAST score 153 E value 5.0e-10 Match length 68 56 % identity NCBI Description (AL035601) putative protein [Arabidopsis thaliana] Seq. No. 12848 26414 1.R1040 Contig ID 5'-most EST  $crh70\overline{0}855155.h1$ Seq. No. 12849 Contig ID 26415 1.R1040 5'-most EST  $seb70\overline{0}651450.h1$ Seq. No. 12850 Contig ID 26428 1.R1040 5'-most EST LIB3170-059-Q1-K1-E12 Method BLASTX NCBI GI g3355471

BLAST score 268 E value 2.0e-23 Match length 116 % identity

NCBI Description (AC004218) putative lysophospholipase [Arabidopsis

thaliana]

12851

Seq. No.

26431 1.R1040 Contig ID 5'-most EST zpv700760620.h1

Seq. No. 12852

26434 1.R1040 Contig ID 5'-most EST leu701151295.h1



Method BLASTX
NCBI GI g2500536
BLAST score 214
E value 3.0e-17
Match length 101
% identity 45

NCBI Description PROBABLE ATP-DEPENDENT RNA HELICASE DBP9

>gi\_1077400\_pir\_\_S51412 hypothetical protein YLR276c yeast (Saccharomyces cerevisiae) >gi\_577189 (U17245)

Ylr276cp [Saccharomyces cerevisiae]

Seq. No. 12853

Contig ID 26437 1.R1040

5'-most EST LIB3051-100-Q1-K1-D4

Seq. No. 12854

Contig ID 26441 1.R1040

5'-most EST uC-gmrominsoy045a08b1

Seq. No. 12855

Contig ID 26446\_1.R1040 5'-most EST kl1701202477.h1

Method BLASTX
NCBI GI g3367576
BLAST score 468
E value 4.0e-46
Match length 197
% identity 49

NCBI Description (AL031135) NAM / CUC2 -like protein [Arabidopsis thaliana]

Seq. No. 12856

Contig ID 26453\_2.R1040

5'-most EST LIB3170-062-Q1-J1-E4

Seq. No. 12857

Contig ID 26456 1.R1040

5'-most EST LIB3170-062-Q1-K1-H4

Seq. No. 12858

Contig ID 26461\_1.R1040

Seq. No. 12859

Contig ID 26462\_1.R1040 5'-most EST fua701039078.h1

Method BLASTX
NCBI GI g3861020
BLAST score 160
E value 6.0e-15
Match length 238
% identity 28

NCBI Description (AJ235271) unknown [Rickettsia prowazekii]

Seq. No. 12860

Contig ID 26471\_1.R1040

5'-most EST LIB3170-015-Q1-J1-A12

Method BLASTN



```
q4519192
NCBI GI
BLAST score
                  44
E value
                  2.0e-15
                  164
Match length
                  82
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MBK21, complete sequence
                  12861
Seq. No.
                  26496 1.R1040
Contig ID
5'-most EST
                  jex70\overline{0}907621.h1
Method
                  BLASTX
NCBI GI
                  g1522681
BLAST score
                  183
E value
                  3.0e-13
                  219
Match length
% identity
                  26
                  (U49240) symplekin [Homo sapiens] >gi 2143262 emb CAA71861
NCBI Description
                   (Y10931) symplekin [Homo sapiens]
                  12862
Seq. No.
                  26505 1.R1040
Contig ID
5'-most EST
                  LIB3051-117-Q1-K1-A3
Seq. No.
                  12863
                  26506 1.R1040
Contig ID
5'-most EST
                   jC-qmro02910025h06d1
                  BLASTX
Method
                   g4512715
NCBI GI
BLAST score
                   252
                   2.0e-21
E value
Match length
                  115
                   48
% identity
NCBI Description
                  (AC006569) unknown protein [Arabidopsis thaliana]
Seq. No.
                   12864
Contig ID
                   26508 1.R1040
                   LIB3051-088-Q1-K1-G7
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3885335
BLAST score
                   155
E value
                   2.0e-10
Match length
                   64
                   52
% identity
NCBI Description
                   (AC005623) ethylene-insensitive3-like protein [Arabidopsis
                   thaliana]
```

Contig ID 26544 1.R1040

5'-most EST LIB3051-002-Q1-E1-A8

Method BLASTX NCBI GI q4510418 BLAST score 236 2.0e-19 E value Match length 116 % identity 44

NCBI Description (AC006929) hypothetical protein [Arabidopsis thaliana]



Contig ID 26547\_1.R1040 5'-most EST crh700854576.h1

Method BLASTX
NCBI GI g3702336
BLAST score 428
E value 3.0e-42
Match length 107
% identity 73

NCBI Description (AC005397) putative 3-methyl-2-oxobutanoate

hydroxy-methyl-transferase [Arabidopsis thaliana]

Seq. No. 12867

Contig ID 26550\_1.R1040

5'-most EST jC-gmle01810062e05a1

Method BLASTX
NCBI GI g4249733
BLAST score 183
E value 7.0e-13
Match length 417
% identity 22

NCBI Description (AF109377) ldlBp [Mus musculus]

Seq. No. 12868

Contig ID 26551\_1.R1040 5'-most EST ssr700558867.h1

Seq. No. 12869

Contig ID 26554\_1.R1040

5'-most EST LIB3051-002-Q1-E1-C7

Seq. No. 12870

Contig ID 26556 1.R1040 5'-most EST seb700653063.h1

Method BLASTX
NCBI GI g2506139
BLAST score 882
E value 5.0e-95
Match length 261
% identity 71

NCBI Description COATOMER DELTA SUBUNIT (DELTA-COAT PROTEIN) (DELTA-COP)

(ARCHAIN) >gi\_1314049\_emb\_CAA91901\_ (Z67962)

archain/delta-COP [Oryza sativa]

Seq. No. 12871

Contig ID 26556 2.R1040

5'-most EST uC-gmrominsoy110h07b1

Method BLASTX
NCBI GI g2506139
BLAST score 612
E value 1.0e-63
Match length 142
% identity 85

NCBI Description COATOMER DELTA SUBUNIT (DELTA-COAT PROTEIN) (DELTA-COP)

(ARCHAIN) >gi 1314049\_emb\_CAA91901\_ (Z67962)

archain/delta-COP [Oryza sativa]



Contig ID 26556\_4.R1040 5'-most EST zhf700957357.h1

Method BLASTX
NCBI GI g2506139
BLAST score 256
E value 2.0e-22
Match length 56
% identity 91

NCBI Description COATOMER DELTA SUBUNIT (DELTA-COAT PROTEIN) (DELTA-COP)

(ARCHAIN) >gi\_1314049\_emb\_CAA91901\_ (Z67962)

archain/delta-COP [Oryza sativa]

Seq. No. 12873

Contig ID 26556\_5.R1040 5'-most EST fua701042255.h1

Method BLASTX
NCBI GI g2506139
BLAST score 163
E value 2.0e-11
Match length 38
% identity 89

NCBI Description COATOMER DELTA SUBUNIT (DELTA-COAT PROTEIN) (DELTA-COP)

(ARCHAIN) >gi 1314049 emb\_CAA91901\_ (Z67962)

archain/delta-COP [Oryza sativa]

Seq. No. 12874

Contig ID 26560 1.R1040

5'-most EST LIB3051-002-Q1-E1-D5

Seq. No. 12875

Contig ID 26562\_2.R1040 5'-most EST ckk700605807.h2

Seq. No. 12876

Contig ID 26572\_1.R1040 5'-most EST crh700851784.h1

Method BLASTX
NCBI GI g4191775
BLAST score 241
E value 3.0e-20
Match length 53
% identity 85

NCBI Description (AC005917) putative acyl-CoA cholesterol acyltransferase

[Arabidopsis thaliana]

Seq. No. 12877

Contig ID 26573\_1.R1040

5'-most EST LIB3051-002-Q1-E1-G8

Method BLASTX
NCBI GI g4567251
BLAST score 219
E value 1.0e-17
Match length 58
% identity 66

NCBI Description (AC007070) unknown protein [Arabidopsis thaliana]



Contig ID 26577\_1.R1040 5'-most EST uC-gmropic098d05b1

Seq. No. 12879

Contig ID 26577\_2.R1040 5'-most EST seb700652490.h1

Seq. No. 12880

Contig ID 26582\_1.R1040 5'-most EST zsg701127538.h1

Method BLASTX
NCBI GI g2281637
BLAST score 264
E value 2.0e-22
Match length 65
% identity 72

NCBI Description (AF003099) AP2 domain containing protein RAP2.6

[Arabidopsis thaliana]

Seq. No. 12881

Contig ID 26582 2.R1040

5'-most EST LIB3093-018-Q1-K1-B4

Seq. No. 12882

Contig ID 26583 1.R1040

5'-most EST LIB3051-003-Q1-E1-A8

Seq. No. 12883

Contig ID 26586\_1.R1040

5'-most EST LIB3051-003-Q1-E1-B8

Seq. No. 12884

Contig ID 26587 1.R1040

5'-most EST LIB3051-003-Q1-E1-B9

Seq. No. 12885

Contig ID 26591\_1.R1040

5'-most EST LIB3170-054-Q1-J1-F4

Seq. No. 12886

Contig ID 26597\_1.R1040

5'-most EST g5606937

Method BLASTX

NCBI GI g1938424

BLAST score 222

E value 3.0e-36

Match length 194

% identity 48

NCBI Description (U97002) similar to acyl-CoA dehydrogenases and epoxide

hydrolases [Caenorhabditis elegans]

Seq. No. 12887

Contig ID 26599 1.R1040 5'-most EST kl1701212237.h1



Seq. No. 12888
Contig ID 26607 1.R1040
5'-most EST LIB3109-027-Q1-K1-H8

Seq. No. 12889
Contig ID 26609 1.R1040
5'-most EST uaw700662779.h1
Method BLASTX

Method BLASTX
NCBI GI g3522937
BLAST score 172
E value 8.0e-12
Match length 166

% identity 34

NCBI Description (AC004411) unknown protein [Arabidopsis thaliana]

Seq. No. 12890

Contig ID 26610\_1.R1040 5'-most EST uC-gmropic063d10b1

Seq. No. 12891

Contig ID 26612 1.R1040

5'-most EST LIB3138-024-Q1-N1-H7

Method BLASTX
NCBI GI g2827519
BLAST score 559
E value 2.0e-57
Match length 144
% identity 68

NCBI Description (ALO21633) predicted protein [Arabidopsis thaliana]

Seq. No. 12892

Contig ID 26613\_1.R1040

5'-most EST fC-gmse7000751180f1

Method BLASTX
NCBI GI g2541876
BLAST score 459
E value 3.0e-45
Match length 340
% identity 33

NCBI Description (D26015) CND41, chloroplast nucleoid DNA binding protein

[Nicotiana tabacum]

Seq. No. 12893

Contig ID 26615 1.R1040

5'-most EST LIB3051-004-Q1-E1-C10

Seq. No. 12894

Contig ID 26616\_1.R1040 5'-most EST eep700865352.h1

Seq. No. 12895

Contig ID 26619\_1.R1040 5'-most EST epx701110205.h1

Seq. No. 12896

Contig ID 26620 1.R1040

5'-most EST LIB3051-004-Q1-E1-C6



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12897
Seq. No.
                  26620 2.R1040
Contig ID
5'-most EST
                  dpv701099808.h1
                  12898
Seq. No.
Contig ID
                  26621 1.R1040
5'-most EST
                  LIB3051-004-Q1-E1-D2
                  12899
Seq. No.
                  26622 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy216h03b1
Seq. No.
                  12900
Contig ID
                  26629 1.R1040
                  leu701154851.h1
5'-most EST
                  12901
Seq. No.
                  26629 2.R1040
Contig ID
5'-most EST
                  asn70\overline{1}135880.h1
                  12902
Seq. No.
                  26631 1.R1040
Contig ID
5'-most EST
                  LIB3051-004-Q1-E1-E8
                   12903
Seq. No.
                  26634 1.R1040
Contig ID
5'-most EST
                   zhf700961501.h1
                  BLASTX
Method
NCBI GI
                   q3927830
BLAST score
                   282
                   6.0e-25
E value
Match length
                   128
% identity
                   50
                  (AC005727) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   12904
                   26634 3.R1040
Contig ID
5'-most EST
                   pmv700890677.h1
Method
                   BLASTX
NCBI GI
                   g3927830
BLAST score
                   141
E value
                   9.0e-09
Match length
                   70
% identity
NCBI Description
                  (AC005727) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   12905
                   26639 1.R1040
Contig ID
5'-most EST
                   LIB3051-004-Q1-E1-G7
Method
                   BLASTN
NCBI GI
                   q3821780
```

NCBI Description Xenopus laevis cDNA clone 27A6-1

35 4.0e-10

36 60

BLAST score

% identity

E value Match length



Contig ID 26640\_1.R1040 5'-most EST uC-gmropic102a05b1

Seq. No. 12907

Contig ID 26640 4.R1040 5'-most EST jex700907390.h1

Seq. No. 12908

Contig ID 26649\_1.R1040

5'-most EST LIB3170-045-Q1-J1-G3

Method BLASTX
NCBI GI g2104558
BLAST score 164
E value 5.0e-11
Match length 125
% identity 30

NCBI Description (AB000216) CCA3 [Rattus norvegicus]

Seq. No. 12909

Contig ID 26651\_1.R1040 5'-most EST bth700847812.h1

Method BLASTX
NCBI GI g2558938
BLAST score 384
E value 9.0e-53
Match length 237
% identity 49

NCBI Description (AF024625) arm repeat containing protein [Brassica napus]

Seq. No. 12910

Contig ID 26652\_1.R1040 5'-most EST fua701040832.h1

Seq. No. 12911

Contig ID 26653 1.R1040

5'-most EST LIB3051-005-Q1-E1-B6

Seq. No. 12912

Contig ID 26654 2.R1040 5'-most EST crh700851905.h1

Seq. No. 12913

Contig ID 26654\_3.R1040 5'-most EST zzp700830073.h1

Seq. No. 12914

Contig ID 26655 1.R1040

5'-most EST LIB30 $\overline{5}1-005-Q1-E1-B9$ 

Seq. No. 12915

Contig ID 26655 2.R1040

5'-most EST jC-gmle01810010d03d1

Seq. No. 12916

Contig ID 26661 1.R1040



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5'-most EST
                  LIB3051-005-Q1-E1-D12
```

26661 2.R1040 Contig ID 5'-most EST  $kmv70\overline{0}743694.h1$ 

Seq. No. 12918

Contig ID 26665 1.R1040

5'-most EST LIB3170-033-Q1-K1-H7

12919 Seq. No.

Contig ID 26667 1.R1040

5'-most EST jC-gmle01810090f11a1

Seq. No. 12920

Contig ID 26668 1.R1040 5'-most EST fua701040656.hl

Method BLASTX NCBI GI q4580461 BLAST score 426 E value 7.0e-42Match length 133 % identity 63

NCBI Description (AC006081) unknown protein [Arabidopsis thaliana]

Seq. No. 12921

26668 4.R1040 Contig ID uaw700661295.h1 5'-most EST

Method BLASTX g4580476 NCBI GI BLAST score 253 1.0e-21 E value Match length 92

% identity 54

NCBI Description (AC006081) unknown protein [Arabidopsis thaliana]

Seq. No.

12922

26675 1.R1040 Contig ID

5'-most EST LIB3051-005-Q1-E1-G12

Seq. No.

12923

Contig ID 26676 1.R1040

5'-most EST LIB3051-005-Q1-E1-G2

Method BLASTX NCBI GI g4325338 BLAST score 793 E value 6.0e-85 Match length 176 % identity

NCBI Description (AF128392) No definition line found [Arabidopsis thaliana]

Seq. No.

12924

26679 1.R1040 Contig ID 5'-most EST  $jex70\overline{0}907733.h1$ 

Seq. No.

12925

Contig ID

26680\_1.R1040



5'-most EST LIB3051-005-Q1-E1-H6

Seq. No. 12926

Contig ID 26681 1.R1040

5'-most EST LIB3051-005-Q1-E1-H7

Seq. No. 12927

Contig ID 26684 1.R1040

5'-most EST uC-gmrominsoy258g10b1

Method BLASTX
NCBI GI g2191168
BLAST score 410
E value 7.0e-40
Match length 163
% identity 53

NCBI Description (AF007270) contains similarity to myosin heavy chain

[Arabidopsis thaliana]

Seq. No. 12928

Contig ID 26684 2.R1040

5'-most EST LIB30 $\overline{5}1$ -006-Q1-E1-A10

Method BLASTX
NCBI GI g3482922
BLAST score 176
E value 2.0e-12
Match length 57
% identity 65

NCBI Description (AC003970) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 12929

Contig ID 26690 1.R1040

5'-most EST LIB3051-006-Q1-E1-B11

Seq. No. 12930

Contig ID 26695 1.R1040

5'-most EST LIB3051-006-Q1-E1-B9

Seq. No. 12931

Contig ID 26702 1.R1040

5'-most EST LIB3051-006-Q1-K1-C9

Seq. No. 12932

Contig ID 26709 1.R1040

5'-most EST LIB3051-006-Q1-E1-D6

Seq. No. 12933

Contig ID 26712\_1.R1040 5'-most EST dpv701101778.h1

Method BLASTX
NCBI GI g1871181
BLAST score 266
E value 3.0e-23
Match length 125
% identity 50

NCBI Description (U90439) ring zinc finger protein isolog [Arabidopsis

thaliana]



Seq. No. 12934 Contig ID 26713

Contig ID 26713\_1.R1040 5'-most EST uC-gmronoir006d03b1

Seq. No. 12935

Contig ID 26720 1.R1040

5'-most EST uC-gmrominsoy177b10b1

Seq. No. 12936

Contig ID 26722\_1.R1040

5'-most EST uC-gmrominsoy086f02b1

Seq. No. 12937

Contig ID 26722 2.R1040 5'-most EST sat701010330.h1

Seq. No. 12938

Contig ID 26727\_1.R1040 5'-most EST gsv701049071.h1

Method BLASTX
NCBI GI g4218121
BLAST score 235
E value 3.0e-19
Match length 168
% identity 31

NCBI Description (AL035353) putative protein [Arabidopsis thaliana]

Seq. No. 12939

Contig ID 26727\_2.R1040 5'-most EST ncj700978159.h1

Seq. No. 12940

Contig ID 26727 3.R1040

5'-most EST jC-gmro02910075c08a1

Seq. No. 12941

Contig ID 26728 1.R1040

5'-most EST LIB3051-006-Q1-E1-H5

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 1.0e-10
Match length 36
% identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 12942

Contig ID 26730\_1.R1040

5'-most EST uC-gmrominsoy074f05b1

Method BLASTX
NCBI GI g2853287
BLAST score 310
E value 6.0e-28
Match length 300
% identity 32

NCBI Description (AF001947) U4/U6-associated RNA splicing factor [Homo

sapiens]



```
12943
Seg. No.
                   26756 1.R1040
Contig ID
5'-most EST
                   LIB3051-006-Q1-K1-E4
Seq. No.
                   12944
                   26762 1.R1040
Contig ID
                   uaw700661389.hl
5'-most EST
Seq. No.
                   12945
                   26762 2.R1040
Contig ID
5'-most EST
                   zpv700760106.h1
Seq. No.
                   12946
                   26763 1.R1040
Contig ID
                   q5606\overline{7}43
5'-most EST
Method
                   BLASTX
                   g3115852
NCBI GI
BLAST score
                   373
E value
                   1.0e-35
Match length
                   137
                   59
% identity
NCBI Description
                   (AL022023) putative protein [Arabidopsis thaliana]
                   12947
Seq. No.
                   26763 2.R1040
Contig ID
5'-most EST
                   q4276928
Method
                   BLASTX
NCBI GI
                   g3115852
BLAST score
                   243
E value
                   2.0e-20
Match length
                   71
% identity
                   68
                   (AL022023) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   12948
                   26764 1.R1040
Contig ID
5'-most EST
                   bth700847488.h1
                   12949
Seq. No.
                   26764 2.R1040
Contig ID
5'-most EST
                   zhf700955283.h1
                   12950
Seq. No.
                   26789 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220102f02a1
                   12951
Seq. No.
                   26793 1.R1040
Contig ID
                   jsh70\overline{1}067683.h1
5'-most EST
                   BLASTX
Method
```

NCBI GI g3786017 BLAST score 191 E value 6.0e-14 Match length 118 % identity 35

NCBI Description (AC005499) putative non-green plastid inner envelope



## membrane protein [Arabidopsis thaliana]

12952 Seq. No. Contig ID 26799 1.R1040 5'-most EST LIB3051-007-Q1-E1-E12 Method BLASTX NCBI GI g4263718 677 BLAST score 3.0e-71E value Match length 187 % identity 71 NCBI Description thaliana]

(AC006223) putative DNA topoisomerase III beta [Arabidopsis

12953 Seq. No.

Contig ID 26800 1.R1040 5'-most EST zsg701124087.h1

Seq. No. 12954

Contig ID 26806 2.R1040

5'-most EST LIB3051-007-Q1-E1-F9

Method BLASTX NCBI GI g4206196 BLAST score 337 E value 1.0e-31 Match length 84 74 % identity

(AF071527) hypothetical protein [Arabidopsis thaliana] NCBI Description

Seq. No. 12955

26807 1.R1040 Contig ID

5'-most EST jC-gmle01810026c12a1

Seq. No. 12956

26809 1.R1040 Contig ID  $zsg70\overline{1}120512.h1$ 5'-most EST

Method BLASTX NCBI GI a1698548 BLAST score 273 5.0e-24 E value Match length 155 % identity 43

NCBI Description (U58971) calmodulin-binding protein [Nicotiana tabacum]

Seq. No. 12957

26812 1.R1040 Contig ID

5'-most EST uC-gmrominsoy111a12b1

Method BLASTX NCBI GI q3033395 BLAST score 256 5.0e-22 E value Match length 71 % identity 65

(AC004238) putative zinc-finger protein [Arabidopsis NCBI Description

thaliana]

Seq. No. 12958



Contig ID 26812\_2.R1040 5'-most EST rca700998284.h1

Method BLASTX
NCBI GI g4490758
BLAST score 250
E value 2.0e-21
Match length 113
% identity 42

NCBI Description (AL035708) putative protein [Arabidopsis thaliana]

Seq. No. 12959

Contig ID 26816\_1.R1040

5'-most EST jC-gmst02400053a08d1

Seq. No. 12960

Contig ID 26818 1.R1040

5'-most EST LIB3051-061-Q1-K1-B12

Seq. No. 12961

Contig ID 26819\_1.R1040 5'-most EST uC-gmropic059c02b1

Seq. No. 12962

Contig ID 26819\_2.R1040

5'-most EST jC-gmro02910066d10a1

Seq. No. 12963

Contig ID 26819 3.R1040 5'-most EST asn701131310.h1

Seq. No. 12964

Contig ID 26819 4.R1040 5'-most EST gsv701053360.h1

Seq. No.

12965

Contig ID 26820\_1.R1040

5'-most EST LIB3051-008-Q1-E1-A9

Seq. No. 12966

Contig ID 26826\_1.R1040 5'-most EST zsg701123932.h1

Seq. No.

12967

Contig ID 26833 1.R1040

5'-most EST LIB30 $\overline{5}1$ -008-Q1-E1-C8

Seq. No.

12968

Contig ID 26843\_1.R1040 5'-most EST rca700996928.h1

Method BLASTN
NCBI GI g871763
BLAST score 181
E value 3.0e-97
Match length 353
% identity 88

NCBI Description V.unguiculata mRNA for basic chitinase clase



Seq. No. 12969

Contig ID 26846\_1.R1040

5'-most EST jC-gmro02910008d08a1

Method BLASTX
NCBI GI g3212865
BLAST score 261
E value 2.0e-22
Match length 115
% identity 53

NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]

Seq. No. 12970

Contig ID 26849\_1.R1040 5'-most EST gsv701055916.h1

Method BLASTX
NCBI GI g4454021
BLAST score 212
E value 7.0e-17
Match length 116
% identity 38

NCBI Description (AL035396) hypothetical protein [Arabidopsis thaliana]

Seq. No. 12971

Contig ID 26851 1.R1040

5'-most EST LIB3051-008-Q1-E1-F11

Seq. No. 12972

Contig ID 26854\_1.R1040 5'-most EST epx701110110.h1

Seq. No. 12973

Contig ID 26858 1.R1040 5'-most EST k11701212046.h1

Seq. No. 12974

Contig ID 26862\_1.R1040 5'-most EST hyd700729971.h1

Seq. No. 12975

Contig ID 26870\_1.R1040

5'-most EST LIB3093-027-Q1-K1-C1

Method BLASTX
NCBI GI g629846
BLAST score 158
E value 1.0e-10
Match length 134
% identity 37

NCBI Description initiator-binding protein - maize >gi\_483444\_emb\_CAA55693\_

(X79086) initiator-binding protein [Zea mays]

Seq. No. 12976

Contig ID 26877\_2.R1040

5'-most EST LIB3170-056-Q1-K1-B2

Seq. No. 12977

Contig ID 26877\_3.R1040 5'-most EST leu701150292.h1



Method BLASTX
NCBI GI g2370497
BLAST score 153
E value 7.0e-10
Match length 77
% identity 34

NCBI Description (Z98944) beta transducin [Schizosaccharomyces pombe]

Seq. No. 12978

Contig ID 26877\_4.R1040 5'-most EST vwf700679503.h1

Seq. No. 12979

Contig ID 26877\_5.R1040 5'-most EST rlr700897701.h1

Seq. No. 12980

Contig ID 26879\_1.R1040 5'-most EST uxk700671945.h1

Seq. No. 12981

Contig ID 26883 1.R1040

5'-most EST jC-gmle01810072c02d1

Seq. No. 12982

Contig ID 26884\_1.R1040

5'-most EST LIB3107-063-Q1-K1-G2

Seq. No. 12983

Contig ID 26893\_1.R1040

5'-most EST LIB3051-009-Q1-E1-E11

Seq. No. 12984

Contig ID 26895\_1.R1040

5'-most EST jC-gmst02400055f03a1

Method BLASTX
NCBI GI g4566495
BLAST score 160
E value 8.0e-11
Match length 87

Match length 87 % identity 39

NCBI Description (AF098300) topoisomerase I-binding RS protein [Homo

sapiens]

Seq. No. 12985

Contig ID 26901\_1.R1040

5'-most EST LIB3139-061-P1-N1-D10

Method BLASTN
NCBI GI g170205
BLAST score 110
E value 1.0e-54
Match length 378
% identity 82

NCBI Description N.plumbaginifolia H+-translocating ATPase mRNA

Seq. No. 12986

Contig ID 26904\_1.R1040



LIB3051-009-Q1-E1-G3 5'-most EST

BLASTN Method q2656024 NCBI GI

46 BLAST score

2.0e-16 E value 280 Match length 85 % identity

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K15E6

12987 Seq. No.

26905 1.R1040 Contig ID xpa700793238.h1 5'-most EST

Seq. No. 12988

26911 1.R1040 Contig ID

jC-gmle01810049a07d1 5'-most EST

12989 Seq. No.

26912 1.R1040 Contig ID

LIB3051-010-Q1-E1-A10 5'-most EST

BLASTX Method g3540202 NCBI GI 207 BLAST score 3.0e-16E value Match length 164 % identity

NCBI Description (AC004260) Hypothetical protein [Arabidopsis thaliana]

12990 Seq. No.

26912 2.R1040 Contig ID gsv701048447.h1 5'-most EST

12991 Seq. No.

26914 1.R1040 Contig ID

LIB3051-010-Q1-E1-A12 5'-most EST

12992 Seq. No.

26917 1.R1040 Contig ID 5'-most EST uaw700666215.hl

12993 Seq. No.

26918 1.R1040 Contig ID

jC-gmf102220125b05a1 5'-most EST

Method BLASTX q3913996 NCBI GI 862 BLAST score 1.0e-106 E value Match length 278 75 % identity

MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR NCBI Description

>qi 2208927 dbj BAA20482 (D85610) ATP-dependent protease

Lon [Spinacia oleracea]

12994 Seq. No.

26920 1.R1040 Contig ID

LIB3051-010-Q1-E1-B3 5'-most EST



```
BLASTX
Method
NCBI GI
                  q4204275
BLAST score
                  161
                  7.0e-11
E value
                  162
Match length
% identity
                   31
NCBI Description
                  (AC004146) Unknown protein [Arabidopsis thaliana]
                  12995
Seq. No.
                   26924 1.R1040
Contig ID
5'-most EST
                  jC-gmro02910031c12a1
Seq. No.
                   12996
                   26933 1.R1040
Contig ID
5'-most EST
                  LIB3139-028-P1-N1-C10
                  BLASTX
Method
                   q3212866
NCBI GI
BLAST score
                   161
                   1.0e-10
E value
Match length
                   171
                   32
% identity
                  (AC004005) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   12997
                   26935 1.R1040
Contig ID
5'-most EST
                  LIB3051-010-Q1-E1-D10
Method
                   BLASTX
                   q4263790
NCBI GI
BLAST score
                   636
                   1.0e-66
E value
Match length
                   156
                   78
% identity
NCBI Description
                  (AC006068) putative ch-TOG protein [Arabidopsis thaliana]
Seq. No.
                   12998
                   26941 1.R1040
Contig ID
                   fua701038762.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2501555
BLAST score
                   327
E value
                   3.0e-30
Match length
                   113
% identity
                   57
                   POSSIBLE APOSPORY-ASSOCIATED PROTEIN C >gi 549984 (U13148)
NCBI Description
                   possible apospory-associated protein [Pennisetum ciliare]
Seq. No.
                   12999
                   26941 2.R1040
Contig ID
5'-most EST
                   LIB3109-035-Q1-K3-A8
Method
                   BLASTX
                   q4539308
NCBI GI
                   289
BLAST score
                   8.0e-26
E value
                   93
Match length
```

[Arabidopsis thaliana]

58

% identity

NCBI Description

(AL049480) possible apospory-associated like protein



```
13000
Seq. No.
Contig ID
                   26942 1.R1040
                   jC-gmro02910061c03d1
5'-most EST
Seq. No.
                   13001
                   26944 1.R1040
Contig ID
                   jC-gmst02400029d11d1
5'-most EST
                   BLASTX
Method
                   g2760321
NCBI GI
                   364
BLAST score
                   2.0e-34
E value
                   95
Match length
                   69
% identity
                  (AC002130) F1N21.6 [Arabidopsis thaliana]
NCBI Description
                   13002
Seq. No.
                   26944 2.R1040
Contig ID
5'-most EST
                   rca70\overline{0}995991.h1
                   BLASTX
Method
                   g2760321
NCBI GI
BLAST score
                   559
                   2.0e-57
E value
                   152
Match length
% identity
                   68
                  (AC002130) F1N21.6 [Arabidopsis thaliana]
NCBI Description
                   13003
Seq. No.
                   26944 3.R1040
Contig ID
5'-most EST
                   trc700565320.h1
                   BLASTX
Method
                   q2760321
NCBI GI
BLAST score
                   302
                   2.0e-27
E value
Match length
                   102
                   52
% identity
                  (AC002130) F1N21.6 [Arabidopsis thaliana]
NCBI Description
                   13004
Seq. No.
Contig ID
                   26946 1.R1040
                   LIB3051-102-Q1-K1-H12
5'-most EST
                   13005
Seq. No.
                   26947 1.R1040
Contig ID
5'-most EST
                   LIB30\overline{5}1-010-Q1-E1-E6
Seq. No.
                   13006
                   26953 1.R1040
Contig ID
5'-most EST
                   sat701008746.h1
Seq. No.
                   13007
                   26955 1.R1040
Contig ID
```

5'-most EST LIB3051-010-Q1-E1-H1

BLASTX Method q1175426 NCBI GI BLAST score 264

E value 1.0e-22



Match length 123 % identity 49

NCBI Description PUTATIVE ATP-DEPENDENT RNA HELICASE C12C2.06

>gi 984214 emb CAA90819\_ (Z54140) probable ATP-dependent

RNA helicase [Schizosaccharomyces pombe]

Seq. No. 13008

Contig ID 26961\_1.R1040 5'-most EST rlr700901296.h1

Method BLASTX
NCBI GI g4432863
BLAST score 208
E value 4.0e-16
Match length 200
% identity 25

NCBI Description (AC006300) putative phosphate/phosphoenolpyruvate

translocator protein [Arabidopsis thaliana]

Seq. No. 13009

Contig ID 26962 1.R1040

5'-most EST LIB3139-118-P1-N1-H4

Method BLASTX
NCBI GI g3820981
BLAST score 307
E value 9.0e-28
Match length 149
% identity 39

NCBI Description (AL031228) dJ1033B10.5 (SAC2 (suppressor of actin mutation

2, yeast, homolog)-LIKE (ARE1)) [Homo sapiens]

Seq. No. 13010

Contig ID 26962 2.R1040

5'-most EST uC-gmflminsoy070e12b1

Seq. No. 13011

Contig ID 26965 1.R1040

5'-most EST LIB3051-011-Q1-E1-A6

Seq. No. 13012

Contig ID 26967 1.R1040 5'-most EST zhf700953919.h1

Seq. No. 13013

Contig ID 26973\_1.R1040 5'-most EST sat701012340.h1

Seq. No. 13014

Contig ID 26975\_1.R1040 5'-most EST crh700850209.h1

Seq. No. 13015

Contig ID 26975\_2.R1040 5'-most EST gsv70\overline{1052579.h1}

Seq. No. 13016

Contig ID 26991\_1.R1040 5'-most EST eep700866189.h1



```
Method
                   BLASTX
NCBI GI
                   g3850821
BLAST score
                   1562
                   1.0e-174
E value
                   360
Match length
                   83
% identity
                   (Y18350) U2 snRNP auxiliary factor, large subunit
NCBI Description
                   [Nicotiana plumbaginifolia]
                   13017
Seq. No.
                   26991 2.R1040
Contig ID
                   g4396457
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3850823
BLAST score
                   286
                   2.0e-25
E value
                   67
Match length
                   78
% identity
                   (Y18351) U2 snRNP auxiliary factor, large subunit
NCBI Description
                   [Nicotiana plumbaginifolia]
                   13018
Seq. No.
                   26991 3.R1040
Contig ID
                   jC-gmf102220101g10a1
5'-most EST
                   BLASTX
Method
                   g3850823
NCBI GI
                   394
BLAST score
                   4.0e-38
E value
                   95
Match length
                   81
% identity
                   (Y18351) U2 snRNP auxiliary factor, large subunit
NCBI Description
                   [Nicotiana plumbaginifolia]
                   13019
Seq. No.
                   26996 1.R1040
Contig ID
5'-most EST
                   uxk70\overline{0}671012.h1
                   13020
Seq. No.
                   27000 1.R1040
Contig ID
5'-most EST
                   seb70\overline{0}651428.h1
Method
                   BLASTX
                   g2673914
NCBI GI
                   1606
BLAST score
                   1.0e-179
E value
Match length
                   546
% identity
                   60
                   (AC002561) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   13021
Seq. No.
                   27004 1.R1040
Contig ID
5'-most EST
                   LIB3051-012-Q1-E1-C6
                   13022
Seq. No.
```

Contig ID 27006\_1.R1040
5'-most EST LIB3051-012-Q1-E1-D11
Method BLASTN
NCBI GI g4519192

```
BLAST score
                  1.0e-11
E value
                  138
Match length
                  82
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MBK21, complete sequence
                  13023
Seq. No.
                   27016 1.R1040
Contig ID
                  LIB3051-066-Q1-K1-D6
5'-most EST
                   13024
Seq. No.
                   27017 1.R1040
Contig ID
                   jC-gmro02910048e01a1
5'-most EST
                   BLASTX
Method
                   g3850113
NCBI GI
                   165
BLAST score
                   4.0e-11
E value
Match length
                   147
                   46
% identity
                   (AL033388) hypothetical integral membrane protein
NCBI Description
                   [Schizosaccharomyces pombe]
                   13025
Seq. No.
                   27022 1.R1040
Contig ID
                   LIB3051-012-Q1-E1-H10
5'-most EST
                   13026
Seq. No.
                   27026 1.R1040
Contig ID
                   jC-gmro02910037b12a1
5'-most EST
                   BLASTX
Method
                   g2894607
NCBI GI
                   332
BLAST score
                   1.0e-30
E value
                   103
Match length
                   59
% identity
                   (AL021889) NAM (no apical meristem) - like protein
NCBI Description
                   [Arabidopsis thaliana]
                   13027
Seq. No.
```

27026 2.R1040 Contig ID

LIB3138-018-Q1-N1-A12 5'-most EST

13028 Seq. No.

27028 1.R1040 Contig ID

LIB3107-031-Q1-K1-E8 5'-most EST

BLASTX Method g2213547 NCBI GI BLAST score 218 2.0e-17 E value Match length 97 % identity 49

(Z97052) putative ubiquinone biosynthesis methyltransferase NCBI Description

[Schizosaccharomyces pombe]

13029 Seq. No.

27032 1.R1040 Contig ID



```
LIB3138-034-Q1-N1-H8
5'-most EST
Seq. No.
                  13030
Contig ID
                  27037 1.R1040
                  LIB3051-013-Q1-E1-C4
5'-most EST
Seq. No.
                  13031
                  27044 1.R1040
Contig ID
                  LIB3051-013-Q1-E1-E7
5'-most EST
                  BLASTX
Method
                  g4512676
NCBI GI
                  257
BLAST score
                  4.0e-22
E value
Match length
                  84
% identity
NCBI Description (AC006931) unknown protein [Arabidopsis thaliana]
                  13032
Seq. No.
                  27045 1.R1040
Contig ID
                  LIB3051-013-Q1-E1-E8
5'-most EST
Seq. No.
                   13033
                   27047 1.R1040
Contig ID
                  LIB3073-004-Q1-K1-H5
5'-most EST
                   BLASTX
Method
                   g2462759
NCBI GI
BLAST score
                   357
                   1.0e-33
E value
                   73
Match length
% identity
                   85
NCBI Description (AC002292) Putative Cytochrome B5 [Arabidopsis thaliana]
                   13034
Seq. No.
                   27047_2.R1040
Contig ID
                   crh700850908.h1
5'-most EST
                   13035
Seq. No.
                   27050 1.R1040
Contig ID
                   uC-gmrominsoy205b11b1
5'-most EST
                   13036
Seq. No.
                   27053 1.R1040
Contig ID
                   kmv70\overline{0}740120.h1
5'-most EST
                   BLASTX
Method
                   g2134385
NCBI GI
                   963
BLAST score
                   1.0e-104
E value
                   317
Match length
                   59
% identity
                   protein kinase - chicken >gi_571460 (U16656) protein kinase
NCBI Description
                   [Gallus gallus]
                   13037
Seq. No.
                   27053 2.R1040
Contig ID
                   uC-gmropic064c11b1
 5'-most EST
Method
                   BLASTX
```

g2134385

NCBI GI



BLAST score 271 E value 2.0e-23 Match length 110 % identity 50

NCBI Description protein kinase - chicken >gi\_571460 (U16656) protein kinase

[Gallus gallus]

Seq. No. 13038

Contig ID 27053 3.R1040

5'-most EST jC-gmro02910005a12a1

Seq. No. 13039

Contig ID 27055\_1.R1040

5'-most EST LIB3051-014-Q1-E1-A1

Seq. No. 13040

Contig ID 27055 2.R1040 5'-most EST ncj700987764.h1

Seq. No. 13041

Contig ID 27059\_1.R1040 5'-most EST zhf700964622.h1

Seq. No. 13042

Contig ID 27061\_1.R1040 5'-most EST rlr700898884.h1

Method BLASTX
NCBI GI g2342682
BLAST score 100
E value 5.0e-15
Match length 126
% identity 46

NCBI Description (AC000106) Contains similarity to Rattus AMP-activated

protein kinase (gb\_X95577). [Arabidopsis thaliana]

Seq. No. 13043

Contig ID 27062\_1.R1040 5'-most EST zhf700954693.h1

Seq. No. 13044

Contig ID 27065\_1.R1040

5'-most EST LIB3109-041-Q1-K1-D1

Method BLASTX
NCBI GI g3451068
BLAST score 425
E value 7.0e-42
Match length 113
% identity 72

NCBI Description (AL031326) putative protein [Arabidopsis thaliana]

Seq. No. 13045

Contig ID 27071\_1.R1040

5'-most EST LIB3051-014-Q1-E1-D8

Method BLASTX
NCBI GI g3152596
BLAST score 238
E value 6.0e-20



Match length 79 % identity (AC002986) YUP8H12R.36 [Arabidopsis thaliana]

NCBI Description

13046

Seq. No. 27073 1.R1040 Contig ID awf700837868.hl 5'-most EST

BLASTX Method g4538981 NCBI GI 219 BLAST score 8.0e-18 E value 130 Match length % identity

(ALO49487) putative protein [Arabidopsis thaliana] NCBI Description

Seq. No.

13047

Contig ID

27077 1.R1040

5'-most EST

LIB3051-014-Q1-E1-E9

Seq. No.

13048

Contig ID

27077 2.R1040

5'-most EST

uC-gmrominsoy090g04b1

BLASTX Method g4314390 NCBI GI BLAST score 318 E value 3.0e-29 142 Match length % identity 47

(AC006232) putative calcium binding protein [Arabidopsis NCBI Description

Seq. No.

13049

thaliana]

Contig ID

27078 1.R1040

5'-most EST

LIB3094-014-Q1-K1-E11

BLASTX Method g2232354 NCBI GI 381 BLAST score 3.0e-36 E value 331 Match length % identity 31

(AF006081) UDPG glucosyltransferase [Solanum berthaultii] NCBI Description

Seq. No.

13050

Contig ID

27078 2.R1040

g4304087 5'-most EST BLASTX Method g2232354 NCBI GI 251 BLAST score E value 1.0e-21 110 Match length

% identity NCBI Description

(AF006081) UDPG glucosyltransferase [Solanum berthaultii]

Seq. No.

13051

45

Contig ID 5'-most EST 27079 1.R1040 trc700561182.hl

Method

BLASTX



```
q4539314
NCBI GI
                  516
BLAST score
                  5.0e-52
E value
Match length
                  212
% identity
                  52
                  (AL035679) kinesin like protein [Arabidopsis thaliana]
NCBI Description
                  13052
Seq. No.
                  27080 1.R1040
Contig ID
                  LIB3051-014-Q1-E1-F5
5'-most EST
Seq. No.
                  13053
                  27085 1.R1040
Contig ID
                  LIB3051-014-Q1-E1-G6
5'-most EST
Seq. No.
                  13054
                  27086 1.R1040
Contig ID
                  LIB3051-014-Q1-E1-G7
5'-most EST
Method
                  BLASTX
NCBI GI
                   q3135268
BLAST score
                   277
E value
                   2.0e-24
Match length
                   149
                   37
% identity
                   (AC003058) putative RNA-binding protein [Arabidopsis
NCBI Description
                   thaliana]
                   13055
Seq. No.
Contig ID
                   27092 1.R1040
                   LIB3051-015-Q1-E1-A7
5'-most EST
Seq. No.
                   13056
                   27100 1.R1040
Contig ID
                   uC-gmrominsoy062a04b1
5'-most EST
                   13057
Seq. No.
                   27102 1.R1040
Contig ID
5'-most EST
                   rlr700897006.h1
Seq. No.
                   13058
                   27103 1.R1040
Contig ID
                   gsv701047882.hl
5'-most EST
                   BLASTX
Method
                   q2832628
NCBI GI
                   634
BLAST score
E value
                   2.0e-65
                   275
Match length
                   52
% identity
                  (AL021711) putative protein [Arabidopsis thaliana]
NCBI Description
                   13059
Seq. No.
Contig ID
                   27103 2.R1040
                   uC-gmropic023b01b1
5'-most EST
```

13060 Seq. No. Contig ID 27103 4.R1040

jC-gmle01810064g09d1

5'-most EST



Seq. No. 13061

Contig ID 27108\_1.R1040

5'-most EST LIB3139-031-P1-N1-F10

Seq. No. 13062

Contig ID 27108\_2.R1040

5'-most EST LIB3051-015-Q1-E1-G8

Seq. No. 13063

Contig ID 27109\_1.R1040

5'-most EST uC-gmrominsoy311b02b1

Method BLASTX
NCBI GI g3879150
BLAST score 244
E value 2.0e-20
Match length 112
% identity 47

NCBI Description (Z70686) Similarity to Yeast hypothetical protein YKEO

(SW:YKE0\_YEAST); cDNA EST yk254g6.3 comes from this gene; cDNA EST yk254g6.5 comes from this gene [Caenorhabditis

elegans]

Seq. No. 13064

Contig ID 27123\_1.R1040

5'-most EST LIB3051-016-Q1-E1-D2

Method BLASTX
NCBI GI g2809250
BLAST score 630
E value 8.0e-66
Match length 158
% identity 73

NCBI Description (AC002560) F21B7.19 [Arabidopsis thaliana]

Seq. No.

13065

Contig ID 27124\_1.R1040

5'-most EST LIB3109-038-Q1-K1-A8

Seq. No.

13066

Contig ID 27125\_1.R1040 5'-most EST bth700846279.h1

Seq. No.

13067

Contig ID 27125\_2.R1040

5'-most EST LIB3109-047-Q1-K1-H1

Seq. No.

13068

Contig ID 27127\_1.R1040 5'-most EST bth700845322.h1

Method BLASTX
NCBI GI g2829926
BLAST score 150
E value 2.0e-09
Match length 61
% identity 54

NCBI Description (AC002291) Hypothetical protein [Arabidopsis thaliana]



```
Seq. No.
Contig ID
                   27133 1.R1040
5'-most EST
                  LIB3051-016-Q1-E1-F8
Seq. No.
                  13070
Contig ID
                   27137 1.R1040
5'-most EST
                  jC-gmro02910007b12a1
Seq. No.
                  13071
Contig ID
                  27140 1.R1040
                  LIB3138-095-Q1-N1-C5
5'-most EST
Method
                  BLASTX
                   g2829889
NCBI GI
BLAST score
                   372
E value
                   3.0e-35
Match length
                   119
% identity
                   66
                  (AC002396) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   13072
                   27140 2.R1040
Contig ID
5'-most EST
                  LIB3106-086-Q1-K1-E1
Seq. No.
                   13073
Contig ID
                   27140 3.R1040
5'-most EST
                   rca700997083.hl
                   BLASTX
Method
NCBI GI
                   g2213621
BLAST score
                   229
E value
                   6.0e-19
Match length
                   98
% identity
                   53
NCBI Description (AC000103) F21J9.26 [Arabidopsis thaliana]
                   13074
Seq. No.
                   27141 1.R1040
Contig ID
5'-most EST
                   epx701105189.h1
                   BLASTX
Method
NCBI GI
                   g2829887
                   273
BLAST score
E value
                   5.0e-24
                   131
Match length
% identity
NCBI Description
                  (AC002396) Hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   13075
Contig ID
                   27142 1.R1040
5'-most EST
                   jC-gmst02400050a04a1
Seq. No.
                   13076
                   27150 1.R1040
Contig ID
```

5'-most EST LIB3051-017-Q1-E1-C7

BLASTX Method NCBI GI q2213600 BLAST score 418 2.0e-40 E value Match length 221



% identity NCBI Description (AC000348) T7N9.20 [Arabidopsis thaliana] 13077 Seq. No. 27152 1.R1040 Contig ID uC-gmrominsoy285d09b1 5'-most EST BLASTX Method g4467147 NCBI GI 754 BLAST score 4.0e-80 E value 251 Match length 63 % identity NCBI Description (AL035540) putative protein [Arabidopsis thaliana] Seq. No. 13078 27159 1.R1040 Contig ID  $smc70\overline{0}748595.h1$ 5'-most EST BLASTX Method g4206122 NCBI GI 1352 BLAST score 1.0e-162 E value 357 Match length 80 % identity (AF097667) protein phosphatase 2C homolog [Mesembryanthemum NCBI Description crystallinum] 13079 Seq. No. 27159 2.R1040 Contig ID q4313<del>9</del>23 5'-most EST BLASTX Method g3608412 NCBI GI 381 BLAST score 2.0e-36 E value 80 Match length 89 % identity (AF079355) protein phosphatase-2c [Mesembryanthemum NCBI Description crystallinum] 13080 Seq. No. 27165 1.R1040 Contig ID LIB3093-032-Q1-K1-H5 5'-most EST Method BLASTX g2582639 NCBI GI 742 BLAST score 1.0e-79 E value Match length 394 31 % identity (AJ002414) hnRNP-like protein [Arabidopsis thaliana] NCBI Description 13081 Seq. No. 27165 2.R1040 Contig ID LIB3107-044-Q1-K1-B5 5'-most EST

Method BLASTX
NCBI GI g2244786
BLAST score 154
E value 6.0e-10
Match length 40



```
% identity
NCBI Description (Z97335) ribonucleoprotein homolog [Arabidopsis thaliana]
                   13082
Seq. No.
                   27165 3.R1040
Contig ID
                   uC-gmropic062a10b1
5'-most EST
                   BLASTX
Method
                   g2582639
NCBI GI
                   217
BLAST score
                   2.0e-35
E value
                   102
Match length
                   81
% identity
NCBI Description (AJ002414) hnRNP-like protein [Arabidopsis thaliana]
Seq. No.
                   13083
                   27168 1.R1040
Contig ID
                   V4L-01-Q1-B1-H4
5'-most EST
                   13084
Seq. No.
                   27171 1.R1040
Contig ID
                   trc700562208.h1
5'-most EST
                   BLASTX
Method
                   g4544409
NCBI GI
                   1271
BLAST score
                   1.0e-140
E value
Match length
                   380
% identity
                   (AC006955) putative transcription factor [Arabidopsis
NCBI Description
                   thaliana]
                   13085
Seq. No.
                   27174 1.R1040
Contig ID
                   LIB3051-105-Q1-K1-F2
5'-most EST
                   BLASTX
Method
                   g1723176
NCBI GI
                    174
BLAST score
                    4.0e-12
E value
                    64
Match length
                    55
% identity
                   HYPOTHETICAL 22.4 KD PROTEIN SLL0615
NCBI Description
                    >gi 1001617_dbj_BAA10348_ (D64002) transmembrane protein
FT27 [Synechocystis sp.] >gi_1256592 (U38892) similar to
                    Mus musculus transmembrane protein (clone pFT27); Method:
                    conceptual translation supplied by author; ORF206
                    [Synechocystis sp.]
                    13086
Seq. No.
                    27178 1.R1040
Contig ID
5'-most EST
                    LIB3051-018-Q1-E1-B8
Method
                    BLASTX
```

Method BLASTX
NCBI GI g3130051
BLAST score 275
E value 4.0e-24
Match length 128
% identity 45

NCBI Description (AL023518) conserved hypothetical protein

[Schizosaccharomyces pombe]



```
13087
Seq. No.
                  27179 1.R1040
Contig ID
                  LIB3051-018-Q1-E1-B9
5'-most EST
                  13088
Seq. No.
                  27180 1.R1040
Contig ID
                  uC-gmflminsoy007c03b1
5'-most EST
                  BLASTX
Method
                  g2827469
NCBI GI
                  901
BLAST score
                  7.0e-97
E value
                   568
Match length
% identity
                   36
```

NCBI Description (AF044255) NOSA [Dictyostelium discoideum]

13089 Seq. No. 27184 1.R1040 Contig ID LIB3051-018-Q1-E1-C7 5'-most EST BLASTN Method g3399678

NCBI GI 74 BLAST score 2.0e-33 E value 206 Match length 84 % identity

Arabidopsis thaliana chromosome 1 BAC F13M7 sequence, NCBI Description

complete sequence [Arabidopsis thaliana]

13090 Seq. No.

27186 1.R1040 Contig ID pmv700895189.h1 5'-most EST

BLASTX Method g136452 NCBI GI 409 BLAST score 6.0e-40 E value 128 Match length 62 % identity

STEM-SPECIFIC PROTEIN TSJT1 >gi\_100383\_pir\_\_S13551 NCBI Description

stem-specific protein - common tobacco
>gi\_20037\_emb\_CAA36525\_ (X52283) stem specific, weakly

expressed in other organs [Nicotiana tabacum]

13091 Seq. No.

27194 1.R1040 Contig ID

5'-most EST LIB3051-018-Q1-E1-F12

13092 Seq. No.

27194 2.R1040 Contig ID

5'-most EST LIB3170-057-Q1-K1-A1

Seq. No. 13093

27197 1.R1040 Contig ID

LIB3051-018-Q1-E1-F8 5'-most EST

13094 Seq. No.

27212 1.R1040 Contig ID 5'-most EST uC-gmropic011b01b1



```
Method
                  BLASTX
                  g4539423
NCBI GI
                  1446
BLAST score
                  1.0e-161
E value
                  323
Match length
                  86
% identity
                  (AL049171) pyrophosphate-dependent phosphofructo-1-kinase
NCBI Description
                   [Arabidopsis thaliana]
                  13095
Seq. No.
                  27212 2.R1040
Contig ID
                  vwf700676527.h1
5'-most EST
Seq. No.
                  13096
                  27213 1.R1040
```

Contig ID LIB3051-019-Q1-E1-B12 5'-most EST BLASTX Method g4220480 NCBI GI BLAST score 604 1.0e-62 E value 170 Match length

40

% identity NCBI Description (AC006069) unknown protein [Arabidopsis thaliana]

Seq. No. 13097 27215 1.R1040 Contig ID kl1701210318.hl 5'-most EST BLASTX Method g3790569 NCBI GI 158 BLAST score

7.0e-24 E value 152 Match length 43 % identity

(AF078822) RING-H2 finger protein RHA2a [Arabidopsis NCBI Description

thaliana]

13098 Seq. No. 27215 2.R1040 Contig ID awf700839479.h1 5'-most EST

13099 Seq. No.

27217 1.R1040 Contig ID uC-gmrominsoy189g03b1 5'-most EST

BLASTX Method NCBI GI g3695063 BLAST score 541 3.0e-55 E value 127 Match length 82 % identity

(AF064789) rac GTPase activating protein 3 [Lotus NCBI Description

japonicus]

13100

Seq. No. Contig ID

27233 1.R1040 5'-most EST fde700875589.hl

Method BLASTX NCBI GI g3927836



288 BLAST score 3.0e-25 E value 224 Match length % identity 36 NCBI Description (AC005727) unknown protein [Arabidopsis thaliana] 13101 Seq. No. 27233 2.R1040 Contig ID LIB3051-019-Q1-E1-D6 5'-most EST BLASTX Method g3927836 NCBI GI 150 BLAST score 2.0e-16 E value 171 Match length 35 % identity NCBI Description (AC005727) unknown protein [Arabidopsis thaliana] 13102 Seq. No. 27236 1.R1040 Contig ID LIB3051-019-Q1-E1-E10 5'-most EST Method BLASTX g3882239 NCBI GI 149 BLAST score 2.0e-09 E value 78 Match length 40 % identity NCBI Description (AB018302) KIAA0759 protein [Homo sapiens] 13103 Seq. No. 27239 1.R1040 Contig ID LIB3051-019-Q1-E1-E3 5'-most EST 13104 Seq. No. 27239 2.R1040 Contig ID LIB3167-017-P1-K1-H3 5'-most EST 13105 Seq. No. 27242 1.R1040 Contig ID LIB3107-039-Q1-K1-E10 5'-most EST 13106 Seq. No. 27248 1.R1040 Contig ID LIB3051-019-Q1-E1-F9 5'-most EST BLASTX Method g4314363 NCBI GI 220 BLAST score 7.0e-18 E value 125 Match length 47 % identity (AC006340) hypothetical protein [Arabidopsis thaliana] NCBI Description 13107 Seq. No. 27250 1.R1040 Contig ID

LIB3051-019-Q1-E1-G3 5'-most EST

BLASTX Method NCBI GI g1871185 BLAST score 621



E value 1.0e-64 Match length 133 % identity 83

NCBI Description (U90439) seven in absentia isolog [Arabidopsis thaliana]

Seq. No. 13108

Contig ID 27253\_1.R1040

5'-most EST LIB3051-019-Q1-E1-H1

Seq. No. 13109

Contig ID 27255\_1.R1040 5'-most EST fC-gmle700560219a1

Method BLASTX
NCBI GI g3925363
BLAST score 1319
E value 1.0e-146
Match length 463
% identity 58

NCBI Description (AF067961) homeodomain protein [Malus domestica]

Seq. No. 13110

Contig ID 27258\_1.R1040

5'-most EST LIB3051-019-Q1-E1-H9

Seq. No. 13111

Contig ID 27258\_2.R1040 5'-most EST g4396758

Seq. No. 13112

Contig ID 27285\_1.R1040

5'-most EST LIB3051-020-Q1-E1-A2

Method BLASTN
NCBI GI g4159701
BLAST score 43
E value 6.0e-15
Match length 116

% identity 90 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K22G18, complete sequence [Arabidopsis thaliana]

Seq. No. 13113

Contig ID 27289 1.R1040

5'-most EST LIB3052-012-Q1-N1-H10

Method BLASTX
NCBI GI g1929067
BLAST score 646
E value 6.0e-67
Match length 518
% identity 32

NCBI Description (Z93777) fadD36 [Mycobacterium tuberculosis]

Seq. No. 13114

Contig ID 27289\_3.R1040 5'-most EST fC-gmst700651302d4

Seq. No. 13115

Contig ID 27294\_1.R1040



```
LIB3051-020-Q1-E1-C10
5'-most EST
                  BLASTX
Method
                  g3080437
NCBI GI
                  153
BLAST score
                  6.0e-10
E value
                  38
Match length
                  79
% identity
                  (AL022605) putative protein [Arabidopsis thaliana]
NCBI Description
                  13116
Seq. No.
                  27298 1.R1040
Contig ID
                  LIB3170-077-Q1-K1-B6
5'-most EST
                  13117
Seq. No.
                  27298 2.R1040
Contig ID
                  wvk700684521.h1
5'-most EST
                   13118
Seq. No.
                   27299 1.R1040
Contig ID
                   jC-gm\overline{l}e01810006f05a1
5'-most EST
                   BLASTN
Method
                   g1871173
NCBI GI
                   79
BLAST score
                   4.0e-36
E value
                   262
Match length
                   84
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC T06D20 genomic
                   sequence, complete sequence
                   13119
Seq. No.
                   27301 1.R1040
Contig ID
                   wvk700682732.hl
5'-most EST
                   BLASTX
Method
                   g1619300
NCBI GI
BLAST score
                   545
                   1.0e-55
E value
                   145
Match length
                   70
% identity
                   (X95269) LRR protein [Lycopersicon esculentum]
NCBI Description
                   13120
Seq. No.
                   27302 1.R1040
Contig ID
                   jC-gmro02800029a08a1
5'-most EST
                   13121
Seq. No.
                   27310 1.R1040
Contig ID
                   uC-gmrominsoy231e06b1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4531444
                   565
BLAST score
E value
                   6.0e-58
                   163
Match length
                   69
 % identity
                   (AC006224) putative protein kinase [Arabidopsis thaliana]
NCBI Description
```

13122

27310\_2.R1040

Seq. No.

Contig ID



```
uC-gmrominsoy206b02b1
5'-most EST
                  13123
Seq. No.
                  27310 3.R1040
Contiq ID
                  jC-gmro02910009b02a1
5'-most EST
                  13124
Seq. No.
                  27325 1.R1040
Contig ID
                  uC-gmropic012h01b1
5'-most EST
                  BLASTX
Method
                  g2462834
NCBI GI
                   402
BLAST score
                   8.0e-39
E value
                   182
Match length
% identity
                   49
NCBI Description (AF000657) hypothetical protein [Arabidopsis thaliana]
                   13125
Seq. No.
                   27328 1.R1040
Contig ID
                   LIB3107-011-Q1-K1-E5
5'-most EST
                   13126
Seq. No.
                   27330 1.R1040
Contig ID
                   hrw701063079.hl
5'-most EST
                   13127
Seq. No.
                   27335 1.R1040
Contig ID
                   zhf700964526.h1
5'-most EST
                   BLASTX
Method
                   g2088651
NCBI GI
                   224
BLAST score
                   3.0e-18
E value
                   119
Match length
                   44
% identity
NCBI Description (AF002109) hypersensitivity-related gene 201 isolog
                   [Arabidopsis thaliana]
                   13128
Seq. No.
                   27345 1.R1040
Contig ID
5'-most EST
                   LIB3051-023-Q1-K1-B7
                   13129
Seq. No.
                   27356 1.R1040
Contig ID
                   uaw70\overline{0}665019.h1
5'-most EST
                   BLASTX
Method
                   q3582779
NCBI GI
BLAST score
                   458
                   9.0e-46
E value
                   139
Match length
% identity
                   44
                   (AF056282) peroxisomal targeting sequence 1 receptor
NCBI Description
                    [Nicotiana tabacum]
```

Seq. No. 13130

Contig ID 27362\_1.R1040

5'-most EST LIB3139-096-P1-N1-B1

Method BLASTX



NCBI GI g4538929 BLAST score 336 E value 7.0e-31 Match length 215 % identity 38

NCBI Description (AL049483) putative nucleic acid binding protein

[Arabidopsis thaliana]

Seq. No. 13131

Contig ID 27371\_1.R1040

5'-most EST LIB3139-028-P1-N1-B5

Method BLASTX
NCBI GI g2894378
BLAST score 240
E value 4.0e-20
Match length 123
% identity 44

NCBI Description (Y14573) putative ribophorin I homologue [Hordeum vulgare]

Seq. No. 13132

Contig ID 27371\_2.R1040

5'-most EST jC-gmle01810041d02a1

Seq. No. 13133

Contig ID 27372\_1.R1040

5'-most EST LIB3051-024-Q1-K1-B4

Seq. No. 13134

Contig ID 27377 1.R1040 5'-most EST uC-gmropic032g12b1

Method BLASTX
NCBI GI 94544409
BLAST score 389
E value 4.0e-37
Match length 120
% identity 62

NCBI Description (AC006955) putative transcription factor [Arabidopsis

thaliana]

Seq. No. 13135

Contig ID 27377\_2.R1040 5'-most EST uC-gmronoir068c10b1

Seq. No. 13136

Contig ID 27377\_5.R1040

5'-most EST LIB3051-024-Q1-K1-C6

Seq. No. 13137

Contig ID 27394\_1.R1040 5'-most EST kl1701203659.h2

Seq. No. 13138

Contig ID 27395\_1.R1040 5'-most EST fC-gmf1700908011a1

Method BLASTX
NCBI GI g4539330
BLAST score 790



E value 3.0e-84
Match length 225
% identity 72

% identity 72
NCBI Description (AL035679) putative receptor-like protein kinase (fragment)

[Arabidopsis thaliana]

Seq. No. 13139

Contig ID 27406 1.R1040

5'-most EST LIB3051-025-Q1-K1-D1

Seq. No. 13140

Contig ID 27407\_1.R1040

5'-most EST LIB30 $\overline{5}$ 1-025-Q1-K1-D10

Seq. No. 13141

Contig ID 27409\_1.R1040

5'-most EST LIB3051-025-Q1-K1-D6

Seq. No. 13142

Contig ID 27413\_1.R1040

5'-most EST LIB3051-025-Q1-K1-E7

Seq. No. 13143

Contig ID 27414\_1.R1040

5'-most EST LIB3139-041-P1-N1-B9

Method BLASTX
NCBI GI g4572676
BLAST score 124
E value 3.0e-13
Match length 150

% identity 33

NCBI Description (AC006954) unknown protein [Arabidopsis thaliana]

Seq. No. 13144

Contig ID 27418\_1.R1040

5'-most EST jC-gmf102220079h01a1

Method BLASTX
NCBI GI g4206122
BLAST score 436
E value 7.0e-43
Match length 171
% identity 50

NCBI Description (AF097667) protein phosphatase 2C homolog [Mesembryanthemum

crystallinum]

Seq. No. 13145

Contig ID 27419\_1.R1040 5'-most EST wvk700682790.h1

Seq. No. 13146

Contig ID 27425 1.R1040

5'-most EST LIB3051-025-Q1-K1-H4

Seq. No. 13147

Contig ID 27426 1.R1040

5'-most EST LIB3093-023-Q1-K1-E10



Seq. No. 1314

Contig ID 27429\_1.R1040 5'-most EST pcp700995406.h1

Seq. No. 13149

Contig ID 27435\_1.R1040 5'-most EST zhf700952773.h1

Seq. No. 13150

Contig ID 27439\_1.R1040 5'-most EST wrg700788979.h2

Method BLASTX
NCBI GI g4415938
BLAST score 332
E value 7.0e-31
Match length 103
% identity 63

NCBI Description (AC006418) unknown protein [Arabidopsis thaliana]

Seq. No. 13151

Contig ID 27445\_1.R1040 5'-most EST zpv700760243.h1

Seq. No. 13152

Contig ID 27446 1.R1040 5'-most EST smc700748391.h1

Method BLASTX
NCBI GI g4249402
BLAST score 525
E value 2.0e-53
Match length 152
% identity 69

NCBI Description (AC006072) unknown protein [Arabidopsis thaliana]

Seq. No.

13153

Contig ID 27451\_1.R1040

5'-most EST jC-gmro02910004d05a1

Method BLASTX
NCBI GI g3873621
BLAST score 305
E value 2.0e-27
Match length 172
% identity 44

NCBI Description (Z98262) similar to Ubiquitin family; cDNA EST EMBL:C11990

comes from this gene; cDNA EST EMBL:C08080 comes from this gene; cDNA EST EMBL:C08013 comes from this gene; cDNA EST EMBL:C08074 comes from this gene; cDNA EST EMBL:C09... >gi\_3875993\_emb\_CAA95799\_ (Z71260) similar to Ubiquitin family; cDNA EST EMBL:C11990 comes from this gene; cDNA EST EMBL:C08080 comes from this gene; cDNA EST EMBL:C08080 comes from this gene; cDNA EST EMBL:C08013

comes from this gene; cDNA EST EMBL: C08074 comes from this

gene; cDNA EST EMBL:C09

Seq. No. 13154

Contig ID 27459\_1.R1040 5'-most EST uaw700661060.h1



Seg. No. 13155

Contig ID 27467 1.R1040

5'-most EST LIB3051-027-Q1-K1-B11

Method BLASTX
NCBI GI g2827561
BLAST score 238
E value 2.0e-19
Match length 164
% identity 35

NCBI Description (AL021635) predicted protein [Arabidopsis thaliana]

>gi\_3292809\_emb\_CAA19799\_ (AL031018) putative protein

[Arabidopsis thaliana]

Seq. No. 13156

Contig ID 27471 1.R1040

5'-most EST LIB3051-027-Q1-K1-C11

Seq. No. 13157

Contig ID 27472 1.R1040

5'-most EST LIB3051-027-Q1-K1-C12

Seq. No. 13158

Contig ID 27474 1.R1040

5'-most EST LIB3094-005-Q1-K1-F6

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 2.0e-10
Match length 47
% identity 65

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 13159

Contig ID 27474\_2.R1040

5'-most EST LIB3051-027-Q1-K1-C8

Seq. No. 13160

Contig ID 27474\_3.R1040 5'-most EST ncj700979102.h1

Seq. No. 13161

Contig ID 27476\_1.R1040

5'-most EST LIB3051-027-Q1-K1-D11

Seq. No. 13162

Contig ID 27477 1.R1040

5'-most EST LIB3051-027-Q1-K1-D3

Seq. No. 13163

Contig ID 27482\_1.R1040

5'-most EST LIB3051-107-Q1-K1-B7

Method BLASTN
NCBI GI g4309719
BLAST score 40
E value 5.0e-13

Match length 44 % identity 98



NCBI Description Arabidopsis thaliana chromosome II BAC T30D6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 13164

Contig ID 27485\_1.R1040

5'-most EST LIB $30\overline{5}1-027-Q1-K1-E6$ 

Seq. No. 13165

Contig ID 27490\_1.R1040 5'-most EST pxt700943003.h1

Method BLASTX
NCBI GI 94406809
BLAST score 308
E value 1.0e-27
Match length 189
% identity 56

NCBI Description (AC006201) unknown protein [Arabidopsis thaliana]

Seq. No.

Contig ID 27494\_1.R1040 5'-most EST leu701154228.h1

Seq. No. 13167

Contig ID 27506\_1.R1040 5'-most EST gsv701046593.h1

Seq. No. 13168

Contig ID 27508 1.R1040

5'-most EST uC-gmflminsoy019d08b1

13166

Seq. No. 13169

Contig ID 27516 1.R1040

5'-most EST LIB3051-071-Q1-K1-H5

Seq. No. 13170

Contig ID 27516\_2.R1040 5'-most EST uaw700662916.h1

Seq. No. 13171

Contig ID 27518 1.R1040

5'-most EST LIB3138-015-Q1-N1-A4

Seq. No. 13172

Contig ID 27518\_2.R1040 5'-most EST leu701145734.h1

Seq. No. 13173

Contig ID 27530\_1.R1040 5'-most EST fde700875726.h1

Seq. No. 13174

Contig ID 27533\_1.R1040

5'-most EST LIB3051-028-Q1-K1-H6

Seq. No. 13175

Contig ID 27537\_1.R1040 5'-most EST uC-gmropic030a10b1



```
BLASTX
Method
                  g4206122
NCBI GI
                   451
BLAST score
                   2.0e-44
E value
                   108
Match length
                   77
% identity
                   (AF097667) protein phosphatase 2C homolog [Mesembryanthemum
NCBI Description
                   crystallinum]
                   13176
Seq. No.
                   27537 2.R1040
Contig ID
                   hyd700727118.h1
5'-most EST
                   13177
Seq. No.
                   27540 2.R1040
Contig ID
                   LIB3051-029-Q1-K1-B11
5'-most EST
                   13178
Seq. No.
                   27542 1.R1040
Contig ID
                   ssr70\overline{0}556214.h1
5'-most EST
                   BLASTX
Method
                   g4538961
NCBI GI
                   704
BLAST score
                   2.0e-78
E value
                   213
Match length
                   76
% identity
                   (ALO49488) isoleucine-tRNA ligase-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   13179
Seq. No.
                   27546 1.R1040
Contig ID
                   fua701041040.hl
5'-most EST
                   BLASTX
Method
                    g3193298
NCBI GI
BLAST score
                    158
                    3.0e-10
E value
                    114
Match length
                    31
 % identity
                   (AF069298) T14P8.17 gene product [Arabidopsis thaliana]
NCBI Description
                    13180
Seq. No.
                    27551 1.R1040
 Contig ID
                    LIB3051-095-Q1-K1-H10
 5'-most EST
                    13181
 Seq. No.
                    27555 1.R1040
 Contig ID
                    LIB3051-029-Q1-K1-E1
 5'-most EST
                    BLASTX
 Method
                    q4262240
 NCBI GI
                    328
 BLAST score
 E value
                    1.0e-30
                    93
 Match length
                    61
 % identity
```

Seq. No. 13182

NCBI Description

Contig ID 27556\_1.R1040

(AC006200) putative stress protein [Arabidopsis thaliana]



5'-most EST crh700852769.h1

Seq. No. 13183

Contig ID 27559\_1.R1040 5'-most EST g4396980

Seq. No. 13184

Contig ID 27559\_2.R1040

5'-most EST LIB3051-029-Q1-K1-F12

Seq. No. 13185

Contig ID 27563\_1.R1040 5'-most EST kl1701210894.h1

Method BLASTX
NCBI GI g556409
BLAST score 284
E value 9.0e-25
Match length 165
% identity 44

NCBI Description (L34551) transcriptional activator protein [Oryza sativa]

Seq. No. 13186

Contig ID 27563\_4.R1040 5'-most EST hrw701063369.h1

Seq. No. 13187

Contig ID 27563\_5.R1040

5'-most EST LIB3093-058-Q1-K1-F12

Seq. No. 13188

Contig ID 27563\_6.R1040

5'-most EST jC-gmst02400075c11d1

Seq. No. 13189

Contig ID 27565\_1.R1040 5'-most EST trc700561432.h1

Seq. No. 13190

Contig ID 27570\_1.R1040

5'-most EST LIB3170-078-Q1-J1-F10

Seq. No. 13191

Contig ID 27575\_1.R1040

5'-most EST LIB3051-030-Q1-K1-B3

Seq. No. 13192

Contig ID 27579\_1.R1040

5'-most EST LIB3170-047-Q1-J1-H8

Seq. No. 13193

Contig ID 27590\_1.R1040

5'-most EST jC-gmst02400025g09d1

Seq. No. 13194

Contig ID 27591\_1.R1040 5'-most EST epx701109029.h1



Seq. No. 13195

Contig ID 27595\_1.R1040 5'-most EST dpv701100885.h1

Method BLASTX
NCBI GI g3776581
BLAST score 223
E value 3.0e-18
Match length 88
% identity 52

% identity 52
NCBI Description (AC005388) Similar to Beta integral membrane protein

homolog gb\_U43629 from A. thaliana. [Arabidopsis thaliana]

Seq. No. 13196

Contig ID 27599 1.R1040 5'-most EST jsh701065450.h1

Method BLASTX
NCBI GI g3880441
BLAST score 175
E value 2.0e-12
Match length 78
% identity 44

NCBI Description (Z82062) similar to Zinc finger, C3HC4 type (RING finger);

cDNA EST EMBL:D76353 comes from this gene; cDNA EST EMBL:D71838 comes from this gene; cDNA EST EMBL:D74561 comes from this gene; cDNA EST EMBL:D73319 comes from this

ge

Seq. No. 13197

Contig ID 27600\_1.R1040

5'-most EST LIB3055-005-Q1-N1-C1

Seq. No. 13198

Contig ID 27609\_1.R1040

5'-most EST LIB3170-005-Q1-J1-D5

Seq. No. 13199

Contig ID 27609\_2.R1040 5'-most EST zzp700836291.h1

Seq. No. 13200

Contig ID 27610\_1.R1040

5'-most EST LIB3107-034-Q1-K1-D2

Seq. No. 13201

Contig ID 27612\_1.R1040

5'-most EST LIB3170-054-Q1-K1-H7

Seq. No. 13202

Contig ID 27612\_2.R1040

5'-most EST LIB3051-088-Q1-K1-D4

Seq. No. 13203

Contig ID 27614\_1.R1040

5'-most EST uC-gmrominsoy025d01b1

Method BLASTX
NCBI GI g3643598
BLAST score 153



```
4.0e-10
E value
                  46
Match length
% identity
                  (AC005395) putative poly(A) polymerase [Arabidopsis
NCBI Description
                  thaliana]
                  13204
Seq. No.
                  27614 2.R1040
Contig ID
                  uC-gmrominsoy253g10b1
5'-most EST
                  BLASTX
Method
                  g3643598
NCBI GI
                  256
BLAST score
                  4.0e-22
E value
                  70
Match length
% identity
                  (AC005395) putative poly(A) polymerase [Arabidopsis
NCBI Description
                  thaliana]
                  13205
Seq. No.
                  27616 1.R1040
Contig ID
                  LIB3139-009-P1-N1-F8
5'-most EST
                  BLASTX
Method
                  g3183981
NCBI GI
                   313
BLAST score
                   4.0e-28
E value
                   302
Match length
% identity
NCBI Description (AJ006341) PMP34 protein [Mus musculus]
                   13206
Seq. No.
                   27616 2.R1040
Contig ID
                   uC-gmrominsoy103b07b1
5'-most EST
                   13207
Seq. No.
                   27618 1.R1040
Contig ID
                   jC-gmst02400054g06a1
5'-most EST
                   13208
 Seq. No.
                   27619 1.R1040
 Contig ID
 5'-most EST
                   LIB3051-031-Q1-K1-E11
                   13209
 Seq. No.
                   27621 1.R1040
 Contig ID
                   asn701140602.h1
 5'-most EST
```

Seq. No. 13210

Contig ID 27622\_1.R1040

5'-most EST jC-gmst02400032a05a1

Seq. No. 13211

Contig ID 27622\_2.R1040 5'-most EST dpv701103053.h1

Seq. No. 13212

Contig ID 27626\_1.R1040 5'-most EST uxk700673237.h1



```
Seq. No. 13213

Contig ID 27629 1.R1040

5'-most EST LIB3051-031-Q1-K1-G9

Method BLASTX

NCBI GI g2160152

BLAST score 221
```

E value 1.0e-17 Match length 158 % identity 40

NCBI Description (AC000375) ESTs gb\_U75592,gb\_T13956,gb\_T43869 come from

from this gene. [Arabidopsis thaliana]

Seq. No. 13214

Contig ID 27631\_1.R1040 5'-most EST sat701011174.h1

Seq. No. 13215

Contig ID 27631\_2.R1040 5'-most EST sat701005058.h1

Seq. No. 13216

Contig ID 27633\_1.R1040 5'-most EST leu701151690.h1

Seq. No. 13217

Contig ID 27635\_1.R1040 5'-most EST fua701041433.h1

Method BLASTX
NCBI GI g3859560
BLAST score 317
E value 8.0e-29
Match length 208
% identity 36

NCBI Description (AF098668) acyl-protein thioesterase [Homo sapiens]

Seq. No. 13218

Contig ID 27635 2.R1040

5'-most EST uC-gmrominsoy201b09b1

Seq. No. 13219

Contig ID 27644\_1.R1040 5'-most EST fde700875423.h1

Method BLASTX
NCBI GI g3879362
BLAST score 97
E value 1.0e-09
Match length 91

% identity 44

NCBI Description (281113) similar to DnaJ, prokaryotic heat shock protein, Zinc finger, C2H2 type; cDNA EST yk290e12.5 comes from this gene; cDNA EST yk290e12.3 comes from this gene; cDNA EST

yk447h4.5 comes from this gene; cDNA EST yk474e4.5 c

Seq. No. 13220

Contig ID 27644 2.R1040 5'-most EST epx701104538.h1



Seq. No. 27646 1.R1040 Contig ID 5'-most EST LIB3051-032-Q1-K1-C9

13222

Seq. No. Contig ID 27652 1.R1040 5'-most EST jC-gmro02910056h02a1 Method BLASTX

NCBI GI q3800878 BLAST score 394 4.0e-38 E value Match length 119 % identity 67

(AF096281) threonine dehydratase/deaminase [Arabidopsis NCBI Description

thaliana]

13223 Seq. No.

27653 1.R1040 Contig ID

5'-most EST LIB3093-006-Q1-K1-B2

Seq. No. 13224

Contig ID 27657 1.R1040

5'-most EST LIB3051-032-Q1-K1-E9

Method BLASTX NCBI GI q3924602 437 BLAST score 4.0e-43 E value Match length 144 % identity 58

(AF069442) predicted OR23 protein of unknown function NCBI Description

[Arabidopsis thaliana]

Seq. No. 13225

27662 1.R1040 Contig ID 5'-most EST zhf700954907.h1

BLASTN Method NCBI GI g3510339 BLAST score 77 E value 4.0e-35 Match length 250 % identity

Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: NCBI Description

K3K7, complete sequence [Arabidopsis thaliana]

Seq. No. 13226

Contig ID 27668 1.R1040 5'-most EST sat701003803.h1

13227 Seq. No.

Contig ID 27670 1.R1040 5'-most EST yz1700967068.h1

Method BLASTX g4490297 NCBI GI BLAST score 1462 1.0e-162 E value Match length 610 % identity 53



```
NCBI Description (AL035678) putative protein [Arabidopsis thaliana]
Seq. No.
                  13228
Contig ID
                  27670 2.R1040
5'-most EST
                  fC-gmro700844911f1
Method
                  BLASTX
NCBI GI
                  q4490297
BLAST score
                  437
E value
                  4.0e-43
Match length
                  131
% identity
                 (AL035678) putative protein [Arabidopsis thaliana]
NCBI Description
                  13229
Seq. No.
Contig ID
                  27673 1.R1040
                  jC-gmle01810087d09a1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q461812
BLAST score
                  253
                  1.0e-21
E value
Match length
                  107
                  44
% identity
NCBI Description CYTOCHROME P450 72 (CYPLXXII) (PROBABLE
                  GERANIOL-10-HYDROXYLASE) (GE10H) >gi_167484 (L10081)
                  Cytochrome P-450 protein [Catharanthus roseus]
                  >gi 445604 prf 1909351A cytochrome P450 [Catharanthus
                  roseus
Seq. No.
                  13230
                  27674 1.R1040
Contig ID
5'-most EST
                  sat701014029.h1
Seq. No.
                  13231
                  27675 1.R1040
Contig ID
5'-most EST
                  LIB3051-033-Q1-K1-A11
Method
                  BLASTX
NCBI GI
                  g3367577
BLAST score
                  224
                  8.0e-18
E value
Match length
                  205
% identity
NCBI Description
                 (AL031135) putative protein [Arabidopsis thaliana]
                  13232
Seq. No.
                  27680 1.R1040
Contig ID
5'-most EST
                  jex700905506.h1
                  13233
Seq. No.
                  27682 1.R1040
Contig ID
5'-most EST
                  vwf700675223.h1
```

Contig ID 27684\_1.R1040

5'-most EST LIB3051-033-Q1-K1-D9

Seq. No. 13235

Contig ID 27688 1.R1040



5'-most EST g4313353

Seq. No. 13236

Contig ID 27689 1.R1040

5'-most EST LIB3109-028-Q1-K1-B6

Method BLASTX
NCBI GI g3600038
BLAST score 494
E value 2.0e-49
Match length 260
% identity 44

NCBI Description (AF080119) similar to Saccharomyces cerevisiae

transcription regulator SPO8 (SW:P41833) [Arabidopsis

thaliana]

Seq. No. 13237

Contig ID 27690 1.R1040

5'-most EST LIB3051-034-Q1-K1-A10

Seq. No. 13238

Contig ID 27693\_1.R1040

5'-most EST LIB3051-034-Q1-K1-A6

Seq. No. 13239

Contig ID 27694 1.R1040

5'-most EST uC-gmrominsoy120h07b1

Method BLASTX
NCBI GI g421843
BLAST score 720
E value 6.0e-76
Match length 272
% identity 57

NCBI Description protein kinase (EC 2.7.1.37) 5 - Arabidopsis thaliana

>gi 217861 dbj BAA01715 (D10909) serine/threonine protein

kinase [Arabidopsis thaliana]

Seq. No. 13240

Contig ID 27694 3.R1040 5'-most EST xpa700795514.h1

Seq. No. 13241

Contig ID 27696 1.R1040

5'-most EST LIB3051-034-Q1-K1-B1

Method BLASTX
NCBI GI g3183405
BLAST score 172
E value 5.0e-12
Match length 63
% identity 49

NCBI Description HYPOTHETICAL 11.3 KD PROTEIN C2C6.07 IN CHROMOSOME I

>gi 3451305 emb CAA20442 (AL031324) very hypothetical

protein [Schizosaccharomyces pombe]

Seq. No. 13242

Contig ID 27698\_1.R1040

5'-most EST LIB3170-085-Q1-J1-C3



Contig ID 27701\_1.R1040

5'-most EST LIB3051-034-Q1-K1-B8

Seq. No. 13244

Contig ID 27702\_1.R1040

5'-most EST LIB3094-089-Q1-K1-A11

Seq. No. 13245

Contig ID 27702\_2.R1040 5'-most EST gsv701045321.h1

Seq. No. 13246

Contig ID 27717\_1.R1040

5'-most EST LIB3051-034-Q1-K1-E9

Seq. No. 13247

Contig ID 27718\_1.R1040

5'-most EST LIB3051-034-Q1-K1-F1

Seq. No. 13248

Contig ID 27722\_1.R1040

5'-most EST LIB3051-034-Q1-K1-G10

Seq. No. 13249

Contig ID 27724 1.R1040 5'-most EST kmv700739591.h1

Seq. No. 13250

Contig ID 27729\_1.R1040

5'-most EST LIB3051-034-Q1-K1-H3

Seq. No. 13251

Contig ID 27731\_1.R1040 5'-most EST leu701156034.h1

Seq. No. 13252

Contig ID 27738\_1.R1040 5'-most EST pmv700894031.h1

Method BLASTX
NCBI GI g1170409
BLAST score 612
E value 3.0e-63
Match length 246

% identity 54

NCBI Description HOMEOBOX-LEUCINE ZIPPER PROTEIN HAT22 (HD-ZIP PROTEIN 22) >gi\_549887 (U09336) homeobox protein [Arabidopsis thaliana]

>gi\_549888 (U09337) homeobox protein [Arabidopsis thaliana] >gi\_4490724\_emb\_CAB38927.1\_ (AL035709) homeobox protein

HAT22 [Arabidopsis thaliana]

Seq. No. 13253

Contig ID 27738\_3.R1040 5'-most EST bth700848689.h1

Seq. No. 13254

Contig ID 27739\_1.R1040

2288



5'-most EST

LIB3051-035-Q1-K1-B2

Seq. No.

13255

Contig ID

27742 1.R1040

5'-most EST

LIB3051-087-Q1-K1-B11

Seq. No.

13256

Contig ID

27744 1.R1040

5'-most EST

LIB3106-021-Q1-K1-A9

Seq. No.

13257

Contig ID 5'-most EST 27745 1.R1040 zhf700954402.h1

Method NCBI GI BLASTX g3176690

BLAST score

192

E value

2.0e-14

Match length

120

% identity

39

NCBI Description

(AC003671) Similar to ubiquitin ligase gb D63905 from S.

cerevisiae. EST gb R65295 comes from this gene.

[Arabidopsis thaliana]

Seq. No.

13258

Contig ID

27748 1.R1040

5'-most EST

LIB3051-035-Q1-K1-C8

Seq. No.

13259

Contig ID

27749 1.R1040

5'-most EST

LIB3051-035-Q1-K1-D10

Seq. No.

13260

Contig ID

27751 1.R1040

5'-most EST

LIB3051-035-Q1-K1-D4

Seq. No.

13261

Contig ID

27752 1.R1040

5'-most EST

LIB3051-035-Q1-K1-D6

Seq. No.

13262

Contig ID

27754 1.R1040

5'-most EST

LIB3051-035-Q1-K1-E10

Seq. No.

13263

Contig ID

27757 1.R1040

5'-most EST

LIB3051-035-Q1-K1-F11

Seq. No.

13264

Contig ID

27769 1.R1040

5'-most EST

uC-gmropic044c07b1

Seq. No.

13265

Contig ID

27769 2.R1040

5'-most EST Method

uC-gmropic047b03b1

NCBI GI

BLASTX

g3688170 372

BLAST score



E value 5.0e-35 Match length 297 % identity 38

NCBI Description (AL031804) putative protein [Arabidopsis thaliana]

Seq. No. 13266

Contig ID 27769 3.R1040

5'-most EST fC-gmro7000746763f1

Method BLASTX
NCBI GI g3688170
BLAST score 305
E value 2.0e-27
Match length 67
% identity 78

NCBI Description (AL031804) putative protein [Arabidopsis thaliana]

Seq. No.

Contig ID 27773 1.R1040

5'-most EST LIB3051-036-Q1-K1-B5

13267

Method BLASTX
NCBI GI g2407790
BLAST score 728
E value 6.0e-77
Match length 212
% identity 19

NCBI Description (AF019910) grr1 [Glycine max]

Seq. No. 13268

Contig ID 27774\_1.R1040 5'-most EST awf700840365.h1

Seq. No. 13269

Contig ID 27781\_1.R1040 5'-most EST uC-gmropic043b12b1

Seq. No. 13270

Contig ID 27781 2.R1040

5'-most EST LIB3051-036-Q1-K1-D1

Seq. No. 13271

Contig ID 27782 1.R1040

5'-most EST LIB3051-036-Q1-K1-D10

Method BLASTX
NCBI GI g1402877
BLAST score 392
E value 8.0e-38
Match length 113
% identity 65

NCBI Description (X98130) unknown [Arabidopsis thaliana]

>gi\_1495257\_emb\_CAA66117\_ (X97485) orf03 [Arabidopsis

thaliana]

Seq. No. 13272

Contig ID 27787\_1.R1040 5'-most EST zzp700831982.h1

Method BLASTX NCBI GI g2459422



BLAST score 225 E value 3.0e-18 Match length 87 % identity 52

NCBI Description (AC002332) unknown protein [Arabidopsis thaliana]

Seq. No.

13273

Contig ID 27801\_1.R1040 5'-most EST kl1701209734.h1

Seq. No. 13274

Contig ID 27801 2.R1040

5'-most EST uC-gmrominsoy091a10b1

Seq. No. 13275

Contig ID 27801 3.R1040

5'-most EST jC-gmf102220056h10a1

Seq. No. 13276

Contig ID 27803 1.R1040

5'-most EST LIB3051-036-Q1-K1-H12

Method BLASTX
NCBI GI g2983719
BLAST score 159
E value 2.0e-10
Match length 103
% identity 35

NCBI Description (AE000732) hypothetical protein [Aquifex aeolicus]

Seq. No. 13277

Contig ID 27803\_2.R1040

5'-most EST LIB3106-046-Q1-K1-A9

Seq. No. 13278

Contig ID 27803 3.R1040

5'-most EST jC-gmst02400031a06d1

Seq. No. 13279

Contig ID 27809\_1.R1040 5'-most EST uC-gmropic061a01b1

Method BLASTX
NCBI GI g2245125
BLAST score 301
E value 6.0e-27
Match length 101
% identity 60

NCBI Description (Z97343) hypothetical protein [Arabidopsis thaliana]

Seq. No. 13280

Contig ID 27809 2.R1040

5'-most EST LIB3094-102-Q1-K1-C8

Seq. No. 13281

Contig ID 27811\_1.R1040 5'-most EST pmv700890214.h1

Method BLASTX NCBI GI g3169073



BLAST score 289
E value 9.0e-26
Match length 105
% identity 55

NCBI Description (AL023705) phenylalanyl-trna synthetase

[Schizosaccharomyces pombe]

Seq. No. 13282

Contig ID 27812\_1.R1040

5'-most EST jC-gmro02910031c02a1

Seq. No. 13283

Contig ID 27812\_2.R1040 5'-most EST zhf700952109.h1

Seq. No. 13284

Contig ID 27812\_3.R1040 5'-most EST ssr700560350.h1

Seq. No. 13285

Contig ID 27812\_4.R1040 5'-most EST uC-gmronoir041h11b1

Seq. No. 13286

Contig ID 27812\_5.R1040

5'-most EST jC-gmst02400009a03a1

Seq. No. 13287

Contig ID 27814 1.R1040 5'-most EST crh700850919.h1

Seq. No. 13288

Contig ID 27816 1.R1040

5'-most EST LIB3055-008-Q1-N1-D9

Method BLASTX
NCBI GI g1082761
BLAST score 301
E value 9.0e-27
Match length 312

% identity 32

NCBI Description brain and reproductive organ-expressed protein - human >gi\_603445 (L38616) brain and reproductive organ-expressed protein [Homo sapiens] >gi\_2353177 (AF015767) brain and

reproductive organ-expressed protein [Homo sapiens]

Seq. No. 13289

Contig ID 27826\_1.R1040 5'-most EST fde700875902.h1

Seq. No. 13290

Contig ID 27826 3.R1040 5'-most EST awf700839030.h1

Seq. No. 13291

Contig ID 27827\_1.R1040

5'-most EST LIB3051-037-Q1-K1-E3



Contig ID 27828\_1.R1040

5'-most EST LIB3106-046-Q1-K1-C5

Method BLASTX
NCBI GI g4469020
BLAST score 271
E value 7.0e-24
Match length 58
% identity 86

NCBI Description (AL035602) putative protein (fragment) [Arabidopsis

thaliana]

Seq. No. 13293

Contig ID 27828\_2.R1040 5'-most EST zhf700953834.h1

Method BLASTX
NCBI GI g4469020
BLAST score 663
E value 1.0e-92
Match length 195
% identity 88

NCBI Description (AL035602) putative protein (fragment) [Arabidopsis

thaliana]

Seq. No. 13294

Contig ID 27830 1.R1040

5'-most EST uC-gmrominsoy175a11b1

Seq. No. 13295

Contig ID 27842 1.R1040

5'-most EST LIB3139-080-P1-N1-C10

Seq. No. 13296

Contig ID 27853\_1.R1040

5'-most EST g5509077

Seq. No. 13297

Contig ID 27855 1.R1040

5'-most EST LIB3051-038-Q1-K1-C5

Seq. No. 13298

Contig ID 27857\_1.R1040

5'-most EST jC-gmf102220067f07a1

Seq. No. 13299

Contig ID 27857 2.R1040

5'-most EST jC-gmro02910073c12a1

Seq. No. 13300

Contig ID 27859\_1.R1040

5'-most EST jC-gmf102220084b01d1

Seq. No. 13301

Contig ID 27860 2.R1040 5'-most EST 6HC-02-Q1-B1-H6

Method BLASTX NCBI GI q4567226



```
BLAST score 209
E value 2.0e-16
Match length 88
% identity 51
```

NCBI Description (AC007119) unknown protein [Arabidopsis thaliana]

Seq. No. 13302

Contig ID 27862\_1.R1040 5'-most EST awf700842474.h1

Seq. No. 13303

Contig ID 27863\_1.R1040 5'-most EST leu701156194.h1

Method BLASTX
NCBI GI g4567278
BLAST score 1380
E value 1.0e-153
Match length 393
% identity 72

NCBI Description (AC006841) putative anthracycline associated resistance ARX

protein [Arabidopsis thaliana]

Seq. No. 13304

Contig ID 27866\_1.R1040

5'-most EST LIB3051-038-Q1-K1-F3

Seq. No. 13305

Contig ID 27867 1.R1040

5'-most EST LIB3051-038-Q1-K1-F6

13307

Seq. No. 13306

Contig ID 27869\_1.R1040 5'-most EST fde700872482.h1

Seq. No.

Contig ID 27872\_1.R1040 5'-most EST kmv700738648.h1

Method BLASTX
NCBI GI g4220480
BLAST score 632
E value 5.0e-66
Match length 168
% identity 38

NCBI Description (AC006069) unknown protein [Arabidopsis thaliana]

Seq. No. 13308

Contig ID 27873\_1.R1040

5'-most EST LIB3051-038-Q1-K1-H12

Method BLASTX
NCBI GI g4416307
BLAST score 143
E value 7.0e-09
Match length 102
% identity 39

NCBI Description (AF105716) hypothetical protein [Zea mays]

Seq. No. 13309

2294



```
27877 1.R1040
Contig ID
                  LIB3138-056-Q1-N1-C10
5'-most EST
                  13310
Seq. No.
                  27879 1.R1040
Contig ID
                  LIB3051-039-Q1-K1-A5
5'-most EST
                  BLASTX
Method
                  q1871192
NCBI GI
                  238
BLAST score
                  7.0e-20
E value
                  70
Match length
                   69
% identity
                  (U90439) Cys3His zinc finger protein isolog [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   13311
                   27880 1.R1040
Contig ID
                   uC-gmflminsoy078c08b1
5'-most EST
                   BLASTX
Method
                   g3953478
NCBI GI
BLAST score
                   250
                   3.0e-21
E value
                   168
Match length
                   35
% identity
NCBI Description (AC002328) F2202.23 [Arabidopsis thaliana]
Seq. No.
                   13312
                   27885 1.R1040
Contig ID
                   LIB3051-039-Q1-K1-B7
5'-most EST
                   BLASTX
Method
                   q4490739
NCBI GI
BLAST score
                   496
                   5.0e-50
E value
                   169
Match length
                   63
% identity
                   (AL035708) putative protein [Arabidopsis thaliana]
NCBI Description
                   13313
Seq. No.
                   27886 1.R1040
Contig ID
                   sat701012802.hl
5'-most EST
                   BLASTX
Method
                   g4455296
NCBI GI
                   204
BLAST score
                   8.0e-16
 E value
                   93
Match length
 % identity
                   47
                   (AL035528) hypothetical protein [Arabidopsis thaliana]
 NCBI Description
                   13314
 Seq. No.
                   27893 1.R1040
 Contig ID
 5'-most EST
                   LIB3139-057-P1-N1-A5
 Seq. No.
                   13315
                   27893 2.R1040
 Contig ID
                   LIB3170-054-Q1-K1-F3
 5'-most EST
```

2295

13316

Seq. No.



Contig ID 27893\_4.R1040 5'-most EST zhf700957612.h1

Seq. No. 13317

Contig ID 27902\_1.R1040

5'-most EST LIB3106-107-Q1-K1-C3

Method BLASTX
NCBI GI g3367537
BLAST score 241
E value 5.0e-20
Match length 125
% identity 46

NCBI Description (AC004392) Contains similarity to ANK repeat region of

Fowlpox virus BamHI-orf7 protein homolog C18F10.7 gi\_485107 from Caenorhabditis elegans cosmid gb\_U00049. This gene is continued from unannotated gene on BAC F19K23 gb\_AC000375.

[Arabid

Seq. No. 13318

Contig ID 27904\_1.R1040

5'-most EST LIB3051-039-Q1-K1-G4

Seq. No. 13319

Contig ID 27908\_2.R1040

5'-most EST LIB3051-039-Q1-K1-H5

Seq. No. 13320

Contig ID 27910 1.R1040 5'-most EST kl1701212154.h1

Seq. No. 13321

Contig ID 27913\_1.R1040

5'-most EST jC-gmst02400051f06a1

Seq. No. 13322

Contig ID 27915\_1.R1040

5'-most EST uC-gmflminsoy046f01b1

Seq. No. 13323

Contig ID 27928\_1.R1040

5'-most EST LIB3051-040-Q1-K1-E5

Seq. No. 13324

Contig ID 27930\_1.R1040

5'-most EST jC-gmro02910005b08a1

Seq. No. 13325

Contig ID 27932\_1.R1040 5'-most EST pmv700891857.h1

Seq. No. 13326

Contig ID 27936\_1.R1040

5'-most EST LIB3051-040-Q1-K1-H4

Seq. No. 13327

Contig ID 27938\_1.R1040

5'-most EST jC-gmf102220073h07a1



BLASTX Method g3955021 NCBI GI 227 BLAST score 1.0e-18 E value 145 Match length 46 % identity

(AJ010811) HB2 homeodomain protein [Populus tremula x NCBI Description

Populus tremuloides]

13328 Seq. No.

27944 1.R1040 Contig ID

LIB3051-041-Q1-K1-B2 5'-most EST

13329 Seq. No.

27948 1.R1040 Contig ID

LIB3051-041-Q1-K1-C11 5'-most EST

Method BLASTX q3776567 NCBI GI 472 BLAST score 6.0e-47E value 267 Match length 39 % identity

(AC005388) Strong similarity to F21B7.33 gi\_2809264 from A. NCBI Description

thaliana BAC gb\_AC002560. EST gb\_N65119 comes from this

gene. [Arabidopsis thaliana]

Seq. No. 13330

27950 1.R1040 Contig ID

LIB3052-007-Q1-B1-G4 5'-most EST

BLASTX Method g3413716 NCBI GI BLAST score 240 4.0e-20 E value 128 Match length % identity

(AC004747) unknown protein [Arabidopsis thaliana] NCBI Description >gi 3643589 (AC005395) unknown protein [Arabidopsis

thaliana]

13331 Seq. No.

27956 1.R1040 Contig ID

uC-gmflminsoy069a01b1 5'-most EST

13332 Seq. No.

27956 2.R1040 Contig ID

LIB3051-041-Q1-K1-E12 5'-most EST

13333 Seq. No.

27959 1.R1040 Contig ID

jC-gmst02400067a08d1 5'-most EST

Seq. No. 13334

27962 1.R1040 Contig ID

LIB3051-041-Q1-K1-F4 5'-most EST

BLASTX Method g1750376 NCBI GI 237 BLAST score



9.0e-20 E value Match length 56 86 % identity

(U80808) ubiquitin activating enzyme [Arabidopsis thaliana] NCBI Description >gi\_3150409 (AC004165) ubiquitin activating enzyme (UBA1)

[Arabidopsis thaliana]

13335 Seq. No.

27973 1.R1040 Contig ID

LIB3051-041-Q1-K1-H3 5'-most EST

13336 Seq. No.

27975\_1.R1040 Contig ID

5'-most EST LIB3051-042-Q1-K1-A12

13337 Seq. No.

27976 1.R1040 Contig ID rca701001653.hl 5'-most EST

13338 Seq. No.

27982 1.R1040 Contig ID

jC-gmst02400005d10a1 5'-most EST

BLASTX Method g3860008 NCBI GI BLAST score 559 4.0e-57 E value 193 Match length

56 % identity

(AF091085) unknown [Homo sapiens] NCBI Description

Seq. No.

27984 1.R1040 Contig ID bth700847157.h1 5'-most EST

Seq. No.

13340

13339

Contig ID 27985 1.R1040

5'-most EST LIB3093-058-Q1-K1-G1

BLASTX Method q4455318 NCBI GI BLAST score 388 4.0e-37 E value 129 Match length % identity

(AL035528) glycine hydroxymethyltransferase-like protein NCBI Description

[Arabidopsis thaliana]

Seq. No.

13341

Contig ID 5'-most EST

27987 1.R1040 ncj700982040.h1

Seq. No. Contig ID 13342

5'-most EST

27987 2.R1040 kl1701212719.hl

Seq. No. Contig ID 13343

5'-most EST

27987 3.R1040 zhf700964176.h1

2298



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Seq. No. 13344
Contig ID 27992_1.R1040
```

5'-most EST LIB3051-042-Q1-K1-F3

Seq. No. 13345

Contig ID 27994\_1.R1040 5'-most EST zsg701119890.h1

Method BLASTX
NCBI GI g3688178
BLAST score 146
E value 1.0e-08
Match length 63
% identity 49

NCBI Description (AL031804) putative protein [Arabidopsis thaliana]

Seq. No. 13346

Contig ID 27997\_1.R1040

5'-most EST LIB3051-042-Q1-K1-H1

Seq. No. 13347

Contig ID 28001\_1.R1040

5'-most EST LIB3051-042-Q1-K1-H8

Seq. No. 13348

Contig ID 28001\_2.R1040 5'-most EST zhf700953749.h1

Seq. No. 13349

Contig ID 28009\_1.R1040

5'-most EST LIB3094-096-Q1-K1-G12

 Method
 BLASTX

 NCBI GI
 g2342674

 BLAST score
 492

 E value
 3.0e-49

Match length 177 % identity 62

NCBI Description (AC000106) Similar to ATP-dependent Clp protease

(gb\_D90915). EST gb\_N65461 comes from this gene.

[Arabidopsis thaliana]

Seq. No. 13350

Contig ID 28009\_2.R1040

5'-most EST LIB3107-036-Q1-K1-B2

Method BLASTX
NCBI GI g2342674
BLAST score 493
E value 1.0e-49
Match length 143
% identity 73

NCBI Description (AC000106) Similar to ATP-dependent Clp protease

(gb D90915). EST gb\_N65461 comes from this gene.

[Arabidopsis thaliana]

Seq. No. 13351

Contig ID 28009 3.R1040 5'-most EST txt700734434.h1



Method BLASTX
NCBI GI g2342674
BLAST score 313
E value 9.0e-29
Match length 101
% identity 64

NCBI Description (AC000106) Similar to ATP-dependent Clp protease (gb D90915). EST gb N65461 comes from this gene.

[Arabidopsis thaliana]

Seq. No. 13352

Contig ID 28011\_1.R1040

5'-most EST LIB3109-021-Q1-K2-A8

Method BLASTX
NCBI GI g4432840
BLAST score 471
E value 5.0e-47
Match length 134
% identity 72

NCBI Description (AC006283) unknown protein [Arabidopsis thaliana]

Seq. No. 13353

Contig ID 28011\_2.R1040

5'-most EST LIB3051-048-Q1-K1-F4

Seq. No. 13354

Contig ID 28011\_3.R1040

5'-most EST uC-gmrominsoy271b02b1

Seq. No. 13355

Contig ID 28011\_4.R1040 5'-most EST sat701003185.h1

Seq. No. 13356

Contig ID 28017\_1.R1040

5'-most EST LIB3072-021-Q1-E1-H7

Seq. No. 13357

Contig ID 28021 1.R1040

5'-most EST LIB3092-041-Q1-K1-G8

Seq. No. 13358

Contig ID 28023 1.R1040

5'-most EST jC-gmst02400060d12a1

Method BLASTX
NCBI GI g3183377
BLAST score 186
E value 1.0e-13
Match length 151
% identity 15

NCBI Description HYPOTHETICAL 79.3 KD PROTEIN C24C9.05C IN CHROMOSOME I >gi 2330788 emb CAB11262\_ (Z98601) hypothetical protein.

[Schizosaccharomyces pombe]

Seq. No. 13359

Contig ID 28025 1.R1040

5'-most EST LIB3106-064-Q1-K1-E12



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Seq. No.
                  13360
                  28025 2.R1040
Contig ID
5'-most EST
                  kl1701212584.h1
                  13361
Seq. No.
                  28026 1.R1040
Contig ID
5'-most EST
                  LIB3106-091-Q1-K1-G1
                  13362
Seq. No.
Contig ID
                  28026 2.R1040
5'-most EST
                  LIB3139-030-P1-N1-F5
                  13363
Seq. No.
                  28027 1.R1040
Contig ID
5'-most EST
                  LIB3170-066-Q1-K1-B8
Seq. No.
                  13364
                  28028 1.R1040
Contig ID
                  jC-gmst02400002a02a1
5'-most EST
                  13365
Seq. No.
Contig ID
                  28028 2.R1040
5'-most EST
                  vzy700753535.hl
                  13366
Seq. No.
                  28032 1.R1040
Contig ID
                  LIB3051-062-Q1-K1-A3
5'-most EST
Method
                  BLASTX
                  q4455198
NCBI GI
                   761
BLAST score
                  7.0e-81
E value
                  237
Match length
% identity
                   64
NCBI Description (AL035440) putative protein [Arabidopsis thaliana]
Seq. No.
                   13367
                   28034 1.R1040
Contig ID
5'-most EST
                   LIB3051-044-Q1-K1-B11
Method
                  BLASTX
                   q4335742
NCBI GI
                   192
BLAST score
                   1.0e-14
E value
Match length
                   86
% identity
                   60
NCBI Description (AC006248) putative AR781 [Arabidopsis thaliana]
Seq. No.
                   13368
                   28036 1.R1040
Contig ID
                   uC-gmropic029f07b1
5'-most EST
```

Contig ID 28039\_1.R1040

5'-most EST LIB3051-044-Q1-K1-C12

Seq. No. 13370

Contig ID 28041\_1.R1040



5'-most EST uC-gmropic058b07b1 13371 Seq. No. 28044 1.R1040 Contig ID 5'-most EST q5753185 13372 Seq. No. Contig ID 28044 2.R1040 5'-most EST jC-gmf102220070c08d1 13373 Seq. No. Contig ID 28054 1.R1040 5'-most EST LIB3107-007-Q1-K1-F9

Method BLASTX NCBI GI g2924521 257 BLAST score 6.0e-22 E value Match length 157

% identity 36

NCBI Description (AL022023) putative protein [Arabidopsis thaliana]

13374 Seq. No.

Contig ID 28062 1.R1040

5'-most EST LIB3093-032-Q1-K1-A3

Method BLASTX NCBI GI g4335719 BLAST score 321 2.0e-29 E value 119 Match length 50 % identity

NCBI Description (AC006248) putative RING-H2 finger protein RHG1a

[Arabidopsis thaliana]

Seq. No. 13375

28070 1.R1040 Contig ID

5'-most EST LIB3051-044-Q1-K1-H8

Seq. No. 13376

Contig ID 28076 1.R1040 5'-most EST kl1701206729.hl

Method BLASTX NCBI GI g3252816 BLAST score 162 7.0e-11 E value Match length 125 % identity 30

(AC004705) hypothetical protein [Arabidopsis thaliana] NCBI Description

>gi\_3810589 (AC005398) hypothetical protein [Arabidopsis

thaliana]

Seq. No. 13377

28076 2.R1040 Contig ID

5'-most EST LIB3138-021-Q1-N1-F11

13378 Seq. No.

Contig ID 28078 1.R1040

5'-most EST LIB3094-043-Q1-K1-G6



Method BLASTX
NCBI GI g1352660
BLAST score 188
E value 1.0e-13
Match length 195
% identity 30

NCBI Description COP-COATED VESICLE MEMBRANE PROTEIN P24 PRECURSOR >qi 924850 (U26264) CHOp24 [Cricetulus griseus]

Seq. No. 13379

Contig ID 28078\_2.R1040 5'-most EST sat701014892.h1

Seq. No. 13380

Contig ID 28082\_1.R1040 5'-most EST pxt700944758.h1

Seq. No. 13381

Contig ID 28085\_1.R1040

5'-most EST LIB3051-046-Q1-K1-C10

Seq. No. 13382

Contig ID 28087 1.R1040

5'-most EST LIB3051-045-Q1-K1-C3

Seq. No. 13383

Contig ID 28089\_1.R1040 5'-most EST ncj700985076.h1

Seq. No. 13384

Contig ID 28090\_1.R1040

5'-most EST LIB3109-048-Q1-K1-E12

Seq. No. 13385

Contig ID 28094 1.R1040

5'-most EST LIB3051-045-Q1-K1-D7

Method BLASTX
NCBI GI g4539321
BLAST score 211
E value 2.0e-16
Match length 95
% identity 42

NCBI Description (AL035679) putative protein [Arabidopsis thaliana]

Seq. No. 13386

Contig ID 28096 1.R1040

5'-most EST LIB3051-045-Q1-K1-E4

Seq. No. 13387

Contig ID 28100\_1.R1040 5'-most EST uaw700665711.h1

Seq. No. 13388

Contig ID 28102\_1.R1040

5'-most EST LIB3051-045-Q1-K1-F6

Seq. No. 13389

% identity

NCBI Description

thaliana]



```
28103 1.R1040
Contig ID
                  LIB3051-045-Q1-K1-F8
5'-most EST
                   13390
Seq. No.
                   28109 1.R1040
Contig ID
                   jC-gm\overline{l}e01810021b06a1
5'-most EST
                   13391
Seq. No.
                   28123 2.R1040
Contig ID
                   kl1701203302.h1
5'-most EST
                   13392
Seq. No.
                   28124_1.R1040
Contig ID
                   LIB3051-046-Q1-K1-B8
5'-most EST
                   13393
Seq. No.
                   28128 1.R1040
Contig ID
                   LIB3051-046-Q1-K1-C9
5'-most EST
Seq. No.
                   13394
                   28132 1.R1040
Contig ID
                   awf700842350.h1
5'-most EST
                   BLASTX
Method
                   g3461844
NCBI GI
                   363
BLAST score
                   3.0e - 34
E value
                   190
Match length
                   36
% identity
NCBI Description (AC005315) hypothetical protein [Arabidopsis thaliana]
                   13395
Seq. No.
                   28138 1.R1040
Contig ID
                   LIB3051-046-Q1-K1-E7
5'-most EST
                   13396
 Seq. No.
                   28144 1.R1040
 Contig ID
                   LIB3051-053-Q1-K2-E1
 5'-most EST
                    13397
 Seq. No.
                    28144 2.R1040
 Contig ID
                    LIB3170-038-Q1-K1-F4
 5'-most EST
                    13398
 Seq. No.
                    28148 1.R1040
 Contig ID
                    LIB3051-046-Q1-K1-G9
 5'-most EST
                    13399
 Seq. No.
                    28149 1.R1040
 Contig ID
 5'-most EST
                    zpv700762007.h1
                    BLASTX
 Method
 NCBI GI
                    q2191152
 BLAST score
                    201
 E value
                    2.0e-15
                    120
 Match length
```

(AF007269) A IG002N01.31 gene product [Arabidopsis



Contig ID 28152 1.R1040

5'-most EST LIB3170-040-Q1-K1-A5

Method BLASTX
NCBI GI g508823
BLAST score 421
E value 3.0e-41
Match length 123
% identity 69

NCBI Description (U11553) putative protein kinase [Pisum sativum]

Seq. No. 13401

Contig ID 28155 1.R1040

5'-most EST LIB3053-010-Q1-N1-H2

Seq. No. 13402

Contig ID 28158 1.R1040

5'-most EST LIB3170-037-Q1-K1-D6

Seq. No. 13403

Contig ID 28159 1.R1040

5'-most EST jC-gmle01810054e07a1

Seq. No. 13404

Contig ID 28161\_1.R1040

5'-most EST LIB3170-037-Q1-K1-E5

Seq. No. 13405

Contig ID 28162\_1.R1040 5'-most EST ssr700554455.h1

Seq. No. 13406

Contig ID 28162\_2.R1040 5'-most EST uC-gmropic071d11b1

Seq. No. 13407

Contig ID 28166 1.R1040

5'-most EST LIB3170-039-Q1-K2-F5

Seq. No. 13408

Contig ID 28172\_1.R1040 5'-most EST zzp700833639.h1

Seq. No. 13409

Contig ID 28172 2.R1040

5'-most EST uC-gmrominsoy231b07b1

Seq. No. 13410

Contig ID 28172\_3.R1040

5'-most EST LIB3051-047-Q1-K1-F10

Seq. No. 13411

Contig ID 28175 1.R1040

5'-most EST jC-gmro02910070a08a1

Method BLASTX NCBI GI q3402684



BLAST score 296 E value 3.0e-26 Match length 178 % identity 38

NCBI Description (AC004697) hypothetical protein [Arabidopsis thaliana]

Seq. No. 13412

Contig ID 28178\_1.R1040

5'-most EST LIB3170-034-Q1-K1-C7

Method BLASTX
NCBI GI g4263775
BLAST score 360
E value 6.0e-34
Match length 110
% identity 64

NCBI Description (AC006068) hypothetical protein [Arabidopsis thaliana]

Seq. No. 13413

Contig ID 28178\_2.R1040

5'-most EST LIB3170-040-Q1-K1-C6

Seq. No. 13414

Contig ID 28180\_1.R1040 5'-most EST awf700840160.h1

Seq. No. 13415

Contig ID 28186\_1.R1040 5'-most EST ncj700980584.h1

Method BLASTN
NCBI GI g2213533
BLAST score 37
E value 2.0e-11
Match length 49
% identity 94

NCBI Description P.sativum mRNA encoding DNA-binding PD1-like protein

Seq. No. 13416

Contig ID 28186 2.R1040 5'-most EST seb700653566.h1

Seq. No. 13417

Contig ID 28191\_1.R1040

5'-most EST LIB3170-037-Q1-K1-G6

Method BLASTX
NCBI GI g4530595
BLAST score 283
E value 5.0e-25
Match length 65
% identity 80

NCBI Description (AF132477) heme oxygenase 2 [Arabidopsis thaliana]

Seq. No. 13418

Contig ID 28193\_1.R1040

5'-most EST LIB3051-048-Q1-K1-B11

Seq. No. 13419

Contig ID 28195\_1.R1040

2306

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5'-most EST
                  LIB3170-039-Q1-K2-A6
                  13420
Seq. No.
Contig ID
                  28196 1.R1040
5'-most EST
                  LIB3087-008-Q1-K1-E7
Seq. No.
                  13421
                  28197 1.R1040
Contig ID
5'-most EST
                  LIB3170-038-Q1-K1-D6
Seq. No.
                  13422
                  28199 1.R1040
Contig ID
5'-most EST
                  LIB3107-052-Q1-K1-H8
Seq. No.
                  13423
                  28203 1.R1040
Contig ID
5'-most EST
                  gsv701046722.h1
Method
                  BLASTX
NCBI GI
                  g1871526
BLAST score
                  168
E value
                  2.0e-11
Match length
                  173
% identity
                  27
NCBI Description (X81997) leucine-rich-repeat protein [Helianthus annuus]
                  13424
Seq. No.
                  28205 1.R1040
Contig ID
5'-most EST
                  zhf700961536.h1
Seq. No.
                  13425
Contig ID
                  28208 1.R1040
5'-most EST
                  LIB3170-039-Q1-K2-H6
                  13426
Seq. No.
                  28209 1.R1040
Contig ID
5'-most EST
                  sat701007122.h1
                  BLASTX
Method
NCBI GI
                  q3924611
BLAST score
                  347
E value
                  2.0e-32
Match length
                  199
```

% identity

NCBI Description (AF069442) hypothetical protein [Arabidopsis thaliana]

13427 Seq. No.

28214 1.R1040 Contig ID 5'-most EST zhf700957774.h1 Method

BLASTX NCBI GI g3142300 BLAST score 1337 E value 1.0e-148 Match length 410 % identity

NCBI Description (AC002411) Contains similarity to pre-mRNA processing

protein PRP39 gb L29224 from S. cerevisiae. ESTs gb R64908 and gb\_T88158, gb\_N38703 and gb\_AA651043 come from this gene. [Arabidopsis thaliana]



Contig ID 28220\_1.R1040 5'-most EST leu701152508.h1

Method BLASTX
NCBI GI g2459425
BLAST score 611
E value 2.0e-63
Match length 149
% identity 77

NCBI Description (AC002332) plastid protein [Arabidopsis thaliana]

Seq. No. 13429

Contig ID 28222 1.R1040 5'-most EST g4314011

Seq. No. 13430

Contig ID 28223 1.R1040

5'-most EST uC-gmflminsoy036e02b1

Seq. No. 13431

Contig ID 28223\_2.R1040 5'-most EST zpv700759543.h1

Seq. No. 13432

Contig ID 28223 3.R1040

5'-most EST LIB3139-098-P1-N1-A9

Seq. No. 13433

Contig ID 28223\_5.R1040 5'-most EST asn701142673.h1

Seq. No. 13434

Contig ID 28224\_1.R1040

5'-most EST LIB3138-095-Q1-N1-B1

Method BLASTX
NCBI GI g3776013
BLAST score 700
E value 1.0e-73
Match length 191
% identity 73

NCBI Description (AJ010470) RNA helicase [Arabidopsis thaliana]

Seq. No. 13435

Contig ID 28225 1.R1040 5'-most EST LIB3139-006-P1-N1-G8

Seq. No. 13436

Contig ID 28230\_1.R1040

5'-most EST LIB3170-039-Q1-K2-C7

Seq. No. 13437

Contig ID 28237\_1.R1040 5'-most EST uC-gmropic028d03b1

Method BLASTX
NCBI GI g4572674
BLAST score 776



2.0e-82

E value Match length 304 % identity 59

NCBI Description (AC006954) unknown protein [Arabidopsis thaliana]

Seq. No.

13438

Contig ID 5'-most EST 28237 2.R1040 dpv701097231.hl

Method NCBI GI BLAST score E value

g4572674 258 3.0e-22

BLASTX

83 Match length % identity 66

NCBI Description (AC006954) unknown protein [Arabidopsis thaliana]

Seq. No.

13439

Contig ID

28238 1.R1040

5'-most EST LIB3106-019-Q1-K1-F3

Seq. No.

13440

Contig ID 5'-most EST 28243\_1.R1040 zsg701117366.hl

Seq. No.

13441

Contig ID

28243 2.R1040

5'-most EST

LIB3051-049-Q1-K1-E7

Seq. No.

13442

Contig ID 5'-most EST

28245 1.R1040 rca700998813.hl

Seq. No.

13443

Contig ID 5'-most EST 28246 1.R1040 leu701155954.h1

Method NCBI GI BLAST score BLASTX g808839 311

E value Match length

3.0e-28

171

% identity

NCBI Description (J04186) unknown protein [Saccharomyces cerevisiae]

Seq. No.

13444

Contig ID

28246 2.R1040

5'-most EST

LIB3051-049-Q1-K1-F1

Seq. No.

13445

Contig ID 5'-most EST 28248 1.R1040 hyd700730845.hl

Seq. No.

13446

Contig ID

28249 1.R1040

5'-most EST

LIB3170-037-Q1-K1-B8

Seq. No.

13447

Contig ID

28254\_1.R1040

2309

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Contig ID

13453

28263 1.R1040



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5'-most EST
                  uC-gmrominsoy212b09b1
                  BLASTX
Method
NCBI GI
                  g1082798
BLAST score
                  452
                  1.0e-44
E value
Match length
                  285
% identity
NCBI Description spliceosome-associated protein SAP 61 - human >gi 508723
                  (U08815) SAP 61 [Homo sapiens]
Seq. No.
                  13448
                  28254 2.R1040
Contig ID
                  wrg700786592.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q3068705
BLAST score
                  446
                  3.0e-44
E value
Match length
                  192
                  48
% identity
NCBI Description (AF049236) unknown [Arabidopsis thaliana]
                  13449
Seq. No.
Contig ID
                  28259 1.R1040
5'-most EST
                  LIB3170-038-Q1-K1-A8
Method
                  BLASTX
NCBI GI
                  g1175386
BLAST score
                  148
                  4.0e-09
E value
Match length
                  121
                  31
% identity
NCBI Description HYPOTHETICAL 37.7 KD PROTEIN C18B11.06 IN CHROMOSOME I
                  >gi_2130289_pir__S58305 hypothetical protein SPAC18B11.06 -
                  fission yeast (Schizosaccharomyces pombe)
                  >qi 929892 emb CAA90591 (Z50728) hypothetical protein
                  [Schizosaccharomyces pombe]
Seq. No.
                  13450
                  28260 1.R1040
Contig ID
5'-most EST
                  LIB3106-098-Q1-K1-H10
                  13451
Seq. No.
                  28260 2.R1040
Contig ID
5'-most EST
                  g5753585
                  13452
Seq. No.
                  28262 1.R1040
Contig ID
5'-most EST
                  LIB3051-050-Q1-K1-A11
Method
                  BLASTX
NCBI GI
                  g4322938
BLAST score
                  299
E value
                  8.0e-27
                  129
Match length
% identity
                  24
NCBI Description (AF096298) DNA-binding protein 1 [Nicotiana tabacum]
```



```
jC-qmf102220140b01d1
5'-most EST
Method
                  BLASTX
                  q2146731
NCBI GI
                  399
BLAST score
                  9.0e-39
E value
                  89
Match length
                  87
% identity
                  FK506-binding protein - Arabidopsis thaliana >gi 1354207
NCBI Description
                  (U49453) rof1 [Arabidopsis thaliana]
                  13454
Seq. No.
                  28263 2.R1040
Contig ID
                  LIB3051-050-Q1-K1-A4
5'-most EST
Seq. No.
                  13455
                  28264 1.R1040
Contig ID
                  LIB3051-050-Q1-K1-A8
5'-most EST
                  13456
Seq. No.
                  28265 2.R1040
Contig ID
                  awf700840564.hl
5'-most EST
                  BLASTX
Method
                  g82045
NCBI GI
                   187
BLAST score
                   5.0e-14
E value
                   74
Match length
                   53
% identity
                  embryonic protein ecp31 - carrot >gi 18337 emb_CAA43046_
NCBI Description
                   (X60593) embryonic cell protein [Daucus carota]
                   13457
Seq. No.
                   28265 3.R1040
Contig ID
                   crh70\overline{0}856141.h1
5'-most EST
                   13458
Seq. No.
                   28267 1.R1040
Contig ID
                   LIB3170-071-Q1-K1-G10
5'-most EST
                   13459
Seq. No.
                   28268 1.R1040
Contig ID
                   wvk700684136.h1
 5'-most EST
                   BLASTX
Method
                   q3183377
NCBI GI
                   261
BLAST score
                   3.0e-22
 E value
                   194
Match length
                   19
 % identity
                   HYPOTHETICAL 79.3 KD PROTEIN C24C9.05C IN CHROMOSOME I
 NCBI Description
                   >gi 2330788 emb CAB11262 (Z98601) hypothetical protein.
                    [Schizosaccharomyces pombe]
                   13460
 Seq. No.
                   28275 1.R1040
 Contig ID
```

5'-most EST LIB3170-037-Q1-K1-D9

Method BLASTN NCBI GI g13075 BLAST score 45



E value 5.0e-16 Match length 55 % identity 95

NCBI Description Lupine mitochondrial gene for initiator tRNA-MET

Seq. No. 13461

28279 1.R1040 Contig ID

5'-most EST  $LIB31\overline{7}0-038-Q1-K1-E9$ 

Seq. No. 13462

28281\_1.R1040 Contig ID

5'-most EST LIB3170-039-Q1-K2-C9

Seq. No. 13463

Contig ID 28282 1.R1040

5'-most EST  $LIB30\overline{5}1-050-Q1-K1-G5$ 

Seq. No. 13464

28283 1.R1040 Contig ID 5'-most EST  $zhf70\overline{0}964027.h1$ 

Seq. No. 13465

Contig ID 28285 1.R1040

5'-most EST LIB3170-039-Q1-K2-H9

Seq. No. 13466

Contig ID 28291 1.R1040 5'-most EST zpv700759008.h1

Seq. No. 13467

Contig ID 28291 2.R1040 5'-most EST vwf700675238.h1

Seq. No. 13468

Contig ID 28294 1.R1040

5'-most EST uC-gmrominsoy074b06b1

Method BLASTX NCBI GI q4512685 BLAST score 441 E value 4.0e-43 Match length 229

% identity 39

(AC006931) hypothetical protein [Arabidopsis thaliana] NCBI Description

>gi\_4559325\_gb\_AAD22987.1\_AC007087\_6 (AC007087)

hypothetical protein [Arabidopsis Thaliana]

Seq. No. 13469

28294 2.R1040 Contig ID

5'-most EST uC-gmrominsoy117b04b1

Seq. No. 13470

Contig ID 28295 1.R1040

5'-most EST jC-gmro02910014d01a1

Seq. No. 13471

Contig ID 28296 1.R1040

5'-most EST LIB3051-051-Q1-K1-C5

```
Seq. No.
                   13472
                   28296 2.R1040
Contig ID
5'-most EST
                   awf700840057.h1
Seq. No.
                   13473
                   28299 1.R1040
Contig ID
5'-most EST
                   LIB3170-040-Q1-K1-F10
Seq. No.
                   13474
                   28301 1.R1040
Contig ID
5'-most EST
                   LIB3051-051-Q1-K1-D3
Seq. No.
                   13475
Contig ID
                   28303 1.R1040
5'-most EST
                  LIB3051-051-Q1-K1-D6
Seq. No.
                   13476
Contig ID
                   28304 1.R1040
5'-most EST
                   LIB3170-061-Q1-J1-A5
Method
                   BLASTX
NCBI GI
                   q2829927
BLAST score
                   209
E value
                   2.0e-16
Match length
                   111
% identity
                   43
NCBI Description (AC002291) Unknown protein [Arabidopsis thaliana]
Seq. No.
                   13477
                   28310 1.R1040
Contig ID
5'-most EST
                  LIB3170-039-Q1-K2-B10
Seq. No.
                   13478
Contig ID
                   28311 1.R1040
5'-most EST
                   ckk700605716.h2
Method
                  BLASTX
NCBI GI
                   q3850577
BLAST score
                   222
E value
                  3.0e-23
Match length
                  115
% identity
NCBI Description (AC005278) This gene may be cut off. [Arabidopsis thaliana]
Seq. No.
                  13479
Contig ID
                  28312 1.R1040
5'-most EST
                  LIB3170-085-Q1-K1-B3
Seq. No.
                  13480
Contig ID
                  28315 1.R1040
5'-most EST
                  taw700656419.h1
```

Contig ID 28315 2.R1040

5'-most EST jC-gmle01810092g12a1

Seq. No. 13482

Contig ID 28316\_2.R1040

2313



5'-most EST jC-qmst02400049f07d1

13483 Seq. No.

28320 1.R1040 Contig ID

LIB3170-038-Q1-K1-D10 5'-most EST

Seq. No. 13484

Contig ID 28321 1.R1040

5'-most EST LIB3170-039-Q1-K2-E10

BLASTX Method NCBI GI q3912953 BLAST score 153 E value 1.0e-09 170 Match length

32 % identity

PUTATIVE 1-AMINOCYCLOPROPANE-1-CARBOXYLATE DEAMINASE (ACC NCBI Description

DEAMINASE)

13485 Seq. No.

28322 1.R1040 Contig ID

5'-most EST  $LIB30\overline{5}1-051-Q1-K1-G8$ 

Seq. No. 13486

Contig ID 28323 1.R1040

5'-most EST q4305440

13487 Seq. No.

Contig ID 28325 1.R1040

5'-most EST LIB3051-051-Q1-K1-H11

Seq. No. 13488

28336 1.R1040 Contig ID

5'-most EST LIB3051-052-Q1-K1-H11

Seq. No. 13489

28338 1.R1040 Contig ID

5'-most EST LIB3051-071-Q1-K1-H6

Seq. No. 13490

28342 1.R1040 Contig ID

5'-most EST LIB3051-067-Q1-K1-F4

Seq. No. 13491

28342 2.R1040 Contig ID

5'-most EST LIB3065-014-Q1-N1-F9

13492 Seq. No.

28342 3.R1040 Contig ID

5'-most EST uC-gmrominsoy128e06b1

13493 Seq. No.

28348 1.R1040 Contig ID

5'-most EST LIB3051-053-Q1-K2-D2

Seq. No. 13494

28354 1.R1040 Contig ID

LIB3170-040-Q1-K1-C12 5'-most EST

5'-most EST

Method NCBI GI



```
13495
Seq. No.
Contig ID
                  28357 1.R1040
                  LIB3170-037-Q1-K1-B12
5'-most EST
                  BLASTX
Method
                  g2462935
NCBI GI
                  107
BLAST score
E value
                  5.0e-11
                  117
Match length
                  38
% identity
                  (Y12321) open reading frame 1 [Brassica oleracea]
NCBI Description
                  13496
Seq. No.
Contig ID
                  28358 1.R1040
                  zsg701129892.h1
5'-most EST
                  BLASTX
Method
                  g3806098
NCBI GI
                  352
BLAST score
                  3.0e-33
E value
                  116
Match length
% identity
                  66
                   (AF079100) arginine-tRNA-protein transferase 1; Ate1p
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  13497
Contig ID
                  28358 2.R1040
5'-most EST
                  uaw700661492.hl
                  BLASTX
Method
                  g3806098
NCBI GI
BLAST score
                   438
                   3.0e-43
E value
                   192
Match length
                   52
% identity
                   (AF079100) arginine-tRNA-protein transferase 1; Atelp
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   13498
Contig ID
                   28358 3.R1040
5'-most EST
                   uC-gmropic063h08b1
Method
                   BLASTX
NCBI GI
                   q3806098
BLAST score
                   449
                   2.0e-44
E value
Match length
                   202
% identity
                   48
                   (AF079100) arginine-tRNA-protein transferase 1; Atelp
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   13499
                   28362 1.R1040
Contig ID
5'-most EST
                   LIB3051-053-Q1-K2-G1
                   13500
Seq. No.
                   28365 1.R1040
Contig ID
```

2315

LIB3170-037-Q1-K1-F12

BLASTX

g2462760



BLAST score 174
E value 3.0e-12
Match length 98
% identity 38

NCBI Description (AC002292) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 13501

Contig ID 28368 1.R1040

5'-most EST LIB3051-053-Q1-K2-H2

Seq. No. 13502

Contig ID 28369 1.R1040

5'-most EST LIB3170-039-Q1-K2-B12

Seq. No. 13503

Contig ID 28370\_1.R1040 5'-most EST ncj700976878.h1

Seq. No. 13504

Contig ID 28372 1.R1040

5'-most EST LIB3139-112-P1-N1-A10

Seq. No. 13505

Contig ID 28373\_1.R1040 5'-most EST zsg701127134.h1

Method BLASTX
NCBI GI g2980765
BLAST score 181
E value 3.0e-13
Match length 73
% identity 58

NCBI Description (AL022198) hypothetical protein [Arabidopsis thaliana]

Seq. No. 13506

Contig ID 28375\_1.R1040

5'-most EST jC-gmle01810067g06a1

Seq. No. 13507

Contig ID 28376 1.R1040

5'-most EST LIB3170-038-Q1-K1-E12

Seq. No. 13508

Contig ID 28378\_1.R1040

5'-most EST LIB3051-054-Q1-K2-B4

Seq. No. 13509

Contig ID 28380 1.R1040

5'-most EST LIB3051-054-Q1-K2-B6

Seq. No. 13510

Contig ID 28382 1.R1040

5'-most EST LIB3051-054-Q1-K2-B9

Seq. No. 13511

Contig ID 28384 1.R1040

5'-most EST LIB3051-054-Q1-K2-C12



```
Seq. No.
                  28387 1.R1040
Contig ID
                  LIB3170-041-Q1-K1-C1
5'-most EST
                  13513
Seq. No.
Contig ID
                  28388 1.R1040
5'-most EST
                  LIB3051-054-Q1-K2-D10
Method
                  BLASTX
NCBI GI
                  q3766368
BLAST score
                  161
E value
                  5.0e-11
Match length
                  66
% identity
                  50
NCBI Description
                   (AL031907) putative trascription factor, ccr4-associated
                  factor homolog [Schizosaccharomyces pombe]
                  13514
Seq. No.
Contig ID
                  28390 1.R1040
5'-most EST
                  LIB3051-054-Q1-K2-D8
Seq. No.
                  13515
Contig ID
                  28393 1.R1040
5'-most EST
                  LIB3109-020-Q1-K1-D1
Seq. No.
                  13516
                  28395 1.R1040
Contig ID
5'-most EST
                  uC-qmronoir032d11b1
Method
                  BLASTX
NCBI GI
                  g3850100
BLAST score
                  260
E value
                  2.0e-22
Match length
                  176
% identity
                  20
                   (AL033388) WD repeat-containing protein
NCBI Description
                   [Schizosaccharomyces pombe]
Seq. No.
                  13517
Contig ID
                  28399 1.R1040
5'-most EST
                  LIB3051-054-Q1-K2-F12
                  13518
Seq. No.
                  28401 1.R1040
Contig ID
                  LIB3170-057-Q1-K1-G5
5'-most EST
Seq. No.
                  13519
                  28409 1.R1040
Contig ID
5'-most EST
                  LIB3093-053-Q1-K1-G9
Method
                  BLASTX
```

NCBI GI g3395441 BLAST score 653 E value 4.0e-68 196 Match length 68 % identity

NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]

Seq. No.

13520

Contig ID

28409 2.R1040



```
LIB3170-044-Q1-K1-H2
5'-most EST
Method
                   BLASTX
NCBI GI
                   a3395441
                   221
BLAST score
                   5.0e-18
E value
                   68
Match length
% identity
                   76
                  (AC004683) unknown protein [Arabidopsis thaliana]
NCBI Description
                   13521
Seq. No.
                   28412 1.R1040
Contig ID
5'-most EST
                   LIB3170-044-Q1-K1-D3
Method
                   BLASTX
                   g3600049
NCBI GI
BLAST score
                   469
                   6.0e-47
E value
                   169
Match length
                   59
% identity
                  (AF080120) similar to initiation factor IF2-beta (Pfam:
NCBI Description
                   GTP EFTU.hmm, score: 226.67) [Arabidopsis thaliana]
                   13522
Seq. No.
Contig ID
                   28433 1.R1040
5'-most EST
                   LIB3170-041-Q1-K1-A5
Seq. No.
                   13523
                   28447 1.R1040
Contig ID
                   eep70\overline{0}868070.h1
5'-most EST
Seq. No.
                   13524
                   28447 2.R1040
Contig ID
5'-most EST
                   zhf700955644.h1
Seq. No.
                   13525
                   28447 3.R1040
Contig ID
5'-most EST
                   zhf700962267.h1
                   13526
Seq. No.
                   28452 1.R1040
Contig ID
                   k1170\overline{1}209179.h1
5'-most EST
Seq. No.
                   13527
                   28455 1.R1040
Contig ID
5'-most EST
                   LIB3109-041-Q1-K1-B10
                   13528
Seq. No.
                   28455 2.R1040
Contig ID
5'-most EST
                   trc700563814.h1
```

Contig ID 28457\_1.R1040 5'-most EST uC-gmropic107b08b1

Seq. No. 13530

Contig ID 28458\_1.R1040

5'-most EST LIB3051-058-Q1-K2-F10

Method BLASTN



NCBI GI g3851647 BLAST score 192 E value 1.0e-104 Match length 365 % identity 90

NCBI Description Rattus norvegicus neural F box protein NFB42 mRNA, complete

cds

Seq. No. 13531

Contig ID 28460\_1.R1040

5'-most EST LIB3170-041-Q1-K1-B4

Seq. No. 13532

Contig ID 28466 1.R1040 5'-most EST eep700865338.h1

Seq. No. 13533

Contig ID 28471\_1.R1040

5'-most EST LIB3051-059-A10T7A

Method BLASTX
NCBI GI g4490303
BLAST score 544
E value 1.0e-55
Match length 143
% identity 70

NCBI Description (AL035678) putative protein [Arabidopsis thaliana]

Seq. No. 13534

Contig ID 28478\_1.R1040

5'-most EST LIB3170-042-Q1-K1-G5

Seq. No. 13535

Contig ID 28481\_1.R1040

5'-most EST LIB3170-042-Q1-K1-H5

Method BLASTX
NCBI GI g1086252
BLAST score 114
E value 8.0e-12
Match length 58
% identity 55

NCBI Description sucrose cleavage protein - Potato >gi\_707001\_bbs\_157931

(S74161) sucrolytic enzyme/ferredoxin homolog [Solanum tuberosum=potatoes, cv. Cara, leaf, Peptide, 322 aa]

[Solanum tuberosum]

Seq. No. 13536

Contig ID 28483 1.R1040

5'-most EST LIB3170-044-Q1-K1-B6

Seq. No. 13537

Contig ID 28483\_2.R1040 5'-most EST ssr700557077.h1

Seq. No. 13538

Contig ID 28484\_1.R1040

5'-most EST LIB3170-041-Q1-K1-B6



Contig ID 28487 1.R1040

5'-most EST LIB3051-059-Q1-K2-C4

Seq. No. 13540

Contig ID 28488 1.R1040

5'-most EST uC-gmrominsoy216b02b1

Seq. No. 13541

Contig ID 28488 2.R1040

5'-most EST uC-gmflminsoy065b12b1

13542 Seq. No.

28490 1.R1040 Contig ID

5'-most EST LIB3170-041-Q1-K1-F6

Seq. No. 13543

28492 1.R1040 Contig ID 5'-most EST ejt700606296.hl

Method BLASTX g3935183 NCBI GI BLAST score 210 2.0e-16 E value Match length 102

% identity 45

NCBI Description (AC004557) F17L21.26 [Arabidopsis thaliana]

13544 Seq. No.

28492 2.R1040 Contig ID

5'-most EST jC-gmf102220089f02d1

Seq. No. 13545

Contig ID 28497 1.R1040

5'-most EST LIB3051-059-Q1-K2-E3

Seq. No. 13546

Contig ID 28498 1.R1040 5'-most EST pxt700942413.hl

Seq. No. 13547

Contig ID 28500 1.R1040

5'-most EST LIB3170-042-Q1-K1-B6

Seq. No. 13548

Contig ID 28501 1.R1040 5'-most EST gsv701047471.hl

13549 Seq. No.

28502 1.R1040 Contig ID

5'-most EST LIB3056-006-Q1-N1-H11

Method BLASTX NCBI GI g3873960 BLAST score 341 E value 2.0e-31 Match length 203 % identity 38

NCBI Description (Z81458) C03E10.4 [Caenorhabditis elegans]



Contig ID 28504\_1.R1040

5'-most EST LIB3051-059-Q1-K2-G8

Seq. No. 13551

Contig ID 28504 2.R1040

5'-most EST LIB3107-075-Q1-K1-B2

Seq. No. 13552

Contig ID 28513 1.R1040

5'-most EST LIB3051-060-Q1-K1-A9

Seq. No. 13553

Contig ID 28518\_1.R1040 5'-most EST zpv700758573.h1

Seq. No. 13554

Contig ID 28525 1.R1040

5'-most EST LIB3072-051-Q1-E1-D11

Method BLASTX
NCBI GI g2370494
BLAST score 125
E value 2.0e-09
Match length 185
% identity 30

NCBI Description (Z98944) hypothetical protein [Schizosaccharomyces pombe]

Seq. No. 13555

Contig ID 28526\_1.R1040 5'-most EST epx701104727.h1

Seq. No. 13556

Contig ID 28528\_1.R1040 5'-most EST awf700839431.h1

Seq. No. 13557

Contig ID 28529 1.R1040

5'-most EST LIB3051-060-Q1-K1-E2

Method BLASTX
NCBI GI g4219092
BLAST score 487
E value 6.0e-49
Match length 120
% identity 80

NCBI Description (AF117707) putative copper/zinc superoxide dismutase copper

chaperone precursor [Lycopersicon esculentum]

Seq. No. 13558

Contig ID 28530 1.R1040

5'-most EST LIB3051-060-Q1-K1-E8

Seq. No. 13559

Contig ID 28531\_1.R1040

5'-most EST LIB3051-060-Q1-K1-E9

Seq. No. 13560

2321



Contig ID 28537\_1.R1040 5'-most EST LIB3051-060-Q1-K1-F7

Seq. No. 13561

Contig ID 28544\_1.R1040

5'-most EST LIB3051-060-Q1-K1-G6

Seq. No. 13562

Contig ID 28545\_1.R1040 5'-most EST fde700874410.h1

Seq. No. 13563

Contig ID 28551\_1.R1040 5'-most EST seb700651742.h1

Seq. No. 13564

Contig ID 28557\_1.R1040 5'-most EST ssr700559677.h1

Method BLASTX
NCBI GI g2244910
BLAST score 214
E value 5.0e-17
Match length 74
% identity 77

NCBI Description (Z97339) unnamed protein product [Arabidopsis thaliana]

Seq. No. 13565

Contig ID 28563\_1.R1040

5'-most EST jC-gmro02910075b06a1

Method BLASTX
NCBI GI g1944132
BLAST score 565
E value 5.0e-58
Match length 128
% identity 81

NCBI Description (AB002560) CUC2 [Arabidopsis thaliana]

Seq. No. 13566

Contig ID 28565\_1.R1040

5'-most EST LIB3170-046-Q1-K1-G9

Seq. No. 13567

Contig ID 28570 1.R1040 5'-most EST leu701151340.h1

Seq. No. 13568

Contig ID 28573\_1.R1040

5'-most EST LIB3051-061-Q1-K1-G10

Seq. No. 13569

Contig ID 28576\_1.R1040 5'-most EST pmv700888884.h1

Seq. No. 13570

Contig ID 28576\_2.R1040

5'-most EST LIB3055-003-Q1-N1-F6



```
13571
Seq. No.
                  28576 3.R1040
Contig ID
                  V4R-0\overline{2}-Q1-B1-H5
5'-most EST
                   13572
Seq. No.
                   28578 1.R1040
Contig ID
                  LIB3051-062-Q1-K1-A10
5'-most EST
                   13573
Seq. No.
                   28582 1.R1040
Contig ID
                   bnu700967634.hl
5'-most EST
                   BLASTX
Method
                   q4406809
NCBI GI
                   204
BLAST score
E value
                   7.0e-16
Match length
                   135
% identity
                   39
NCBI Description (AC006201) unknown protein [Arabidopsis thaliana]
                   13574
Seq. No.
                   28584 1.R1040
Contig ID
                   gsf700698465.hl
5'-most EST
                   13575
Seq. No.
                   28586_1.R1040
Contig ID
                   LIB3051-062-Q1-K1-C3
5'-most EST
                   13576
Seq. No.
                   28587 1.R1040
Contig ID
                   jC-gmro02910067c04a1
5'-most EST
                   BLASTX
Method
                   g3334276
NCBI GI
                   360
BLAST score
                   5.0e-34
E value
                   175
Match length
                   42
% identity
NCBI Description AUTOANTIGEN NGP-1 >gi_179285 (L05425) autoantigen [Homo
                   sapiens]
                   13577
Seq. No.
                   28589 1.R1040
Contig ID
                   LIB3109-036-Q1-K1-C3
 5'-most EST
                   13578
 Seq. No.
                   28597 1.R1040
 Contig ID
                   zhf700963663.h1
 5'-most EST
                    13579
 Seq. No.
                    28599 1.R1040
 Contig ID
                    LIB3051-062-Q1-K1-G6
 5'-most EST
 Method
                    BLASTX
                    q3033379
 NCBI GI
```

BLAST score 332 8.0e-31 E value 91 Match length 68 % identity

NCBI Description (AC004238) putative DNA-binding protein [Arabidopsis



## thaliana]

Seq. No. 13580

Contig ID 28599\_2.R1040 5'-most EST seb700651386.h1

Seq. No. 13581

Contig ID 28600\_1.R1040 5'-most EST vzy700756156.h1

Seq. No. 13582

Contig ID 28601\_1.R1040 5'-most EST fua701041611.h1

Method BLASTX
NCBI GI g2642448
BLAST score 486
E value 1.0e-48
Match length 154
% identity 29

NCBI Description (AC002391) hypothetical protein [Arabidopsis thaliana]

>gi 3169187 (AC004401) hypothetical protein [Arabidopsis

thaliana]

Seq. No. 13583

Contig ID 28602 1.R1040

5'-most EST LIB3051-063-Q1-K1-A1

Seq. No. 13584

Contig ID 28603 1.R1040

5'-most EST LIB3139-113-P1-N1-D9

Method BLASTN
NCBI GI g1684854
BLAST score 213
E value 1.0e-116
Match length 273
% identity 95

NCBI Description Phaseolus vulgaris ubiquitin-like protein mRNA, complete

cds

Seq. No. 13585

Contig ID 28605 1.R1040

5'-most EST LIB3051-063-Q1-K1-A3

Method BLASTX
NCBI GI g2653885
BLAST score 341
E value 5.0e-32
Match length 123
% identity 60

NCBI Description (AF027408) phospholipase D-gamma; PLD-gamma [Arabidopsis

thaliana]

Seq. No. 13586

Contig ID 28606\_1.R1040

5'-most EST LIB3170-047-Q1-K1-H11

Seq. No. 13587

Contig ID 28610 1.R1040

2324



```
5'-most EST
                  LIB3170-045-Q1-K1-C12
Method
                  BLASTX
NCBI GI
                  q913227
BLAST score
                  177
                  6.0e-13
E value
Match length
                  54
                  67
% identity
NCBI Description
                  transcription factor X1DP-1 [Xenopus laevis, embryos,
                  Peptide, 409 aa]
                  13588
Seq. No.
Contig ID
                  28613 1.R1040
5'-most EST
                  uC-gmropic006f07b1
Method
                  BLASTX
NCBI GI
                  g3858935
BLAST score
                  880
E value
                  1.0e-94
Match length
                  218
% identity
                  76
NCBI Description
                  (AL021636) synaptobrevin-like protein [Arabidopsis
                  thaliana] >qi 4103357 (AF025332) vesicle-associated
                  membrane protein 7C; synaptobrevin 7C [Arabidopsis
                  thaliana]
Seq. No.
                  13589
Contig ID
                  28616 1.R1040
5'-most EST
                  trc700564238.h1
Seq. No.
                  13590
                  28617 1.R1040
Contig ID
5'-most EST
                  epx701105324.h1
Seq. No.
                  13591
                  28619 1.R1040
Contig ID
5'-most EST
                  jC-gmro02800031d02d1
Method
                  BLASTX
                  g3021344
NCBI GI
BLAST score
                  190
E value
                  3.0e-14
Match length
                  75
% identity
NCBI Description (AJ004959) hypothetical protein [Cicer arietinum]
                  13592
Seq. No.
                  28622 1.R1040
Contig ID
5'-most EST
                  LIB3051-063-Q1-K1-G7
                  13593
Seq. No.
Contig ID
                  28623 1.R1040
```

5'-most EST uxk700668033.h1

Seq. No. 13594

Contig ID 28624 1.R1040

5'-most EST LIB3170-046-Q1-J1-G12

Seq. No. 13595

Contig ID 28624 2.R1040



```
5'-most EST
                  LIB3051-111-Q1-K1-H4
                  13596
Seq. No.
                  28625 1.R1040
Contig ID
5'-most EST
                  LIB3053-009-Q1-N1-B4
                  13597
Seq. No.
Contig ID
                  28625 2.R1040
5'-most EST
                  uC-gmropic098e04b1
                  13598
Seq. No.
                  28625 3.R1040
Contig ID
5'-most EST
                  LIB3107-053-Q1-K1-C7
Seq. No.
                  13599
Contig ID
                  28626 1.R1040
5'-most EST
                  LIB3051-064-Q1-K1-A10
                  13600
Seq. No.
Contig ID
                  28627 1.R1040
                  pcp700993636.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3738306
BLAST score
                  643
                  5.0e-67
E value
Match length
                  284
% identity
NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]
                  13601
Seq. No.
                  28628 1.R1040
Contig ID
5'-most EST
                  asn701135956.h1
                  BLASTX
Method
                  g3746071
NCBI GI
BLAST score
                  757
E value
                  1.0e-80
Match length
                  182
% identity
NCBI Description (AC005311) putative GTP-binding protein [Arabidopsis
                  thaliana]
                  13602
Seq. No.
                  28630 1.R1040
Contig ID
5'-most EST
                  LIB3170-049-Q1-K2-B7
                  13603
Seq. No.
                  28634 1.R1040
```

Contig ID

5'-most EST jC-gmTe01810020c10a1

Seq. No. 13604

28634 2.R1040 Contig ID

5'-most EST LIB3051-064-Q1-K1-C10

13605 Seq. No.

28638 1.R1040 Contig ID 5'-most EST ssr700558502.h1



```
Seq. No.
                  13606
                  28640 1.R1040
Contig ID
5'-most EST
                  LIB3051-064-Q1-K1-D5
                  13607
Seq. No.
Contig ID
                  28649 1.R1040
                  LIB3170-051-Q1-K2-C1
5'-most EST
Method
                  BLASTX
                  q4388730
NCBI GI
BLAST score
                  330
E value
                  2.0e-30
Match length
                  76
% identity
NCBI Description (AC006413) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  13608
                  28649 2.R1040
Contig ID
5'-most EST
                  LIB3170-051-Q1-K1-C7
Seq. No.
                  13609
Contig ID
                  28651 1.R1040
5'-most EST
                  LIB3051-064-Q1-K1-G10
                  BLASTX
Method
NCBI GI
                  g3360289
BLAST score
                  182
E value
                  2.0e-13
Match length
                  50
% identity
                  58
NCBI Description (AF023164) leucine-rich repeat transmembrane protein kinase
                  1 [Zea mays]
Seq. No.
                  13610
Contig ID
                  28652 1.R1040
5'-most EST
                  LIB3051-064-Q1-K1-G11
Method
                  BLASTX
NCBI GI
                  g2894596
                  260
BLAST score
E value
                  7.0e-23
                  77
Match length
% identity
                  69
NCBI Description (AL021889) putative protein [Arabidopsis thaliana]
Seq. No.
                  13611
Contig ID
                  28653 1.R1040
5'-most EST
                  LIB3170-051-Q1-K2-E1
Method
                  BLASTN
NCBI GI
                  g3821780
BLAST score
                  36
E value
                  2.0e-10
Match length
                  37
% identity
                  61
NCBI Description Xenopus laevis cDNA clone 27A6-1
```

Contig ID 28655\_1.R1040 5'-most EST uC-gmropic014f04b1

Method BLASTX

% identity



```
q1778095
NCBI GI
                   1683
BLAST score
                   0.0e + 00
E value
                   507
Match length
                   67
% identity
                   (U64903) putative sugar transporter; member of major
NCBI Description
                   facilitative superfamily; integral membrane protein [Beta
                   vulgaris]
                   13613
Seq. No.
                   28655 2.R1040
Contig ID
                   zhf70\overline{0}953153.h1
5'-most EST
                   BLASTX
Method
                   g3047114
NCBI GI
                   962
BLAST score
                   1.0e-104
E value
                   462
Match length
```

(AF058919) No definition line found [Arabidopsis thaliana] NCBI Description 13614

Seq. No. 28655 6.R1040 Contig ID jC-gmle01810035g01d1 5'-most EST

44

13615 Seq. No. 28659 1.R1040 Contig ID LIB3170-052-Q1-K1-A2 5'-most EST

13616 Seq. No. 28661 1.R1040 Contig ID fde700874519.hl 5'-most EST

13617 Seq. No. 28662 1.R1040 Contig ID LIB3170-049-Q1-K2-A2 5'-most EST

13618 Seq. No. 28664 1.R1040 Contig ID awf700842849.hl 5'-most EST BLASTX Method q2956717 NCBI GI 589 BLAST score

5.0e-61 E value 136 Match length % identity

(Y09722) beta-carotene hydroxylase 2 [Capsicum annuum] NCBI Description

13619 Seq. No. 28669 1.R1040 Contig ID 5'-most EST ssr700555061.hl

13620 Seq. No. 28671 1.R1040 Contig ID LIB3051-065-Q1-K1-C4 5'-most EST

13621 Seq. No. 28673\_1.R1040 Contig ID



5'-most EST LIB3051-065-Q1-K1-D11 BLASTN Method NCBI GI g2062705 BLAST score 37 3.0e-11 E value 37 Match length 38 % identity NCBI Description Human butyrophilin (BTF5) mRNA, complete cds 13622 Seq. No.

28675 1.R1040 Contig ID 5'-most EST LIB3051-065-Q1-K1-D2 Method BLASTX

NCBI GI g4325354 BLAST score 237 E value 7.0e-20 Match length 113 % identity 42

(AF128395) contains similarity to retrovirus-related NCBI Description polyproteins and to CCHC zinc finger protein (Pfam:

PF00098, Score=16.3, E=0.051, E= 1) [Arabidopsis thaliana]

Seq. No. 13623

28680 1.R1040 Contig ID

5'-most EST LIB3051-065-Q1-K1-E5

Seq. No. 13624

28681 1.R1040 Contig ID 5'-most EST crh700850923.h1

Seq. No. 13625

28682 1.R1040 Contig ID

5'-most EST LIB3170-051-Q1-K1-D2

13626 Seq. No.

Contig ID 28688 1.R1040

5'-most EST LIB3051-065-Q1-K1-G8

Method BLASTX NCBI GI g3043612 BLAST score 328 E value 5.0e-30 Match length 180 42 % identity

NCBI Description (AB011116) KIAA0544 protein [Homo sapiens]

Seq. No. 13627

Contig ID 28688\_2.R1040 5'-most EST

g4289761

Seq. No. 13628

Contig ID 28690 1.R1040

5'-most EST LIB3051-065-Q1-K1-H10

Seq. No. 13629

Contig ID

28694 1.R1040

5'-most EST LIB3051-066-Q1-K1-A12



Contig ID 28696 1.R1040

5'-most EST LIB3170-049-Q1-K2-F3

Seq. No. 13631

Contig ID 28698\_2.R1040

5'-most EST LIB3051-066-Q1-K1-C1

Seq. No. 13632

Contig ID 28702\_1.R1040 5'-most EST sat701015280.h1

Method BLASTN
NCBI GI g3241927
BLAST score 39
E value 1.0e-12
Match length 91
% identity 86

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MTE17, complete sequence [Arabidopsis thaliana]

Seq. No. 13633

Contig ID 28704 1.R1040

5'-most EST LIB3094-090-Q1-K1-B9

Seq. No. 13634

Contig ID 28709 1.R1040

5'-most EST LIB30 $\overline{5}1$ -066-Q1-K1-E3

Seq. No. 13635

Contig ID 28712 1.R1040

5'-most EST LIB3170-051-Q1-K2-E3

Seq. No. 13636

Contig ID 28713\_1.R1040

5'-most EST LIB3170-051-Q1-K2-F3

Seq. No. 13637

Contig ID 28724\_1.R1040 5'-most EST seb700651482.h1

Method BLASTX
NCBI GI g1168328
BLAST score 271
E value 1.0e-23
Match length 107
% identity 49

NCBI Description ACTIN-LIKE PROTEIN 3 >gi 629878 pir S48844 actin-like

protein - slime mold (Dictyostelium discoideum)

>gi\_2130164\_pir\_\_S69002 actin-like protein - slime mold
(Dictyostelium discoideum) >gi\_563346\_emb\_CAA86553\_
(Z46418) actin-like protein [Dictyostelium discoideum]

Seq. No. 13638

Contig ID 28726\_1.R1040

5'-most EST LIB3170-049-Q1-K2-E4

Seq. No. 13639

Contig ID 28729 1.R1040



5'-most EST LIB3051-067-Q1-K1-A8

Seq. No. 13640

Contig ID 28732\_1.R1040 5'-most EST rca701001509.h1

Seq. No. 13641

Contig ID 28734\_1.R1040

5'-most EST LIB3170-051-Q1-K2-B4

Seq. No. 13642

Contig ID 28739 1.R1040

5'-most EST LIB3051-067-Q1-K1-D12

Method BLASTX
NCBI GI 94371285
BLAST score 197
E value 3.0e-15
Match length 85

% identity 53

NCBI Description (AC006260) hypothetical protein [Arabidopsis thaliana]

Seq. No. 13643

Contig ID 28740 1.R1040

5'-most EST LIB3170-051-Q1-K1-G4

Seq. No. 13644

Contig ID 28745\_1.R1040 5'-most EST awf700841094.h1

Seq. No. 13645

Contig ID 28747 1.R1040

5'-most EST LIB3051-067-Q1-K1-F12

Method BLASTX
NCBI GI g3786014
BLAST score 143
E value 7.0e-09
Match length 57
% identity 58

NCBI Description (AC005499) hypothetical protein [Arabidopsis thaliana]

Seq. No. 13646

Contig ID 28750\_1.R1040 5'-most EST hyd700725920.h1

Seq. No. 13647

Contig ID 28751\_1.R1040

5'-most EST LIB3051-067-Q1-K1-F8

Seq. No. 13648

Contig ID 28752\_1.R1040 5'-most EST zzp700834069.h1

Seq. No. 13649

Contig ID 28753\_1.R1040

5'-most EST LIB3051-067-Q1-K1-G1

Seq. No. 13650



Contig ID 28759\_1.R1040

5'-most EST LIB3092-028-Q1-K1-C7

Method BLASTX
NCBI GI g3738302
BLAST score 482
E value 3.0e-48
Match length 144
% identity 62

NCBI Description (AC005309) tubby-like protein [Arabidopsis thaliana]

>gi 4249398 (AC006072) putative tubby protein [Arabidopsis

thaliana]

Seq. No. 13651

Contig ID 28759\_2.R1040 5'-most EST smc700749895.h1

Method BLASTX
NCBI GI g3738302
BLAST score 923
E value 1.0e-100
Match length 246
% identity 68

NCBI Description (AC005309) tubby-like protein [Arabidopsis thaliana]

>gi 4249398 (AC006072) putative tubby protein [Arabidopsis

thaliana]

Seq. No. 13652

Contig ID 28760\_1.R1040 5'-most EST smc700748436.h1

Method BLASTX
NCBI GI g2191165
BLAST score 425
E value 3.0e-41
Match length 131
% identity 66

NCBI Description (AF007270) A IG002P16.14 gene product [Arabidopsis

thaliana]

Seq. No. 13653

Contig ID 28764\_1.R1040

5'-most EST LIB3093-041-Q1-K1-D3

Seq. No. 13654

Contig ID 28767\_1.R1040
5'-most EST g5752993
Method BLASTX
NCBI GI g3135269
BLAST score 151
E value 1.0e-19
Match length 170

Match length 170 % identity 42

NCBI Description (AC003058) unknown protein [Arabidopsis thaliana]

Seq. No. 13655

Contig ID 28771 1.R1040

5'-most EST LIB3051-068-Q1-K1-B4

Method BLASTN NCBI GI q3821780



BLAST score 36 E value 1.0e-10 Match length 48 67 % identity

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. Contig ID 13656 28772 1.R1040

5'-most EST

LIB3051-068-Q1-K1-B6

Seq. No.

13657

Contig ID

28773 1.R1040

5'-most EST

LIB3051-068-Q1-K1-B7

Method BLASTX NCBI GI g4378848 196 BLAST score 7.0e-15 E value

75 Match length % identity 53

NCBI Description (AF124349) hydrolase [Zymomonas mobilis]

Seq. No.

13658

Contig ID

28773\_2.R1040

5'-most EST

LIB3107-071-Q1-K1-E1

Method BLASTX NCBI GI q4378848 BLAST score 439 E value 2.0e-43 Match length 150 % identity 59

NCBI Description (AF124349) hydrolase [Zymomonas mobilis]

Seq. No.

13659

Contig ID 5'-most EST

28774 1.R1040 LIB3051-068-Q1-K1-B8

Seq. No.

13660

Contig ID

28776 1.R1040

5'-most EST

LIB3051-068-Q1-K1-C1

Seq. No.

13661

Contig ID

28777 1.R1040

5'-most EST

LIB3051-068-Q1-K1-C4

Seq. No.

13662

Contig ID

28778\_1.R1040

5'-most EST

LIB3051-068-Q1-K1-C6 BLASTN

Method NCBI GI

g3821780

BLAST score

36

E value Match length 1.0e-10

% identity

36 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No.

13663

Contig ID

28780\_1.R1040



```
5'-most EST
                  LIB3051-068-Q1-K1-D7
Seq. No.
                  13664
Contig ID
                  28781 1.R1040
5'-most EST
                  LIB3051-112-Q1-K1-C12
Method
                  BLASTX
                  g732161
NCBI GI
BLAST score
                  152
                  2.0e-09
E value
Match length
                  60
                  52
% identity
                 HYPOTHETICAL 55.9 KD PROTEIN IN MDS1-RPL13 INTERGENIC
NCBI Description
                  REGION >gi_1077952 pir_ S50396 hypothetical protein YMR140w
                  - yeast (Saccharomyces cerevisiae) >gi 606438 emb_CAA87354
                  (Z47071) unknown [Saccharomyces cerevisiae]
                  13665
Seq. No.
Contig ID
                  28781 2.R1040
5'-most EST
                  jC-gmf102220077b08a1
Method
                  BLASTX
NCBI GI
                  g732161
BLAST score
                  152
E value
                  7.0e-10
Match length
                  60
% identity
                  52
                  HYPOTHETICAL 55.9 KD PROTEIN IN MDS1-RPL13 INTERGENIC
NCBI Description
                  REGION >gi_1077952_pir__S50396 hypothetical protein YMR140w
                   - yeast (Saccharomyces cerevisiae) >gi 606438 emb CAA87354
                  (Z47071) unknown [Saccharomyces cerevisiae]
Seq. No.
                  13666
Contig ID
                  28782 1.R1040
5'-most EST
                  LIB3051-068-Q1-K1-E6
                  BLASTX
Method
NCBI GI
                  q4490704
BLAST score
                  160
E value
                  1.0e-10
Match length
                  57
% identity
                  53
NCBI Description (AL035680) putative protein [Arabidopsis thaliana]
Seq. No.
                  13667
Contig ID
                  28789 1.R1040
5'-most EST
                  kl1701209521.h1
Seq. No.
                  13668
                  28800 1.R1040
Contig ID
```

Contig ID 28800 1.RI040 5'-most EST rlr700895388.h1 Method BLASTX

Method BLASTX
NCBI GI g3135493
BLAST score 184
E value 2.0e-13
Match length 195
% identity 31

NCBI Description (AF060248) unknown [Arabidopsis thaliana]

Seq. No. 13669

Buckeyer



```
Contig ID
                  28802 1.R1040
5'-most EST
                  LIB3051-069-Q1-K1-C3
Seq. No.
                  13670
Contig ID
                  28803 1.R1040
5'-most EST
                  rca701000358.h1
Seq. No.
                  13671
                  28804 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy196a10b1
                  BLASTX
Method
                  g2911058
NCBI GI
BLAST score
                  633
E value
                  8.0e-66
                  333
Match length
% identity
                  44
NCBI Description (AL021961) putative protein [Arabidopsis thaliana]
Seq. No.
                  13672
                  28804_3.R1040
Contig ID
                  gbt700548051.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q3822225
BLAST score
                  150
E value
                  1.0e-09
Match length
                  64
                  52
% identity
NCBI Description
                  (AF079183) RING-H2 finger protein RHG1a [Arabidopsis
                  thaliana]
Seq. No.
                  13673
Contig ID
                  28805 1.R1040
5'-most EST
                  LIB3170-050-Q1-K1-A6
Method
                  BLASTN
NCBI GI
                  g2062691
BLAST score
                  36
                  2.0e-10 ·
E value
                  39
Match length
% identity
NCBI Description Human sodium phosphate transporter (NPT4) mRNA, complete
                  cds
                  13674
Seq. No.
                  28808 1.R1040
Contig ID
5'-most EST
                  hrw701059684.h1
Method
                  BLASTX
NCBI GI
                  g3822036
BLAST score
                  304
E value
                  1.0e-27
Match length
                  155
% identity
                  43
NCBI Description (AF072326) endo-1,3-1,4-beta-D-glucanase [Zea mays]
```

Seq. No. 13675

Contig ID 28811\_1.R1040

5'-most EST jC-gmro02910025d02d1



Contig ID 28814\_1.R1040 5'-most EST rca700996069.h1

Method BLASTX
NCBI GI g4204282
BLAST score 145
E value 1.0e-08
Match length 181
% identity 30

NCBI Description (AC004146) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 13677

Contig ID 28817\_1.R1040 5'-most EST ncj700980677.h1

Seq. No. 13678

Contig ID 28819 1.R1040

5'-most EST uC-gmflminsoy069h05b1

Seq. No. 13679

Contig ID 28819 3.R1040 5'-most EST fua701038953.h1

Seq. No. 13680

Contig ID 28822\_1.R1040

5'-most EST LIB3051-069-Q1-K1-F9

Seq. No. 13681

Contig ID 28830\_1.R1040

5'-most EST LIB3051-069-Q1-K1-H6

Seq. No. 13682

Contig ID 28836 1.R1040

5'-most EST LIB3051-070-Q1-K1-A7

Seq. No. 13683

Contig ID 28837\_1.R1040

5'-most EST LIB3051-070-Q1-K1-B10

Method BLASTX
NCBI GI g4454459
BLAST score 153
E value 9.0e-21
Match length 115
% identity 56

NCBI Description (AC006234) unknown protein [Arabidopsis thaliana]

Seq. No. 13684

Contig ID 28839\_1.R1040

5'-most EST LIB3051-070-Q1-K1-B8

Seq. No. 13685

Contig ID 28843 1.R1040

5'-most EST LIB3051-070-Q1-K1-C9

Seq. No. 13686

Contig ID 28844 1.R1040 5'-most EST gsv701054290.h1



Method BLASTX
NCBI GI g4239845
BLAST score 159
E value 8.0e-11
Match length 77
% identity 44

NCBI Description (AB015855) transcription factor TEIL [Nicotiana tabacum]

Seq. No. 13687

Contig ID 28847 1.R1040

5'-most EST LIB3056-010-Q1-N1-E5

Method BLASTX
NCBI GI g2131420
BLAST score 155
E value 7.0e-10
Match length 181
% identity 30

NCBI Description hypothetical protein YDR299w - yeast (Saccharomyces

cerevisiae) >gi 849214 (U28374) Ydr299wp [Saccharomyces

cerevisiae]

Seq. No. 13688

Contig ID 28848 1.R1040

5'-most EST LIB3051-070-Q1-K1-E5

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 1.0e-10
Match length 36
% identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 13689

Contig ID 28851\_1.R1040 5'-most EST pcp700989169.h1

Seq. No. 13690

Contig ID 28852 1.R1040

5'-most EST LIB30 $\overline{5}1$ -070-Q1-K1-F8

Method BLASTX
NCBI GI g4314357
BLAST score 170
E value 4.0e-12
Match length 84
% identity 29

NCBI Description (AC006340) putative nucleic acid binding protein

[Arabidopsis thaliana]

Seq. No. 13691

Contig ID 28854\_1.R1040

5'-most EST LIB3051-070-Q1-K1-G10

Seq. No. 13692



BLAST score 648 E value 1.0e-67 Match length 197 % identity 64

NCBI Description (AC006072) unknown protein [Arabidopsis thaliana]

Seq. No. 13693

Contig ID 28868 2.R1040 5'-most EST trc700565744.h1

Method BLASTX
NCBI GI g3738309
BLAST score 940
E value 1.0e-107
Match length 301
% identity 67

NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]

Seq. No. 13694

Contig ID 28869\_1.R1040 5'-most EST ncj700988615.h1

Seq. No. 13695

Contig ID 28875\_1.R1040

5'-most EST jC-gmf102220094b02a1

Method BLASTX
NCBI GI g4063751
BLAST score 237
E value 4.0e-25
Match length 231
% identity 36

NCBI Description (AC005851) putative white protein [Arabidopsis thaliana]

>gi\_4510409\_gb\_AAD21495.1\_ (AC006929) putative white

protein [Arabidopsis thaliana]

Seq. No. 13696

Contig ID 28876\_1.R1040

5'-most EST  $g4396\overline{9}31$ 

Seq. No. 13697

Contig ID 28884 1.R1040

5'-most EST LIB3170-049-Q1-K2-E9

Seq. No. 13698

Contig ID 28885 1.R1040

5'-most EST LIB3170-049-Q1-K2-F9

Seq. No. 13699

Contig ID 28886 1.R1040

5'-most EST LIB3051-071-Q1-K1-E10

Seq. No. 13700

Contig ID 28888 1.R1040

5'-most EST LIB3170-051-Q1-K2-A9

Seq. No. 13701

Contig ID 28893\_1.R1040

5'-most EST LIB30 $\overline{5}1$ -071-Q1-K1-F2



```
13702
Seq. No.
Contig ID
                  28894 1.R1040
5'-most EST
                  LIB3170-051-Q1-K1-C9
Method
                  BLASTN
NCBI GI
                  g3821780
BLAST score
                  36
                  9.0e-11
E value
                  36
Match length
                  100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  13703
Seq. No.
Contig ID
                  28896 1.R1040
5'-most EST
                  LIB3138-092-Q1-N1-H6
Method
                  BLASTX
NCBI GI
                  q4567312
BLAST score
                  469
E value
                  1.0e-46
                  117
Match length
% identity
                  73
NCBI Description (AC005956) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  13704
                   28897 1.R1040
Contig ID
                  kl1701209414.h1
5'-most EST
                   13705
Seq. No.
                  28897 2.R1040
Contig ID
                  kmv70\overline{0}742617.h1
5'-most EST
Seq. No.
                  13706
                   28900 1.R1040
Contig ID
5'-most EST
                  LIB3051-071-Q1-K1-G12
Seq. No.
                   13707
Contig ID
                   28901 1.R1040
5'-most EST
                  LIB3170-051-Q1-K1-F9
Method
                  BLASTX
NCBI GI
                  g2088641
BLAST score
                   303
E value
                   1.0e-27
Match length
                  120
                   48
% identity
NCBI Description (AF002109) Myb isolog [Arabidopsis thaliana] >gi 2642168
                   (AC003000) myb-like protein [Arabidopsis thaliana]
Seq. No.
                   13708
Contig ID
                   28919 1.R1040
5'-most EST
                   kl1701212308.h1
Method
                  BLASTX
NCBI GI
                   q1001794
BLAST score
                   431
                   5.0e-42
E value
```

2339

NCBI Description (D64005) hypothetical protein [Synechocystis sp.]

149

54

Match length % identity



```
Seq. No.
                  13709
Contig ID
                  28919 2.R1040
5'-most EST
                  LIB3170-049-Q1-K2-F10
Seq. No.
                  13710
                  28923 1.R1040
Contig ID
5'-most EST
                  jC-qmro02910066e08a1
                  BLASTX
Method
NCBI GI
                  g3668082
BLAST score
                  226
                  3.0e-18
E value
Match length
                  71
% identity
                  61
NCBI Description (AC004667) putative DAL1 protein [Arabidopsis thaliana]
                  13711
Seq. No.
                  28923 2.R1040
Contig ID
5'-most EST
                  LIB3093-033-Q1-K1-B6
Method
                  BLASTX
NCBI GI
                  g1200205
                  339
BLAST score
E value
                  1.0e-31
Match length
                  122
% identity
                  53
NCBI Description (X95753) DAG [Antirrhinum majus]
Seq. No.
                  13712
Contig ID
                   28924 1.R1040
5'-most EST
                  LIB3051-072-Q1-K1-D3
Seq. No.
                   13713
                  28927_1.R1040
Contig ID
5'-most EST
                   jC-gmf102220051e09a1
                  BLASTX
Method
NCBI GI
                  g117314
                  219
BLAST score
E value
                   2.0e-17
                  78
Match length
                   51
% identity
NCBI Description
                  COLD-REGULATED PROTEIN 2 >gi 419794 pir B45512
                   cold-regulated protein 2 - barley (fragment) >gi 167028
                   (M60733) cold-regulated [Hordeum vulgare]
                   13714
Seq. No.
                   28932 1.R1040
Contig ID
                   sat701006131.hl
5'-most EST
Seq. No.
                   13715
Contig ID
                   28933 1.R1040
5'-most EST
                  g4105<del>6</del>87
```

Contig ID 28934\_1.R1040

5'-most EST uC-gmrominsoy101c09b1

Seq. No. 13717



Contig ID 28936\_1.R1040 5'-most EST bth700845977.h1

Seq. No. 13718

Contig ID 28942 1.R1040

5'-most EST LIB3051-072-Q1-K1-H3

Method BLASTX
NCBI GI g2495120
BLAST score 304
E value 9.0e-28
Match length 130
% identity 51

NCBI Description POSSIBLE THIOPHENE AND FURAN OXIDATION PROTEIN THDF

>gi\_1652979\_dbj\_BAA17896\_ (D90910) thiophen and furan

oxidation protein [Synechocystis sp.]

Seq. No. 13719

Contig ID 28943 1.R1040

5'-most EST LIB3051-072-Q1-K1-H4

Seq. No. 13720

Contig ID 28945\_1.R1040

5'-most EST LIB30 $\overline{5}$ 1-072-Q1-K1-H6

Seq. No. 13721

Contig ID 28948\_1.R1040 5'-most EST kl1701209532.h1

Method BLASTX
NCBI GI g2522534
BLAST score 313
E value 3.0e-28
Match length 189
% identity 41

NCBI Description (AF027302) TNF-alpha stimulated ABC protein [Homo sapiens]

Seq. No. 13722

Contig ID 28949 1.R1040

5'-most EST LIB3051-073-Q1-K1-A12

Method BLASTX
NCBI GI g4455325
BLAST score 214
E value 3.0e-17
Match length 86
% identity 49

NCBI Description (AL035525) putative protein [Arabidopsis thaliana]

Seq. No. 13723

Contig ID 28954 1.R1040

5'-most EST LIB3167-049-P1-K1-E2

Seq. No. 13724

Contig ID 28954\_2.R1040 5'-most EST smc700749610.h1

Seq. No. 13725

Contig ID 28954\_3.R1040 5'-most EST hrw701062025.h1



Contig ID 28955\_1.R1040 5'-most EST txt700733109.h1

Seq. No. 13727

Contig ID 28958 1.R1040

5'-most EST LIB3051-073-Q1-K1-D12

Seq. No. 13728

Contig ID 28964\_1.R1040

5'-most EST jC-gmst02400063g06d1

Seq. No. 13729

Contig ID 28967\_1.R1040

5'-most EST LIB3170-049-Q1-K1-G12

Seq. No. 13730

Contig ID 28968\_1.R1040

5'-most EST LIB3051-074-Q1-K1-A5

Method BLASTX
NCBI GI g3894189
BLAST score 749
E value 2.0e-79
Match length 281
% identity 56

NCBI Description (AC005662) hypothetical protein [Arabidopsis thaliana]

Seq. No. 13731

Contig ID 28972 1.R1040

5'-most EST LIB3072-023-Q1-E1-H1

Method BLASTX
NCBI GI g3738285
BLAST score 270
E value 2.0e-23
Match length 161
% identity 39

NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]

Seq. No. 13732

Contig ID 28975\_1.R1040

5'-most EST LIB3109-038-Q1-K1-E4

Seq. No. 13733

Contig ID 28975\_2.R1040 5'-most EST pmv700890886.h1

Seq. No. 13734

Contig ID 28992\_1.R1040

5'-most EST LIB3170-053-Q1-K1-F2

Seq. No. 13735

Contig ID 28993\_1.R1040

5'-most EST uC-gmronoir013a08b1

Seq. No. 13736

Contig ID 28994\_1.R1040



```
5'-most EST
                  jC-gmst02400007f01d1
                  13737
Seq. No.
                  28996 1.R1040
Contig ID
5'-most EST
                  asn701136720.h1
Method
                  BLASTX
                  q4490331
NCBI GI
BLAST score
                  515
                  9.0e-54
E value
                  127
Match length
% identity
                  81
NCBI Description (AL035656) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  13738
Contig ID
                  28996 2.R1040
5'-most EST
                  hrw701059527.h1
Method
                  BLASTX
                  g4490331
NCBI GI
BLAST score
                  382
                  9.0e-37
E value
                  85
Match length
                  89
% identity
NCBI Description (AL035656) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  13739
                   28996 3.R1040
Contig ID
5'-most EST
                  hrw701059282.hl
Method
                  BLASTX
NCBI GI
                  g4490331
BLAST score
                   467
                  1.0e-46
E value
                  103
Match length
% identity
                  88
NCBI Description (AL035656) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  13740
                  28998 1.R1040
Contig ID
5'-most EST
                  LIB3170-056-Q1-K1-E1
Seq. No.
                  13741
Contig ID
                   29000 1.R1040
5'-most EST
                  xpa700795968.h1
Method
                  BLASTX
NCBI GI
                  q136071
BLAST score
                  142
E value
                   1.0e-08
Match length
                  163
                  26
% identity
NCBI Description TROPOMYOSIN 1, SMOOTH MUSCLE (GIZZARD BETA-TROPOMYOSIN)
                   (SMOOTH-MUSCLE ALPHA-TROPOMYOSIN) (TROPOMYOSIN BETA CHAIN,
                   SMOOTH MUSCLE) >gi_71602_pir__TMCHS1 tropomyosin 1, smooth
                   muscle - chicken >gi 212807 (K02446) alpha-tropomyosin
```

Contig ID 29010 1.R1040 5'-most EST gsv701055606.h1

(smooth muscle) [Gallus gallus]



Method BLASTN NCBI GI q3779217

BLAST score 45 E value 5.0e-16 Match length 101 % identity 86

NCBI Description Solanum tuberosum protein kinase CPK1 mRNA, complete cds

Seq. No. 13743

Contig ID 29011\_1.R1040

5'-most EST LIB3109-044-Q1-K1-H5

Seq. No. 13744

Contig ID 29020\_1.R1040 5'-most EST asn701140039.h1

Seq. No. 13745

Contig ID 29022\_1.R1040

5'-most EST LIB3051-075-Q1-K1-C1

Seq. No. 13746

Contig ID 29022 2.R1040

5'-most EST LIB3065-016-Q1-N1-G9

Method BLASTX
NCBI GI g132732
BLAST score 166
E value 1.0e-11
Match length 82
% identity 51

NCBI Description 50S RIBOSOMAL PROTEIN L18, CHLOROPLAST PRECURSOR (CL18)

>gi\_71262\_pir\_\_R5PM18 ribosomal protein PsCL18 precursor,
chloroplast - garden pea >gi\_20869\_emb\_CAA32186\_ (X14021)
PsCL18 ribosomal preprotein (AA -49 to 96) [Pisum sativum]

Seq. No. 13747

Contig ID 29022 3.R1040 5'-most EST 2DC-01-Q1-B1-B5

Seq. No. 13748

Contig ID 29026 1.R1040

5'-most EST LIB30 $\overline{5}1$ -075-Q1-K1-C9

Method BLASTX
NCBI GI g4104321
BLAST score 142
E value 1.0e-08
Match length 96
% identity 35

NCBI Description (AF034582) vesicle associated protein [Rattus norvegicus]

Seq. No. 13749

Contig ID 29027\_1.R1040
5'-most EST g5508999

Method BLASTX
NCBI GI g1711355

BLAST score 199
E value 2.0e-15

Match length 62



% identity 58

NCBI Description SHORT-CHAIN TYPE DEHYDROGENASE/REDUCTASE

>gi\_421786\_pir\_\_S34678 short-chain alcohol dehydrogenase Norway spruce >gi\_395223\_emb\_CAA52213\_ (X74115) short-chain

alcohol dehydrogenase [Picea abies]

Seq. No. 13750

Contig ID 29028 1.R1040

5'-most EST LIB3170-053-Q1-K1-C2

Seq. No. 13751

Contig ID 29029\_1.R1040 5'-most EST uC-gmropic033c04b1

Seq. No. 13752

Contig ID 29037\_1.R1040

5'-most EST LIB31 $\overline{7}$ 0-056-Q1-K1-F2

Seq. No. 13753

Contig ID 29041\_1.R1040 5'-most EST ncj700986807.h1

Seq. No. 13754

Contig ID 29042 1.R1040 5'-most EST zhf700964249.h1

Seq. No. 13755

Contig ID 29042 2.R1040 5'-most EST jex700908849.h1

Seq. No. 13756

Contig ID 29043 1.R1040 5'-most EST crh700850269.h1

Seq. No. 13757

Contig ID 29046 1.R1040

5'-most EST LIB3051-075-Q1-K1-H4

Method BLASTX
NCBI GI g1234787
BLAST score 409
E value 3.0e-39
Match length 448
% identity 32

NCBI Description (U37373) up-regulated by thyroid hormone in tadpoles;

expressed specifically in the tail and only at

metamorphosis; membrane bound or extracellular protein;

C-terminal basic region [Xenopus laevis]

Seq. No. 13758

Contig ID 29053 1.R1040

5'-most EST LIB30 $\overline{5}$ 1-111-Q1-K1-D2

Seq. No. 13759

Contig ID 29053\_2.R1040 5'-most EST jex700909489.h1

Seq. No. 13760



Contig ID 29058 1.R1040

5'-most EST LIB3170-046-Q1-K1-E10

Seq. No. 13761

Contig ID 29061 1.R1040

5'-most EST LIB3051-077-Q1-K1-C10

Seq. No. 13762

Contig ID 29062 1.R1040

5'-most EST LIB3051-107-Q1-K1-G1

13763 Seq. No.

Contig ID 29063 1.R1040

5'-most EST LIB3170-056-Q1-K1-H3

13764 Seq. No.

29064 1.R1040 Contig ID

5'-most EST LIB3051-077-Q1-K1-C3

Seq. No. 13765

29065 1.R1040 Contig ID

5'-most EST LIB3170-056-Q1-K1-G3

Seq. No. 13766

Contig ID 29068\_1.R1040

LIB3106-006-Q1-K2-E9 5'-most EST

BLASTX Method NCBI GI a4159995 BLAST score 342 E value 1.0e-31 281 Match length

9 % identity

NCBI Description (AF063095) SEL1L [Mus musculus]

Seq. No.

29070 1.R1040 Contig ID

5'-most EST LIB3051-077-Q1-K1-D8

13767

13768 Seq. No.

29073 1.R1040 Contig ID

5'-most EST LIB3051-077-Q1-K1-E4

Seq. No. 13769

Contig ID 29076 1.R1040 5'-most EST vwf700678753.h1

Method BLASTX NCBI GI q4056460 BLAST score 153 8.0e-10 E value Match length 177 % identity 32

(AC005990) Contains similarity to gb L26505 Met30p from NCBI Description Saccharomyces cerevisiae. ESTs gb\_F14133, gb\_T46217,

gb AA404758 and gb Z37647 come from this gene. [Arabidopsis

thalianal

Seq. No. 13770



```
Contig ID
                   29078 1.R1040
5'-most EST
                   LIB3051-077-Q1-K1-F12
                   BLASTX
Method
NCBI GI
                   q4510407
BLAST score
                   341
E value
                   1.0e-31
Match length
                   255
% identity
NCBI Description (AC006587) unknown protein [Arabidopsis thaliana]
Seq. No.
                   13771
                   29079 1.R1040
Contig ID
5'-most EST
                   LIB30\overline{5}1-077-Q1-K1-F7
Seq. No.
                   13772
Contig ID
                   29084 1.R1040
5'-most EST
                   LIB3170-054-Q1-K1-H3
                   13773
Seq. No.
                   29093_1.R1040
Contig ID
5'-most EST
                   LIB3170-053-Q1-K1-B4
Method
                   BLASTX
NCBI GI
                   g2136141
BLAST score
                   146
E value
                    4.0e-09
Match length
                   80
% identity
NCBI Description serine C-palmitoyltransferase (EC 2.3.1.50) Lcb2 chain -
                   human (fragment)
                   13774
Seq. No.
Contig ID
                   29098 1.R1040
5'-most EST
                   LIB3051-078-Q1-K1-A5
Method
                   BLASTX
NCBI GI
                   q2252863
BLAST score
                   218
                   2.0e-17
E value
Match length
                    100
% identity
NCBI Description (AF013294) similar to nucleolin protein [Arabidopsis
                   thaliana]
                   13775
Seq. No.
Contig ID
                    29103 1.R1040
5'-most EST
                    jC-gmf102220068h05a1
Method
                   BLASTX
NCBI GI
                   q1708972
BLAST score
                   159
E value
                    1.0e-10
Match length
                    35
% identity
NCBI Description
                    (R)-MANDELONITRILE LYASE ISOFORM 3 PRECURSOR
                    (HYDROXYNITRILE LYASE 3) ((R)-OXYNITRILASE 3) >qi 1262279
                   (U51562) (R)-(+)-mandelonitrile lyase isoform MDL\overline{3} precursor [Prunus serotina] >gi_2343181 (AF013161)
                    (R)-(+)-mandelonitrile lyase isoform MDL3 precursor [Prunus
```

serotina]



```
13776
Seq. No.
                  29110 1.R1040
Contig ID
                  LIB3170-054-Q1-K1-E4
5'-most EST
                  13777
Seq. No.
                  29113 1.R1040
Contig ID
                  LIB3170-055-Q1-K1-G4
5'-most EST
                  13778
Seq. No.
                  29115_1.R1040
Contig ID
                  LIB3170-054-Q1-K1-H4
5'-most EST
                  BLASTX
Method
                   g3036816
NCBI GI
                   204
BLAST score
                   8.0e-16
E value
                   158
Match length
                   37
% identity
                  (AL022373) myosin-like protein [Arabidopsis thaliana]
NCBI Description
                   13779
Seq. No.
                   29117_1.R1040
Contig ID
                   LIB3170-056-Q1-K1-B5
5'-most EST
Seq. No.
                   13780
                   29119 1.R1040
Contig ID
                   LIB3106-098-Q1-K1-G4
5'-most EST
                   13781
Seq. No.
                   29130 1.R1040
Contig ID
                   jC-gm\overline{f}102220099d10a1
5'-most EST
                   BLASTX
Method
                   q2190548
NCBI GI
BLAST score
                   161
                   5.0e-11
E value
Match length
                   31
% identity
                   90
                   (AC001229) EST gb ATTS1121 comes from this gene.
NCBI Description
                   [Arabidopsis thaliana]
                   13782
Seq. No.
                   29130 2.R1040
Contig ID
                   LIB3051-079-Q1-K1-B4
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3152616
```

143 BLAST score 1.0e-08 E value 26

Match length % identity 92 (AC004482) hypothetical protein [Arabidopsis thaliana] NCBI Description >gi 3242726 (AC003040) hypothetical protein [Arabidopsis

thaliana]

13783 Seq. No.

29134 1.R1040 Contig ID g5126525 5'-most EST



```
13784
Seq. No.
                  29135 1.R1040
Contig ID
                  LIB3051-079-Q1-K1-C8
5'-most EST
                  BLASTX
Method
                  q113311
NCBI GI
                  155
BLAST score
                  4.0e-10
E value
                  127
Match length
                   32
% identity
                  ACETYL-COENZYME A SYNTHETASE (ACETATE--COA LIGASE)
NCBI Description
                   (ACYL-ACTIVATING ENZYME) >gi_68571_pir__SYASAA acetate--CoA
                   ligase (EC 6.2.1.1) - Emericella nidulans
                  >gi_2341_emb_CAA34858_ (X16990) acetate--CoA ligase
                   [Emericella nidulans]
                   13785
Seq. No.
                   29137 1.R1040
Contig ID
                   LIB3051-079-Q1-K1-D1
5'-most EST
                   13786
Seq. No.
                   29146_1.R1040
Contig ID
                   LIB3051-079-Q1-K1-F2
5'-most EST
                   BLASTX
Method
                   g2623304
NCBI GI
                   199
BLAST score
                   4.0e-17
E value
                   130
Match length
                   39
% identity
                   (AC002409) similar to Medicago nodulin N21 [Arabidopsis
NCBI Description
                   thalianal
                   13787
Seq. No.
                   29148 1.R1040
Contig ID
                   jC-gmst02400075h01a1
5'-most EST
                   BLASTX
Method
                   q3096947
NCBI GI
                   500
BLAST score
                   1.0e-110
E value
                   284
Match length
                   75
 % identity
                   (Y16327) putative cyclic nucleotide-regulated ion channel
 NCBI Description
                    [Arabidopsis thaliana]
                    13788
 Seq. No.
                    29151 1.R1040
 Contig ID
                   LIB3170-056-Q1-K1-F6
 5'-most EST
                    13789
 Seq. No.
                    29152 1.R1040
 Contig ID
```

LIB3051-079-Q1-K1-H2 5'-most EST

13790 Seq. No.

29159 1.R1040 Contig ID

5'-most EST LIB3170-055-Q1-K1-F6

13791 Seq. No.

29162\_1.R1040 Contig ID



LIB3051-080-Q1-K1-D9 5'-most EST

BLASTX Method q2342685 NCBI GI 230 BLAST score 4.0e-19 E value 102 Match length

42 % identity (AC000106) Contains similarity to Rhodococcus amidase NCBI Description (gb\_D16207). ESTs gb\_T20504, gb\_H36650, gb\_N97423, gb\_H36595

come from this gene. [Arabidopsis thaliana]

13792 Seq. No.

29168 1.R1040 Contig ID kl1701204679.hl 5'-most EST

13793 Seq. No.

29170 1.R1040 Contig ID kl1701210885.hl 5'-most EST

13794 Seq. No.

29172 1.R1040 Contig ID

LIB3051-080-Q1-K1-H12 5'-most EST

13795 Seq. No.

29173 1.R1040 Contig ID

jC-gmle01810033d04d1 5'-most EST

13796 Seq. No.

29180 1.R1040 Contig ID sat701010805.hl 5'-most EST

Method BLASTX q3451078 NCBI GI 147 BLAST score 6.0e-09 E value 107 Match length 38 % identity

NCBI Description (AL031326) putative protein [Arabidopsis thaliana]

13797 Seq. No.

29181 1.R1040 Contig ID bth700848713.h1 5'-most EST

Seq. No.

13798 29181 2.R1040 Contig ID zzp700831518.h15'-most EST

Seq. No.

13799

29183 1.R1040 Contig ID

LIB3170-035-Q1-J1-C1 5'-most EST

13800 Seq. No.

29188 1.R1040 Contig ID

jC-gmf102220070b12a1 5'-most EST

13801 Seq. No.

29191 1.R1040 Contig ID

LIB3051-081-Q1-K1-G4 5'-most EST



Method BLASTN
NCBI GI g18729
BLAST score 57
E value 3.0e-23
Match length 57
% identity 100

NCBI Description Soybean (Glycine max) 18S ribosomal RNA

Seq. No.

13802

Contig ID

29195\_1.R1040

5'-most EST

LIB3051-081-Q1-K1-H1

Method BLASTX
NCBI GI g1351636
BLAST score 500
E value 1.0e-50
Match length 154
% identity 30

NCBI Description HYPOTHETICAL 143.3 KD TRP-ASP REPEATS CONTAINING PROTEIN

C12G12.13C IN CHROMOSOME I >gi\_2130260\_pir\_\_S62544 hypothetical protein SPAC12G12.13c ~ fission yeast

(Schizosaccharomyces pombe)

Seq. No.

Contig ID 29197 1.R1040 5'-most EST leu701145614.h1

Seq. No. 13804

Contig ID 29197 2.R1040 5'-most EST ncj700976814.h1

Seq. No. 13805

Contig ID 29200\_1.R1040 5'-most EST dpv701103081.h1

Seq. No.

13806

13803

Contig ID 29204\_1.R1040

5'-most EST LIB3170-054-Q1-K1-D7

Seq. No. 13807

Contig ID 29214 1.R1040

5'-most EST jC-gmst02400020a10a1

Seq. No.

13808 29217 1.R1040

Contig ID 29217\_1.R1040 5'-most EST bth700849579.h1

Method BLASTX
NCBI GI g401621
BLAST score 159
E value 9.0e-11
Match length 105
% identity 36

NCBI Description HYPOTHETICAL 20.4 KD PROTEIN IN TNAB-BGLB INTERGENIC REGION

>gi\_290561 (L10328) o188 [Escherichia coli] >gi\_1790149
(AE000448) orf, hypothetical protein [Escherichia coli]

Seq. No. 13809

Contig ID 29217\_2.R1040



```
5'-most EST LIB3092-053-Q1-K1-C6
```

Contig ID 29220 1.R1040

5'-most EST uC-gmflminsoy031c06b1

86

Method BLASTN
NCBI GI g4220643
BLAST score 55
E value 6.0e-22
Match length 190

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MWD22, complete sequence [Arabidopsis thaliana]

Seq. No. 13811

% identity

Contig ID 29224\_1.R1040

5'-most EST LIB3051-082-Q1-K1-F11

Seq. No. 13812

Contig ID 29225 1.R1040

5'-most EST LIB3170-053-Q1-K1-G8

Seq. No. 13813

Contig ID 29226 1.R1040

5'-most EST LIB30 $\overline{5}1$ -082-Q1-K1-F2

Seq. No. 13814

Contig ID 29230\_1.R1040

5'-most EST LIB3051-082-Q1-K1-G12

Seq. No. 13815

Contig ID 29235 1.R1040

5'-most EST LIB3170-055-Q1-K1-C8

Seq. No. 13816

Contig ID 29236\_1.R1040

5'-most EST LIB3051-082-Q1-K1-H5

Seq. No. 13817

Contig ID 29237\_1.R1040 5'-most EST wrg700788810.h2

Method BLASTX
NCBI GI g4455246
BLAST score 227
E value 9.0e-19
Match length 83
% identity 57

NCBI Description (AL035523) putative protein [Arabidopsis thaliana]

Seq. No. 13818

Contig ID 29240\_1.R1040

5'-most EST LIB3051-083-Q1-K1-B3

Seq. No. 13819

Contig ID 29243\_1.R1040 5'-most EST awf700839751.h1



```
13820
Seq. No.
Contig ID
                  29243 2.R1040
5'-most EST
                  gsv701047628.h1
Seq. No.
                  13821
Contig ID
                  29246 1.R1040
5'-most EST
                  zsq701119988.h1
Seq. No.
                  13822
Contig ID
                  29247_1.R1040
5'-most EST
                  LIB3051-083-Q1-K1-E8
                  13823
Seq. No.
Contig ID
                  29249 1.R1040
5'-most EST
                  LIB3138-079-P1-N1-A7
                  BLASTN
Method
                  g577088
NCBI GI
BLAST score
                  333
E value
                  0.0e + 00
Match length
                  477
% identity
                  92
NCBI Description P.sativum mRNA for ribosomal protein L1
Seq. No.
                  13824
                  29249 2.R1040
Contig ID
5'-most EST
                  LIB3092-036-Q1-K1-E6
Method
                  BLASTN
NCBI GI
                  g577088
BLAST score
                  190
                  1.0e-102
E value
                  322
Match length
% identity
                  90
NCBI Description P.sativum mRNA for ribosomal protein L1
                  13825
Seq. No.
Contig ID
                  29249 3.R1040
5'-most EST
                  LIB3170-053-Q1-K1-C9
Method
                  BLASTN
NCBI GI
                  g577088
BLAST score
                  79
E value
                  3.0e-36
Match length
                  119
                   92
% identity
NCBI Description P.sativum mRNA for ribosomal protein L1
Seq. No.
                  13826
                  29254 1.R1040
Contig ID
5'-most EST
                  LIB3170-053-Q1-J1-G9
Method
                  BLASTX
NCBI GI
                  g1652475
BLAST score
                  187
E value
                  2.0e-13
```

185 29

Match length

% identity

NCBI Description (D90905) hypothetical protein [Synechocystis sp.]



Contig ID 29254\_2.R1040

5'-most EST LIB3170-053-Q1-K1-G9

Seq. No. 13828

Contig ID 29255 1.R1040

5'-most EST LIB3170-056-Q1-K1-H9

Seq. No. 13829

Contig ID 29257 1.R1040

5'-most EST jC-gmle01810012c09a1

Method BLASTX
NCBI GI g1143711
BLAST score 183
E value 2.0e-13
Match length 121
% identity 45

NCBI Description (U13631) non-green plastid inner envelope membrane protein

precursor [Brassica oleracea]

Seq. No. 13830

Contig ID 29257 2.R1040

5'-most EST uC-gmflminsoy010g04b1

Seq. No. 13831

Contig ID 29260\_1.R1040 5'-most EST jsh701068131.h1

Seq. No. 13832

Contig ID 29261 1.R1040

5'-most EST LIB3170-054-Q1-K1-B9

Seq. No. 13833

Contig ID 29262 1.R1040

5'-most EST jC-gmst02400023c06d1

Seq. No. 13834

Contig ID 29263\_1.R1040 5'-most EST leu701152365.h1

Seq. No. 13835

Contig ID 29268\_1.R1040

5'-most EST LIB3051-084-Q1-K1-D5

Method BLASTX
NCBI GI 94455302
BLAST score 283
E value 4.0e-42
Match length 237
% identity 58

NCBI Description (AL035528) putative protein [Arabidopsis thaliana]

Seq. No. 13836

Contig ID 29268 2.R1040

5'-most EST LIB3170-054-Q1-K1-D11

Seq. No. 13837

Contig ID 29268\_3.R1040

5'-most EST LIB3093-009-Q1-K1-G4



```
Method
                  BLASTX
NCBI GI
                  g4455302
BLAST score
                  321
E value
                  2.0e-29
Match length
                  150
% identity
                  58
NCBI Description (AL035528) putative protein [Arabidopsis thaliana]
Seq. No.
                  13838
Contig ID
                  29270 1.R1040
```

LIB3051-084-Q1-K1-D7

Seq. No. 13839

5'-most EST

Contig ID 29274 1.R1040 5'-most EST awf700839942.h1

Method BLASTX
NCBI GI g3702632
BLAST score 201
E value 3.0e-15
Match length 244
% identity 29

NCBI Description (AL031824) putative transcriptional regulator

[Schizosaccharomyces pombe] >gi\_3859080\_emb\_CAA21957\_

(AL033406) putative alcohol dehydrogenase repressor protein

[Schizosaccharomyces pombe]

Seq. No. 13840

Contig ID 29274 2.R1040

5'-most EST LIB3051-114-Q1-K1-E9

Seq. No. 13841

Contig ID 29275\_1.R1040

5'-most EST LIB3170-055-Q1-K1-H9

Method BLASTX
NCBI GI g3193286
BLAST score 231
E value 4.0e-19
Match length 91
% identity 54

NCBI Description (AF069298) T14P8.22 gene product [Arabidopsis thaliana]

Seq. No. 13842

Contig ID 29276 1.R1040

5'-most EST LIB3139-109-P1-N1-G2

Method BLASTX
NCBI GI 94204268
BLAST score 632
E value 6.0e-66
Match length 169
% identity 80

NCBI Description (AC005223) 62134 [Arabidopsis thaliana]

Seq. No. 13843

Contig ID 29279\_1.R1040 5'-most EST zsg701127441.h1

Seq. No. 13844



Contig ID 29281\_1.R1040 5'-most EST zhf700964740.h1

Seq. No. 13845

Contig ID 29283 1.R1040

5'-most EST LIB3051-084-Q1-K1-H2

Seq. No. 13846

Contig ID 29284 1.R1040

5'-most EST LIB3051-084-Q1-K1-H3

Method BLASTX
NCBI GI g4432835
BLAST score 407
E value 1.0e-39
Match length 131
% identity 57

NCBI Description (AC006283) unknown protein [Arabidopsis thaliana]

Seq. No. 13847

Contig ID 29288\_1.R1040

5'-most EST LIB3170-056-Q1-K1-G10

Method BLASTN
NCBI GI g1218003
BLAST score 53
E value 8.0e-21
Match length 53
% identity 100

NCBI Description Glycine max dynamin-like protein SDL5A mRNA, complete cds

Seq. No. 13848

Contig ID 29290\_1.R1040

5'-most EST LIB3170-086-Q1-K1-E5

Method BLASTX
NCBI GI g3763916
BLAST score 198
E value 5.0e-15
Match length 130
% identity 36

NCBI Description (AC004450) unknown protein [Arabidopsis thaliana]

>gi\_4531439\_gb\_AAD22124.1\_AC006224\_6 (AC006224) unknown

protein [Arabidopsis thaliana]

Seq. No. 13849

Contig ID 29291\_1.R1040

5'-most EST LIB3051-085-Q1-K1-A5

Seq. No. 13850

Contig ID 29304\_1.R1040

5'-most EST LIB30 $\overline{5}1$ -085-Q1-K1-C8

Method BLASTX
NCBI GI g2565010
BLAST score 177
E value 6.0e-13
Match length 78
% identity 47

NCBI Description (AC002983) putative microfibril-associated protein

[Arabidopsis thaliana] >gi 3377811 (AF076275) contains



similarity to ATP synthase B/B' (Pfam: ATP-synt\_B.hmm, score: 11.71) [Arabidopsis thaliana]

Seq. No. 13851

Contig ID 29304\_2.R1040 5'-most EST awf700838279.h1

Method BLASTX
NCBI GI g2565010
BLAST score 265
E value 4.0e-23
Match length 98
% identity 54

NCBI Description (AC002983) putative microfibril-associated protein

[Arabidopsis thaliana] >gi\_3377811 (AF076275) contains similarity to ATP synthase B/B' (Pfam: ATP-synt\_B.hmm,

score: 11.71) [Arabidopsis thaliana]

Seq. No. 13852

Contig ID 29305\_1.R1040

5'-most EST LIB3170-054-Q1-K1-C10

Seq. No. 13853

Contig ID 29306\_1.R1040

5'-most EST LIB3051-085-Q1-K1-D1

Method BLASTX
NCBI GI g2911076
BLAST score 314
E value 9.0e-29
Match length 90
% identity 68

NCBI Description (AL021960) putative protein [Arabidopsis thaliana]

Seq. No. 13854

Contig ID 29307\_1.R1040 5'-most EST epx701106025.h1

Seq. No.

13855

Contig ID 29308\_1.R1040

5'-most EST LIB3051-085-Q1-K1-D2

Seq. No. 13856

Contig ID 29316\_1.R1040 5'-most EST uxk700670374.h1

Method BLASTX
NCBI GI g3025276
BLAST score 207
E value 3.0e-16
Match length 226
% identity 34

NCBI Description HYPOTHETICAL 62.8 KD PROTEIN IN SSE1-CAR1 INTERGENIC REGION >gi\_2132982\_pir\_\_S62012 probable membrane protein YPL109c -

yeast (Saccharomyces cerevisiae) >gi\_1163104 (U43503)

Lph17p [Saccharomyces cerevisiae]

Seq. No. 13857

Contig ID 29316\_2.R1040

5'-most EST LIB3051-085-Q1-K1-F7



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13858
Seq. No.
                  29317 1.R1040
Contig ID
                  LIB3170-054-Q1-K1-H10
5'-most EST
                  13859
Seq. No.
                  29318 1.R1040
Contig ID
                  LIB3051-085-Q1-K1-G1
5'-most EST
                  13860
Seq. No.
                  29321 1.R1040
Contig ID
                   jC-gm\overline{f}102220106g09d1
5'-most EST
                   BLASTX
Method
                   g4006850
NCBI GI
                   247
BLAST score
                   8.0e-21
E value
                   102
Match length
                   67
% identity
NCBI Description (Z99707) cytochrome like protein [Arabidopsis thaliana]
                   13861
Seq. No.
                   29324_1.R1040
Contig ID
                   crh700856289.hl
5'-most EST
                   BLASTX
Method
                   g4204295
NCBI GI
                   314
BLAST score
                   1.0e-28
E value
                   256
Match length
                   36
% identity
                   (AC003027) lcl_prt_seq No definition line found
NCBI Description
                   [Arabidopsis thaliana]
                   13862
Seq. No.
                   29325 1.R1040
Contig ID
                   uC-gmflminsoy042h12b1
5'-most EST
                   13863
 Seq. No.
                   29329 1.R1040
 Contig ID
                   LIB3170-056-Q1-K1-H11
 5'-most EST
                   13864
 Seq. No.
                   29334 1.R1040
 Contig ID
                   hyd700726082.hl
 5'-most EST
                   BLASTX
 Method
                    g4263784
 NCBI GI
 BLAST score
                    315
                    8.0e-29
 E value
                    78
 Match length
 % identity
                    74
                   (AC006068) putative glycogenin-2 protein [Arabidopsis
 NCBI Description
```

thaliana]

13865 Seq. No.

29334 2.R1040 Contig ID

LIB3170-047-Q1-J1-H4 5'-most EST

BLASTX Method g2245015 NCBI GI

2358



BLAST score 186
E value 5.0e-14
Match length 53
% identity 68
NCBI Description (Z97341) unnamed protein product [Arabidopsis thaliana]
Seq. No. 13866
Contig ID 29338\_1.R1040

5'-most EST pmv700888814.h1
Method BLASTX
NCBI GI g4432846
BLAST score 304
E value 2.0e-27
Match length 203

Match length 203 % identity 41

NCBI Description (AC006283) unknown protein [Arabidopsis thaliana]

Seq. No. 13867

Contig ID 29339 1.R1040

5'-most EST LIB3051-086-Q1-K1-B9

Seq. No. 13868

Contig ID 29340 1.R1040

5'-most EST LIB3170-054-Q1-K1-H11

Method BLASTX
NCBI GI g2191136
BLAST score 179
E value 6.0e-13
Match length 142
% identity 35

NCBI Description (AF007269) Similar to UTP-Glucose Glucosyltransferase; coded for by A. thaliana cDNA T46230; coded for by A.

thaliana cDNA H76538; coded for by A. thaliana cDNA H76290

[Arabidancia thaliana]

[Arabidopsis thaliana]

Seq. No. 13869

Contig ID 29341\_1.R1040 5'-most EST uC-gmropic035b10b1

Method BLASTX
NCBI GI g3004662
BLAST score 149
E value 4.0e-09
Match length 77
% identity 43

NCBI Description (AF017777) small optic lobes [Drosophila melanogaster]

Seq. No. 13870

Contig ID 29342 1.R1040

5'-most EST LIB3051-086-Q1-K1-C7

Seq. No. 13871

Contig ID 29345 1.R1040

5'-most EST LIB3051-086-Q1-K1-D2

Seq. No. 13872

Contig ID 29352 1.R1040 5'-most EST uxk700669128.h1



Method BLASTX
NCBI GI g1723832
BLAST score 210
E value 3.0e-16
Match length 102
% identity 37

NCBI Description HYPOTHETICAL 15.9 KD PROTEIN IN OLE1-DUP1 INTERGENIC REGION >gi\_2132531\_pir\_\_ S64058 probable membrane protein YGL054c - yeast (Saccharomyces cerevisiae) >gi\_1322550 emb CAA96756

(Z72576) ORF YGL054c [Saccharomyces cerevisiae]

Seq. No. 13873

Contig ID 29356 1.R1040

5'-most EST LIB3051-086-Q1-K1-F2

Seq. No. 13874

Contig ID 29357\_1.R1040 5'-most EST wrg700787566.h1

Method BLASTX
NCBI GI 94038043
BLAST score 152
E value 1.0e-09
Match length 111
% identity 41

NCBI Description (AC005936) putative DNA-binding protein [Arabidopsis

thaliana]

Seq. No. 13875

Contig ID 29360 1.R1040

5'-most EST uC-gmflminsoy075g10b1

Method BLASTX
NCBI GI g1170239
BLAST score 1569
E value 1.0e-175
Match length 463
% identity 69

NCBI Description FERROCHELATASE PRECURSOR (PROTOHEME FERRO-LYASE) (HEME

SYNTHETASE) >gi 474968 dbj BAA05102 (D26106)

ferrochelatase [Cucumis sativus]

Seq. No. 13876

Contig ID 29360\_2.R1040

5'-most EST uC-gmflminsoy070e05b1

Seq. No. 13877

Contig ID 29364 1.R1040

5'-most EST LIB3139-029-P1-N1-H9

Method BLASTX
NCBI GI g1946369
BLAST score 262
E value 3.0e-32
Match length 223
% identity 30

NCBI Description (U93215) unknown protein [Arabidopsis thaliana]

Seq. No. 13878

Contig ID 29367 1.R1040



LIB3170-054-Q1-K1-C12 5'-most EST Seq. No. 13879 29369 1.R1040 Contig ID LIB3051-086-Q1-K1-H9 5'-most EST 13880 Seq. No. 29371\_1.R1040 Contig ID jC-gmro02910009d04a1 5'-most EST BLASTX Method g3763916 NCBI GI 213 BLAST score 7.0e-17 E value 123 Match length % identity 38 (AC004450) unknown protein [Arabidopsis thaliana] NCBI Description >qi 4531439 gb AAD22124.1 AC006224\_6 (AC006224) unknown protein [Arabidopsis thaliana] 13881 Seq. No. 29372 1.R1040 Contig ID LIB3170-055-Q1-K1-E12 5'-most EST 13882 Seq. No. 29374 1.R1040 Contig ID uC-gmrominsoy180g04b1 5'-most EST BLASTX Method q4510346 NCBI GI 935 BLAST score 1.0e-111 E value 269 Match length 78 % identity (AC006921) hypothetical protein [Arabidopsis thaliana] NCBI Description 13883 Seq. No. 29374 2.R1040 Contig ID LIB3051-087-Q1-K1-B1 5'-most EST BLASTX Method q4510346 NCBI GI BLAST score 146 3.0e-09 E value 39 Match length 69 % identity (AC006921) hypothetical protein [Arabidopsis thaliana] NCBI Description 13884 Seq. No. 29377 1.R1040 Contig ID LIB3051-087-Q1-K1-B9 5'-most EST 13885 Seq. No. 29379 1.R1040 Contig ID epx701110447.h1 5'-most EST BLASTX Method

Method BLASTX
NCBI GI g4376650
BLAST score 390
E value 2.0e-37
Match length 182



```
% identity
NCBI Description
                  (AE001621) GcpE Protein [Chlamydia pneumoniae]
Seq. No.
                  13886
                  29379 2.R1040
Contig ID
5'-most EST
                  jC-gmro02910050h07d1
                  13887
Seq. No.
Contig ID
                  29380 1.R1040
5'-most EST
                  LIB3093-013-Q1-K1-D11
Method
                  BLASTX
NCBI GI
                  g3510253
BLAST score
                  334
                  7.0e-31
E value
Match length
                  156
% identity
                  65
                  (AC005310) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  13888
Seq. No.
Contig ID
                  29384 1.R1040
5'-most EST
                  LIB3107-053-Q1-K1-G4
Method
                  BLASTX
NCBI GI
                  q4567250
BLAST score
                  212
                  2.0e-16
E value
Match length
                  95
% identity
                   43
NCBI Description (AC007070) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  13889
                  29387 1.R1040
Contig ID
5'-most EST
                  LIB3051-087-Q1-K1-E3
                  13890
Seq. No.
Contig ID
                  29396 1.R1040
5'-most EST
                  LIB3051-087-Q1-K1-G10
Seq. No.
                  13891
Contig ID
                  29402 1.R1040
5'-most EST
                  uC-gmrominsoy210c03b1
Method
                  BLASTX
NCBI GI
                   g2673918
BLAST score
                   350
E value
                   2.0e-32
Match length
                   410
```

% identity 32

NCBI Description (AC002561) unknwon protein [Arabidopsis thaliana]

13892 Seq. No. Contig ID

29407\_1.R1040

5'-most EST LIB3107-054-Q1-K1-B2

13893 Seq. No.

Contig ID 29408 1.R1040

5'-most EST LIB3170-058-Q1-K1-E1

Seq. No. 13894



Contig ID 29408 2.R1040 5'-most EST

LIB3087-006-Q1-K1-C1

Seq. No. 13895

29410 1.R1040 Contig ID 5'-most EST vwf700675915.h1

Method BLASTX q3183285 NCBI GI BLAST score 472 2.0e-47 E value 272 Match length 45 % identity

NCBI Description HYPOTHETICAL 54.4 KD PROTEIN IN AROH-NLPC INTERGENIC REGION

>gi\_1742787\_dbj\_BAA15475\_ (D90813) ORF\_ID:o322#7; similar to [SwissProt Accession Number Q06373] [Escherichia coli]

>gi 1787999 (AE000266) orf, hypothetical protein

[Escherichia coli]

Seq. No. 13896

Contig ID 29411 1.R1040

5'-most EST uC-gmflminsoy079d11b1

Seq. No. 13897

29412 1.R1040 Contig ID 5'-most EST q5753250

13898 Seq. No.

29414 1.R1040 Contig ID

5'-most EST LIB3170-060-Q1-K1-A2

Seq. No. 13899

29414 2.R1040 Contig ID 5'-most EST hyd700727356.h1

Seq. No. 13900

Contig ID 29417 1.R1040 5'-most EST uaw700664741.h1

Seq. No. 13901

Contig ID 29417 2.R1040

5'-most EST jC-gmst02400020a07a1

Seq. No. 13902

Contig ID 29418 1.R1040

5'-most EST LIB3051-088-Q1-K1-D12

13903 Seq. No.

Contig ID 29421 1.R1040 5'-most EST seb700651666.h1

Seq. No. 13904

29422 1.R1040 Contig ID

5'-most EST LIB3109-003-Q1-K1-F5

Method BLASTX NCBI GI g3860262 BLAST score 966 E value 1.0e-105



```
257
Match length
                  70
% identity
                  (AC005824) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  13905
                  29424 1.R1040
Contig ID
                  zhf700951982.hl
5'-most EST
                  BLASTX
Method
                  g3202042
NCBI GI
BLAST score
                  360
                   6.0e-34
E value
                   146
Match length
                   58
% identity
                   (AF069324) 26S proteasome regulatory subunit S5A
NCBI Description
                   [Mesembryanthemum crystallinum]
                   13906
Seq. No.
                   29424 2.R1040
Contig ID
                   fC-gmse700670286a1
5'-most EST
                   BLASTN
Method
                   g3202041
NCBI GI
BLAST score
                   46
                   1.0e-16
E value
                   110
Match length
                   85
% identity
                   Mesembryanthemum crystallinum 26S proteasome regulatory
NCBI Description
                   subunit S5A mRNA, complete cds
                   13907
Seq. No.
                   29425 1.R1040
Contig ID
                   jC-gmf102220051c05a1
5'-most EST
                   BLASTX
Method
                   g4512707
NCBI GI
                   1200
BLAST score
                   1.0e-132
E value
                   318
Match length
                   74
% identity
                   (AC006569) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   13908
Seq. No.
                   29425 2.R1040
Contig ID
                   dpv701103688.h1
5'-most EST
                   BLASTX
Method
                   g4512707
NCBI GI
                   170
```

Method BLASTX
NCBI GI g4512707
BLAST score 170
E value 3.0e-12
Match length 36
% identity 94

NCBI Description (AC006569) hypothetical protein [Arabidopsis thaliana]

Seq. No. 13909

Contig ID 29426\_1.R1040

5'-most EST LIB3051-088-Q1-K1-F10

Method BLASTX
NCBI GI g4580469
BLAST score 162
E value 5.0e-11

Match length 88 % identity 50 NCBI Description (AC006081) putative zinc finger protein [Arabidopsis 13910 Seq. No. 29434 1.R1040 Contig ID 5'-most EST jC-gmf102220058g04a1 13911 Seq. No. 29434 3.R1040 Contig ID 5'-most EST sat701007136.h1 Seq. No. 13912 29436 1.R1040 Contig ID 5'-most EST xpa700793082.h1 Seq. No. 13913 29436 2.R1040 Contig ID 5'-most EST sat701011049.h1 Seq. No. 13914 Contig ID 29438 1.R1040

5'-most EST jC-qmf102220056h06a1

Method BLASTX NCBI GI g3702333 BLAST score 551 E value 3.0e-56 Match length 166 68 % identity

NCBI Description (AC005397) hypothetical protein [Arabidopsis thaliana]

Seq. No. 13915

Contig ID 29446 1.R1040

5'-most EST LIB3051-090-Q1-K1-A11

Method BLASTX NCBI GI g421953 BLAST score 201 E value 2.0e-15 Match length 59

% identity 68

NCBI Description hypothetical protein 2 - potato transposon Tst1

>gi\_21432\_emb\_CAA36614\_ (X52387) ORF2 [Solanum tuberosum]

13916 Seq. No.

Contig ID 29452 1.R1040

5'-most EST LIB3170-059-Q1-K1-F7

Seq. No. 13917

Contig ID 29459 1.R1040 5'-most EST gsv701051562.h1

Seq. No. 13918

29460 1.R1040 Contig ID

5'-most EST LIB3051-113-Q1-K1-C5

Seq. No. 13919



Contig ID 29464 1.R1040 5'-most EST LIB3051-090-Q1-K1-D9

Seq. No. 13920

Contig ID 29472\_1.R1040

5'-most EST uC-gmrominsoy320d01b1

Method BLASTX
NCBI GI g4314357
BLAST score 184
E value 2.0e-13
Match length 113
% identity 21

NCBI Description (AC006340) putative nucleic acid binding protein

[Arabidopsis thaliana]

Seq. No. 13921

Contig ID 29473 1.R1040

5'-most EST LIB3093-035-Q1-K1-A4

Method BLASTN
NCBI GI g169960
BLAST score 83
E value 2.0e-38
Match length 261
% identity 85

NCBI Description Glycine max G-box binding factor (GBF2B) mRNA, 3' end

Seq. No. 13922

Contig ID 29478\_1.R1040

5'-most EST LIB3051-090-Q1-K1-H5

Seq. No. 13923

Contig ID 29479\_1.R1040 5'-most EST 2hf700953227.h1

Seq. No. 13924

Contig ID 29479 2.R1040 5'-most EST jex700908603.h1

Seq. No. 13925

Contig ID 29482 1.R1040

5'-most EST LIB3051-091-Q1-K1-A8

Seq. No. 13926

Contig ID 29485 1.R1040

5'-most EST LIB3051-091-Q1-K1-B12

Seq. No. 13927

Contig ID 29488\_1.R1040

5'-most EST LIB3051-091-Q1-K1-C3

Seq. No. 13928

Contig ID 29489 1.R1040

5'-most EST LIB3051-091-Q1-K1-C5

Seq. No. 13929

Contig ID 29489 2.R1040

5'-most EST LIB3093-014-Q1-K1-F1



Seq. No. 13930

Contig ID 29489\_3.R1040 5'-most EST zzp700834613.h1

Seq. No. 13931

Contig ID 29496\_1.R1040 5'-most EST zhf700959670.h1

Seq. No. 13932

Contig ID 29500 1.R1040

5'-most EST LIB3051-091-Q1-K1-F9

Seq. No. 13933

Contig ID 29509 1.R1040

5'-most EST LIB3170-046-Q1-J1-D3

Method BLASTX
NCBI GI g2828289
BLAST score 505
E value 5.0e-54
Match length 200
% identity 50

NCBI Description (AL021687) hypothetical protein [Arabidopsis thaliana]

Seq. No. 13934

Contig ID 29514 1.R1040

5'-most EST LIB3051-092-Q1-K1-C6

Seq. No. 13935

Contig ID 29516 1.R1040

5'-most EST LIB3051-092-Q1-K1-D7

Seq. No. 13936

Contig ID 29520 1.R1040

5'-most EST LIB3170-059-Q1-K1-C10

Seq. No. 13937

Contig ID 29522 1.R1040

5'-most EST LIB3170-058-Q1-K1-D5

Seq. No. 13938

Contig ID 29522\_2.R1040

5'-most EST jC-gmro02800040c07a1

Method BLASTX
NCBI GI g2244898
BLAST score 604
E value 1.0e-62
Match length 184
% identity 61

NCBI Description (Z97338) strong similarity to protein phosphatase 2A

regulatory chain, 74K [Arabidopsis thaliana]

Seq. No. 13939

Contig ID 29531\_1.R1040 5'-most EST wvk700683473.h1

Method BLASTX NCBI GI q4490756



BLAST score E value 1.0e-26 Match length 141 % identity 43

NCBI Description (AL035708) hypothetical protein [Arabidopsis thaliana]

Seq. No.

13940

Contig ID 5'-most EST

29531 2.R1040 trc700566049.h1

Seq. No.

13941

Contig ID 5'-most EST 29533 1.R1040  $k1170\overline{1}211907.h1$ 

Seq. No.

13942

Contig ID 5'-most EST 29536 1.R1040

LIB3051-093-Q1-K1-A8

Seq. No.

13943

Contig ID

29537 1.R1040

5'-most EST LIB3051-093-Q1-K1-A9

Seq. No.

13944

Contig ID 5'-most EST 29544\_1.R1040

LIB3051-093-Q1-K1-C4

Seq. No.

13945

Contig ID 5'-most EST

29545 1.R1040 jsh701070241.h1

Seq. No.

13946

Contig ID 5'-most EST 29548 1.R1040

LIB3051-103-Q1-K1-A3

Seq. No.

13947

Contig ID 5'-most EST 29550 1.R1040 LIB3107-034-Q1-K1-F6

Seq. No.

13948

Contig ID

29553 1.R1040

5'-most EST

LIB3170-057-Q1-K1-G6

Seg. No.

13949

Contig ID

29559 1.R1040

5'-most EST

LIB3170-058-Q1-K1-C6

Seq. No.

13950

Contig ID

29562 1.R1040

5'-most EST

LIB3106-114-Q1-K1-E6

Seg. No.

13951

Contig ID 5'-most EST

29562 2.R1040 xpa700793009.h1

Seq. No.

13952

Contig ID 5'-most EST 29562 3.R1040

zsg701119507.h1

```
Seq. No. 13953
Contig ID 29562_4.R1040
5'-most EST epx701104354.h1

Seq. No. 13954
Contig ID 29563_1.R1040
5'-most EST LIB3051-093-Q1-K1-H1

Seq. No. 13955
```

Seq. No.

Contig ID

5'-most EST

29566 1.R1040

sat701009552.h1

 Seq. No.
 13956

 Contig ID
 29566\_2.R1040

 5'-most EST
 epx701108383.h1

 Seq. No.
 13957

 Contig ID
 29566\_3.R1040

 5'-most EST
 asn701135822.h1

Seq. No. 13958 Contig ID 29567\_1.R1040

5'-most EST LIB3092-020-Q1-K1-F8

 Seq. No.
 13959

 Contig ID
 29568\_1.R1040

 5'-most EST
 LIB3051-094-Q1-K1-B1

Seq. No. 13960 Contig ID 29578\_1.R1040

5'-most EST LIB3051-094-Q1-K1-E10
Method BLASTX
NCBI GI g3786012

NCBI GI g3786012
BLAST score 362
E value 2.0e-34
Match length 126
% identity 56

NCBI Description (AC005499) putative acid phosphatase [Arabidopsis thaliana]

Seq. No. 13961

Contig ID 29580\_1.R1040 5'-most EST uC-gmronoir013a01b1

Seq. No. 13962

Contig ID 29580\_2.R1040

5'-most EST LIB31 $\overline{3}$ 8-095-Q1-N1-H11

Method BLASTX
NCBI GI g2632254
BLAST score 616
E value 5.0e-64
Match length 146
% identity 80

NCBI Description (Y12465) serine/threonine kinase [Sorghum bicolor]

Seq. No. 13963

Contig ID 29581\_1.R1040



```
LIB3051-094-Q1-K1-F1
5'-most EST
                   13964
Seq. No.
                   29582 1.R1040
Contig ID
                   LIB3051-094-Q1-K1-F3
5'-most EST
                   13965
Seq. No.
                   29588 1.R1040
Contig ID
                   LIB3051-094-Q1-K1-G8
5'-most EST
                   13966
Seq. No.
                   29588 2.R1040
Contig ID
                   zzp700834515.h1
5'-most EST
                   13967
Seq. No.
                   29595 1.R1040
Contig ID
                   rca700997548.hl
5'-most EST
                   13968
Seq. No.
                   29596 1.R1040
Contig ID
                   LIB3051-095-Q1-K1-B8
5'-most EST
                   13969
Seq. No.
                   29597_1.R1040
Contig ID
                   LIB3051-095-Q1-K1-C10
5'-most EST
                   BLASTX
Method
                   g3878874
NCBI GI
                   181
BLAST score
                   3.0e-13
E value
                   82
Match length
                   43
% identity
                   (Z69793) R03A10.3 [Caenorhabditis elegans]
NCBI Description
                   13970
Seq. No.
                    29598 1.R1040
Contig ID
                   LIB3170-058-Q1-K1-E8
 5'-most EST
                    13971
 Seq. No.
                    29599 1.R1040
 Contig ID
                    kl1701206533.h1
 5'-most EST
 Seq. No.
                    13972
                    29600 1.R1040
 Contig ID
                    LIB3170-058-Q1-J1-C4
 5'-most EST
                    13973
 Seq. No.
                    29601 1.R1040
 Contig ID
                    LIB30\overline{5}1-095-Q1-K1-D11
 5'-most EST
 Method
                    BLASTX
                    g3894168
 NCBI GI
```

210 BLAST score 2.0e-16 E value 119 Match length 33 % identity

(ACO05312) similar to phloem-specific lectin [Arabidopsis NCBI Description

thaliana]



```
13974
Seq. No.
                  29607 1.R1040
Contig ID
                  LIB3051-095-Q1-K1-E6
5'-most EST
                  BLASTX
Method
NCBI GI
                   q3608144
BLAST score
                  169
                   2.0e-12
E value
                   52
Match length
% identity
NCBI Description (AC005314) unknown protein [Arabidopsis thaliana]
                   13975
Seq. No.
                   29609 1.R1040
Contig ID
                   LIB3051-095-Q1-K1-F10
5'-most EST
                   13976
Seq. No.
Contig ID
                   29610 1.R1040
                   LIB3170-057-Q1-K1-C9
5'-most EST
                   13977
Seq. No.
                   29610 2.R1040
Contig ID
5'-most EST
                   asn701135788.h1
                   13978
Seq. No.
                   29614 1.R1040
Contig ID
                   LIB3107-065-Q1-K1-A1
5'-most EST
                   13979
Seq. No.
                   29623 1.R1040
Contig ID
                   LIB3051-096-Q1-K1-B2
5'-most EST
Seq. No.
                   13980
                   29626 1.R1040
Contig ID
                   kmv70\overline{0}742908.h1
5'-most EST
                   BLASTX
Method
                   g2760832
NCBI GI
                   298
BLAST score
                   7.0e-27
E value
                   108
Match length
                   62
 % identity
                   (AC003105) similar to barley ids-4 gene product
NCBI Description
                    [Arabidopsis thaliana]
                   13981
 Seq. No.
                   29627 1.R1040
 Contig ID
                   zzp700830252.hl
 5'-most EST
                   13982
 Seq. No.
                    29631 1.R1040
 Contig ID
                    jC-gmro02910046f06a1
```

5'-most EST

Seq. No. 13983

29632 1.R1040 Contig ID

LIB3170-057-Q1-K1-C10 5'-most EST

13984 Seq. No.

29637 1.R1040 Contig ID

2371



```
ssr700555259.hl
5'-most EST
```

13985 Seq. No.

29640 1.R1040 Contig ID

LIB3139-013-P1-N1-C5 5'-most EST

Method BLASTX q3757522 NCBI GI 590 BLAST score 1.0e-60 E value 250 Match length % identity

(AC005167) putative splicing factor [Arabidopsis thaliana] NCBI Description

13986 Seq. No.

29646 1.R1040 Contig ID 5'-most EST asn701137687.h1

13987 Seq. No.

29654 1.R1040 Contig ID

LIB3051-100-Q1-K1-A12 5'-most EST

BLASTX Method NCBI GI q481812 249 BLAST score 3.0e-21 E value 80 Match length % identity

DNA-binding protein GT-2 - Arabidopsis thaliana NCBI Description

>gi 416490\_emb\_CAA51289\_ (X72780) GT-2 factor [Arabidopsis

thaliana]

Seq. No. Contig ID 13988

29655 1.R1040 uC-gmronoir004b04b1 5'-most EST

Seq. No.

13989

29661 1.R1040 Contig ID uC-gmropic006c10b1 5'-most EST

Seq. No.

13990

29668 1.R1040 Contig ID

LIB3107-066-Q1-K1-G4 5'-most EST

Seq. No.

13991

29668 3.R1040 Contig ID

LIB3051-101-Q1-K1-A7 5'-most EST

Seq. No.

13992

29670 1.R1040 Contig ID

LIB3139-023-P1-N1-D12 5'-most EST

Seq. No.

13993

29673 1.R1040 Contig ID

LIB3170-064-Q1-K1-F2 5'-most EST

Seq. No.

13994

29673 2.R1040 Contig ID

LIB3092-006-Q1-K1-E1 5'-most EST



Method BLASTX
NCBI GI g2245061
BLAST score 681
E value 2.0e-71
Match length 251
% identity 67
NCBI Description (Z97342)

NCBI Description (Z97342) Clp proteinase homolog [Arabidopsis thaliana]

Seq. No. 13995

Contig ID 29676\_1.R1040

5'-most EST jC-gmle01810010g06a1

Seq. No. 13996

Contig ID 29677\_1.R1040

5'-most EST LIB3051-101-Q1-K1-E10

Method BLASTX
NCBI GI g2760843
BLAST score 295
E value 1.0e-26
Match length 121
% identity 58

NCBI Description (AC003105) unknown protein [Arabidopsis thaliana]

Seq. No. 13997

Contig ID 29679 1.R1040

5'-most EST jC-gmro02910008c09a1

Seq. No. 13998

Contig ID 29682\_1.R1040

5'-most EST LIB3051-101-Q1-K1-F12

Method BLASTX
NCBI GI g4490735
BLAST score 480
E value 4.0e-48
Match length 135
% identity 65

NCBI Description (AL035708) putative protein [Arabidopsis thaliana]

Seq. No. 13999

Contig ID 29689\_1.R1040

5'-most EST LIB3065-025-Q1-N1-F8

Seq. No. 14000

Contig ID 29695\_1.R1040 5'-most EST uxk700667182.h1

Method BLASTX
NCBI GI g4454026
BLAST score 601
E value 3.0e-62
Match length 173
% identity 69

NCBI Description (AL035394) phosphatase like protein [Arabidopsis thaliana]

Seq. No. 14001

Contig ID 29695\_2.R1040

5'-most EST jC-gmro02910063c11d1

Method BLASTX



```
NCBI GI g4454026
BLAST score 297
E value 8.0e-27
Match length 69
% identity 78
NCBI Description (AL035394) phosphata
```

NCBI Description (AL035394) phosphatase like protein [Arabidopsis thaliana]

Seq. No. 14002

Contig ID 29703\_1.R1040

5'-most EST LIB3170-061-Q1-K2-F3

Seq. No. 14003

Contig ID 29710 1.R1040

5'-most EST LIB3051-102-Q1-K1-D7

Seq. No. 14004

Contig ID 29713\_1.R1040 5'-most EST fC-gmse700671032z1

Seq. No. 14005

Contig ID 29724 1.R1040

5'-most EST LIB3051-102-Q1-K1-H7

Seq. No. 14006

Contig ID 29726\_1.R1040

5'-most EST LIB3139-016-P1-N1-G11

Method BLASTX
NCBI GI g3915436
BLAST score 205
E value 4.0e-18
Match length 148
% identity 45

NCBI Description HYPOTHETICAL 53.4 KD PROTEIN IN PRP9-NAT1 INTERGENIC REGION

>gi\_2131316\_pir\_\_S67569 hypothetical protein YDL036c yeast (Saccharomyces cerevisiae) >gi\_1279680\_emb\_CAA96453\_

(Z71781) unknown [Saccharomyces cerevisiae] >gi\_1431018\_emb\_CAA98595\_ (Z74084) ORF YDL036c

[Saccharomyces cerevisiae]

Seq. No. 14007

Contig ID 29727 1.R1040

5'-most EST LIB3170-064-Q1-K1-A4

Seq. No. 14008

Contig ID 29736\_1.R1040 5'-most EST zhf700964761.h1

Method BLASTX
NCBI GI g4105269
BLAST score 243
E value 2.0e-20
Match length 123
% identity 43

NCBI Description (AF044574) putative peroxisomal 2,4-dienoyl-CoA reductase

[Rattus norvegicus]

Seq. No. 14009

Contig ID 29736 2.R1040



5'-most EST wvk700682265.h1

Seq. No. 14010

Contig ID 29739\_1.R1040

5'-most EST LIB3051-103-Q1-K1-C2

Seq. No. 14011

Contig ID 29740\_1.R1040

5'-most EST LIB3170-061-Q1-K2-D4

Seq. No. 14012

Contig ID 29741\_1.R1040

5'-most EST LIB3170-064-Q1-K1-E4

Seq. No. 14013

Contig ID 29744 1.R1040

5'-most EST LIB3093-044-Q1-K1-D5

Seq. No. 14014

Contig ID 29746\_1.R1040 5'-most EST awf700843306.h1

Seq. No. 14015

Contig ID 29748\_1.R1040

5'-most EST LIB3051-103-Q1-K1-F10

Seq. No. 14016

Contig ID 29757\_1.R1040

5'-most EST uC-gmflminsoy044g03b1

Seq. No. 14017

Contig ID 29763\_1.R1040

5'-most EST LIB30 $\overline{5}$ 1-104-Q1-K1-A7

Seq. No. 14018

Contig ID 29763\_2.R1040 5'-most EST uaw700661059.h1

Seq. No. 14019

Contig ID 29780\_1.R1040 5'-most EST fC-qmle700558924f2

Method BLASTX
NCBI GI g4262225
BLAST score 421
E value 2.0e-41

Match length 132 % identity 57

NCBI Description (AC006200) putative phosphatidic acid phosphatase

[Arabidopsis thaliana]

Seq. No. 14020

Contig ID 29780\_2.R1040

5'-most EST LIB3051-104-Q1-K1-F8

Method BLASTX
NCBI GI g4262225
BLAST score 311
E value 1.0e-28

2375



Match length 130 % identity 47

NCBI Description (AC006200) putative phosphatidic acid phosphatase

[Arabidopsis thaliana]

Seq. No. 14021

Contig ID 29781 1.R1040

5'-most EST jC-gmle01810021c03a1

Seq. No. 14022

Contig ID 29785\_1.R1040

5'-most EST LIB30 $\overline{5}1-106-Q1-K1-B4$ 

Seq. No. 14023

Contig ID 29803 1.R1040

5'-most EST LIB3170-064-Q1-K1-H6

Seq. No. 14024

Contig ID 29805\_1.R1040 5'-most EST uC-gmropic034h05b1

Seq. No. 14025

Contig ID 29807\_1.R1040 5'-most EST g5057992 Method BLASTX NCBI GI g2739385

BLAST score 657
E value 9.0e-94
Match length 262
% identity 69

NCBI Description (AC002505) putative beta-1,3-glucanase [Arabidopsis

thaliana]

Seq. No. 14026

Contig ID 29808\_1.R1040

5'-most EST LIB3051-105-Q1-K1-D10

Seq. No. 14027

Contig ID 29810 1.R1040

5'-most EST uC-gmflminsoy117d01b1

Seq. No. 14028

Contig ID 29818\_1.R1040 5'-most EST zhf700962609.h1

Method BLASTX
NCBI GI g3152572
BLAST score 341
E value 2.0e-31
Match length 292
% identity 44

NCBI Description (AC002986) Contains homology to DNAJ heatshock protein

gb\_U32803 from Haemophilus influenzae. [Arabidopsis

thaliana]

Seq. No. 14029

Contig ID 29825 1.R1040

5'-most EST LIB3170-064-Q1-K1-B7



14030 Seq. No.

Contig ID 29830 1.R1040 5'-most EST pxt700943809.h1

Method BLASTX g4455159 NCBI GI BLAST score 229 1.0e-18 E value 76 Match length 59 % identity

NCBI Description (AL021687) putative protein [Arabidopsis thaliana]

14031 Seq. No.

Contig ID 29832 1.R1040 5'-most EST g5342427

14032 Seq. No.

29833 1.R1040 Contig ID

5'-most EST LIB3170-061-Q1-K2-F7

14033 Seq. No.

Contig ID 29837 1.R1040

5'-most EST LIB3051-106-Q1-K1-B11

Seq. No. 14034

Contig ID 29838 1.R1040 5'-most EST ssr700559171.h1

14035 Seq. No.

Contig ID 29840 1.R1040

5'-most EST LIB3138-055-Q1-N1-C9

14036 Seq. No.

29840 2.R1040 Contig ID 5'-most EST ncj700985914.h1

Seq. No.

14037 29842 1.R1040 Contig ID

5'-most EST LIB3051-106-Q1-K1-C10

14038 Seq. No.

29844 1.R1040 Contig ID

5'-most EST LIB3051-106-Q1-K1-C2

14039 Seq. No.

29845\_1.R1040 Contig ID

LIB3170-062-Q1-K1-C7 5'-most EST

Seq. No. 14040

29846 1.R1040 Contig ID

5'-most EST LIB3051-106-Q1-K1-D10

Seq. No. 14041

29847 1.R1040 Contig ID 5'-most EST uC-gmropic059h06b1

14042 Seq. No.



```
29855 1.R1040
Contig ID
                   fua701042683.h1
5'-most EST
                   BLASTX
Method
                   g2623297
NCBI GI
BLAST score
                   527
E value
                   4.0e-53
                   299
Match length
                   42
% identity
                   (AC002409) unknown protein [Arabidopsis thaliana]
NCBI Description
                   >gi_3790583 (AF079180) RING-H2 finger protein RHCla
                   [Arabidopsis thaliana]
                   14043
Seq. No.
                   29855 2.R1040
Contig ID
                   uC-qmflminsoy099b03b1
5'-most EST
Seq. No.
                   14044
                   29857 1.R1040
Contig ID
                   LIB30\overline{5}1-106-Q1-K1-G2
5'-most EST
                   14045
Seq. No.
                   29860 1.R1040
Contig ID
                   hyd700728963.hl
5'-most EST
                   14046
Seq. No.
                   29861 1.R1040
Contig ID
                   LIB3051-106-Q1-K1-H11
5'-most EST
                   14047
Seq. No.
                   29863 1.R1040
Contia ID
                   q5606043
5'-most EST
Method
                   BLASTX
                   q4510354
NCBI GI
                   258
BLAST score
                   5.0e-22
E value
                   155
Match length
                   46
% identity
                   (AC006921) unknown protein [Arabidopsis thaliana]
NCBI Description
                   14048
Seq. No.
                   29865 1.R1040
Contig ID
                   LIB3051-106-Q1-K1-H6
5'-most EST
                   14049
Seq. No.
                   29872 1.R1040
Contig ID
                   xpa700792592.h1
 5'-most EST
                    14050
Seq. No.
                    29878 1.R1040
 Contig ID
                    LIB3051-107-Q1-K1-D11
 5'-most EST
                    BLASTX
Method
                    q4455335
 NCBI GI
 BLAST score
                    566
 E value
                    2.0e-58
```

2378

NCBI Description (AL035525) putative protein [Arabidopsis thaliana]

160

27

Match length % identity



Seq. No. 14051

Contig ID 29887\_1.R1040

5'-most EST LIB3051-107-Q1-K1-F11

Method BLASTX
NCBI GI 94512666
BLAST score 322
E value 7.0e-30
Match length 124
% identity 34

NCBI Description (AC006931) putative mei2 protein [Arabidopsis thaliana]

Seq. No. 14052

Contig ID 29888\_1.R1040 5'-most EST bth700845386.h1

Method BLASTX
NCBI GI 94262241
BLAST score 470
E value 1.0e-46
Match length 163
% identity 64

NCBI Description (AC006200) unknown protein [Arabidopsis thaliana]

Seq. No. 14053

Contig ID 29889\_1.R1040 5'-most EST awf700836974.h1

Seq. No. 14054

Contig ID 29892\_1.R1040

5'-most EST LIB3051-107-Q1-K1-H10

Seq. No. 14055

Contig ID 29901\_1.R1040 5'-most EST V4L-02-Q1-B1-D11

Method BLASTX
NCBI GI g3250675
BLAST score 1519
E value 1.0e-169
Match length 503
% identity 63

NCBI Description (AL024486) putative protein [Arabidopsis thaliana]

Seq. No. 14056

Contig ID 29901\_2.R1040 5'-most EST fC-gmst700661765d3

Seq. No. 14057

Contig ID 29901\_4.R1040 5'-most EST pxt700941325.h1

Seq. No. 14058

Contig ID 29903\_1.R1040 5'-most EST wvk700680036.h2

Method BLASTX
NCBI GI g2583126
BLAST score 150
E value 1.0e-17



Match length 102 % identity 68

NCBI Description (AC002387) putative DNA repair protein (RAD57) [Arabidopsis

thaliana]

Seq. No. 14059

Contig ID 29903 2.R1040

5'-most EST LIB3093-009-Q1-K1-C7

Method BLASTX
NCBI GI g2583126
BLAST score 229
E value 5.0e-19
Match length 108
% identity 51

NCBI Description (AC002387) putative DNA repair protein (RAD57) [Arabidopsis

thaliana]

Seq. No. 14060

Contig ID 29905\_1.R1040 5'-most EST zhf700962367.h1

Seq. No. 14061

Contig ID 29910\_1.R1040

5'-most EST LIB3109-019-Q1-K1-A3

Seq. No. 14062

Contig ID 29914\_1.R1040

5'-most EST LIB3106-056-Q1-K1-G2

Seq. No. 14063

Contig ID 29917\_1.R1040

5'-most EST LIB3051-108-Q1-K1-F10

Seq. No. 14064

Contig ID 29918\_1.R1040 5'-most EST kl1701204362.h2

Seq. No. 14065

Contig ID 29919\_1.R1040

5'-most EST LIB3051-108-Q1-K1-F5

Seq. No. 14066

Contig ID 29921\_1.R1040 5'-most EST fC-gmst700662670f1

Method BLASTX
NCBI GI g3805760
BLAST score 217
E value 2.0e-17
Match length 94
% identity 55

NCBI Description (AC005693) unknown protein [Arabidopsis thaliana]

Seq. No. 14067

Contig ID 29921\_2.R1040 5'-most EST gsv70\overline{1}052918.h1

Seq. No. 14068



```
29921 3.R1040
Contig ID
                  uaw700664809.hl
5'-most EST
                   14069
Seq. No.
                   29922 1.R1040
Contig ID
                  LIB3051-108-Q1-K1-G10
5'-most EST
                  BLASTX
Method
                   q3757522
NCBI GI
                   148
BLAST score
                   2.0e-09
E value
Match length
                   43
% identity
                   63
NCBI Description (AC005167) putative splicing factor [Arabidopsis thaliana]
                   14070
Seq. No.
                   29924 1.R1040
Contig ID
                   zhf700956251.h1
5'-most EST
                   BLASTX
Method
                   g4455293
NCBI GI
                   261
BLAST score
                   3.0e-22
E value
Match length
                   61
                   85
% identity
                   (AL035528) putative protein [Arabidopsis thaliana]
NCBI Description
                   14071
Seq. No.
                   29924 2.R1040
Contig ID
                   gsv70\overline{1}053640.h1
5'-most EST
                   BLASTX
Method
                   g4455293
NCBI GI
                   248
BLAST score
                   4.0e-34
E value
                   229
Match length
% identity
                   (AL035528) putative protein [Arabidopsis thaliana]
NCBI Description
                   14072
Seq. No.
                   29924 3.R1040
Contig ID
                   jC-gmst02400044h05a1
5'-most EST
                   BLASTX
Method
                   a4455293
NCBI GI
                   154
BLAST score
E value
                   5.0e-10
                   32
Match length
% identity
                   (AL035528) putative protein [Arabidopsis thaliana]
NCBI Description
                   14073
Seq. No.
                   29925 1.R1040
Contig ID
5'-most EST
                   jsh701067609.hl
                   14074
Seq. No.
                    29928 1.R1040
 Contig ID
                   LIB30\overline{5}1-108-Q1-K1-H2
 5'-most EST
```

2381

14075

29929 1.R1040

Seq. No.

Contig ID



```
LIB3170-061-Q1-J1-E10
5'-most EST
                  14076
Seq. No.
Contig ID
                  29930 1.R1040
                  LIB3051-108-Q1-K1-H6
5'-most EST
                  14077
Seq. No.
                  29933 1.R1040
Contig ID
                  LIB3170-061-Q1-K2-G10
5'-most EST
                  14078
Seq. No.
                  29938 1.R1040
Contig ID
                  smc700745368.hl
5'-most EST
                  BLASTX
Method
                  g2642158
NCBI GI
                  674
BLAST score
                  1.0e-70
E value
                  162
Match length
                  75
% identity
NCBI Description (AC003000) hypothetical protein [Arabidopsis thaliana]
                  14079
Seq. No.
                  29938 2.R1040
Contig ID
                  jsh701065776.hl
5'-most EST
                  BLASTX
Method
                  g2642158
NCBI GI
                   460
BLAST score
                  1.0e-45
E value
                  110
Match length
                   74
% identity
NCBI Description (AC003000) hypothetical protein [Arabidopsis thaliana]
                   14080
Seq. No.
Contig ID
                   29938 3.R1040
                   zhf700955287.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2642158
                   211
BLAST score
                   1.0e-16
E value
Match length
                   58
% identity
                   66
                  (AC003000) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   14081
Seq. No.
                   29944 1.R1040
Contig ID
5'-most EST
                   LIB3051-109-Q1-K1-C10
                   14082
Seq. No.
                   29947 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy028e04b1
                   14083
Seq. No.
                   29950 1.R1040
```

Contig ID 29950\_1.R1040 5'-most EST pst700645864.h1

Seq. No. 14084

Contig ID 29951\_1.R1040



```
uC-qmropic042d11b1
5'-most EST
                  BLASTX
Method
                  g3785991
NCBI GI
                  211
BLAST score
                  2.0e-35
E value
                  153
Match length
                  58
% identity
                  (AC005560) putative MAP kinase [Arabidopsis thaliana]
NCBI Description
                  14085
Seq. No.
                  29951 2.R1040
Contig ID
                   kl1701212281.hl
5'-most EST
                  BLASTX
Method
                   q4512667
NCBI GI
                   339
BLAST score
                   5.0e-32
E value
                   92
Match length
                   67
% identity
                  (AC006931) putative MAP kinase [Arabidopsis thaliana]
NCBI Description
                   14086
Seq. No.
                   29953 1.R1040
Contig ID
                   LIB3170-064-Q1-K1-G11
5'-most EST
Seq. No.
                   14087
                   29954 1.R1040
Contig ID
                   kl1701204392.h2
5'-most EST
                   14088
Seq. No.
                   29958 1.R1040
Contig ID
                   asn701134395.h1
5'-most EST
                   BLASTX
Method
                   q4185599
NCBI GI
BLAST score
                   159
                   1.0e-10
E value
Match length
                   145
% identity
                   (AB010708) Anthocyanin 5-aromatic acyltransferase [Gentiana
NCBI Description
                   triflora]
                   14089
Seq. No.
                   29960 1.R1040
Contig ID
                   LIB30\overline{5}1-109-Q1-K1-G5
5'-most EST
                   14090
Seq. No.
                   29963 1.R1040
Contig ID
                   LIB3170-064-Q1-K1-C12
5'-most EST
Method
                   BLASTX
                   q2464864
NCBI GI
                   172
BLAST score
                   4.0e-12
E value
                   75
Match length
                   30
 % identity
                   (Z99707) putative protein [Arabidopsis thaliana]
```

14091 Seq. No.

NCBI Description

29966 1.R1040 Contig ID



```
LIB3051-110-Q1-K1-A5
5'-most EST
Seq. No.
                  14092
                  29969 1.R1040
Contig ID
                  LIB3051-110-Q1-K1-B12
5'-most EST
                  14093
Seq. No.
                  29971 1.R1040
Contig ID
                  LIB3170-064-Q1-K1-E12
5'-most EST
                   14094
Seq. No.
                   29974 1.R1040
Contig ID
                   jC-gmf102220143a01a1
5'-most EST
                   BLASTX
Method
                   q4559380
NCBI GI
BLAST score
                   711
                   4.0e-75
E value
                   222
Match length
                   61
% identity
                  (AC006526) putative auxin-responsive GH3 protein
NCBI Description
                   [Arabidopsis thaliana]
                   14095
Seq. No.
                   29974 2.R1040
Contig ID
                   uxk70\overline{0}667953.h1
5'-most EST
Method
                   BLASTX
                   g4559380
NCBI GI
BLAST score
                   177
                   6.0e-13
E value
                   80
Match length
                   50
% identity
                  (AC006526) putative auxin-responsive GH3 protein
NCBI Description
                   [Arabidopsis thaliana]
                   14096
Seq. No.
                   29975 1.R1040
Contig ID
                   LIB3051-110-Q1-K1-D5
5'-most EST
                   14097
Seq. No.
                   29978 1.R1040
Contig ID
                   LIB3051-110-Q1-K1-D8
5'-most EST
                   BLASTX
Method
                   g4415911
NCBI GI
                   251
BLAST score
                   2.0e-21
E value
                   70
Match length
 % identity
NCBI Description (AC006282) putative polyA binding protein [Arabidopsis
                    thaliana]
 Seq. No.
                    14098
                    29979 1.R1040
 Contig ID
```

Contig ID 29979 1.R1040 5'-most EST rlr700899426.h1

Method BLASTX
NCBI GI g4263517
BLAST score 817
E value 3.0e-87



Match length % identity NCBI Description

297 57

(AC004044) similar to PHZF, catalyzing the hydroxylation of

phenazine-1-carboxylic acid to

2-hydroxy-phenazine-1-carboxylic acid [Arabidopsis

thaliana]

Seq. No.

14099

Contig ID 5'-most EST 29979\_3.R1040 6HC-02-Q1-B1-C9

Method NCBI GI BLAST score BLASTX g4263517 149

E value
Match length
% identity

9.0e-10 43 70

NCBI Description

(AC004044) similar to PHZF, catalyzing the hydroxylation of

phenazine-1-carboxylic acid to

2-hydroxy-phenazine-1-carboxylic acid [Arabidopsis

thaliana]

Seq. No.

14100

Contig ID

29980\_1.R1040

5'-most EST

LIB3051-110-Q1-K1-E4

Seq. No.

14101

Contig ID

29982\_1.R1040

5'-most EST

LIB3051-110-Q1-K1-E6

Seq. No.

14102

Contig ID

29987\_1.R1040

5'-most EST

LIB3106-070-P1-K1-C9

Seq. No.

14103

Contig ID

29998 1.R1040

5'-most EST

LIB3170-067-Q1-K1-A5

Seq. No.

14104

Contig ID 5'-most EST

30006\_1.R1040 awf700841929.h1

Method NCBI GI BLASTX q3643090

NCB1 G1 BLAST score g3643090 405

E value Match length

2.0e-39 174

% identity
NCBI Description

57 (AF075582) protein phosphatase-2C; PP2C [Mesembryanthemum

crystallinum]

Seq. No.

14105

Contig ID 5'-most EST

30007\_1.R1040 epx701105122.h1

Seq. No.

14106

Contig ID

30009 1.R1040

5'-most EST

LIB3051-111-Q1-K1-C5



Seq. No.	14107
Contig ID	30011_1.R1040
5'-most EST	LIB3051-111-Q1-K1-D12

Seq. No. 14108 Contig ID 30013\_1.R1040 5'-most EST LIB3092-049-Q1-K1-E4

Seq. No. 14109
Contig ID 30015\_1.R1040
5'-most EST LIB3170-066-Q1-K1-E1

 Seq. No.
 14110

 Contig ID
 30016\_1.R1040

 5'-most EST
 LIB3170-067-Q1-K1-G1

 Seq. No.
 14111

 Contig ID
 30017\_1.R1040

 5'-most EST
 hrw701061690.h1

 Seq. No.
 14112

 Contig ID
 30019\_1.R1040

 5'-most EST
 sat701002777.h2

 Seq. No.
 14113

 Contig ID
 30021\_1.R1040

 5'-most EST
 jC-gmf102220091f02d1

Seq. No. 14114 Contig ID 30022\_1.R1040 5'-most EST dpv701100006.h2

 Seq. No.
 14115

 Contig ID
 30027 1.R1040

 5'-most EST
 LIB3051-111-Q1-K1-G4

Seq. No. 14116
Contig ID 30028\_1.R1040
5'-most EST LIB3170-054-Q1-J1-C8

Seq. No. 14117 Contig ID 30030\_1.R1040 5'-most EST LIB3170-065-Q1-K1-C2

 Seq. No.
 14118

 Contig ID
 30032 1.R1040

 5'-most EST
 LIB3170-065-Q1-K1-D2

Seq. No. 14119
Contig ID 30033\_1.R1040
5'-most EST LIB3051-111-Q1-K1-H7

 Seq. No.
 14120

 Contig ID
 30036\_1.R1040

 5'-most EST
 trc700564735.h1

 Method
 BLASTX

 NCBI GI
 g3608155

2386



402 BLAST score 7.0e-39 E value Match length 89 % identity 81

NCBI Description (AC005314) putative RNA helicase [Arabidopsis thaliana]

14121 Seq. No.

30038 1.R1040 Contig ID  $jex70\overline{0}904842.h1$ 5'-most EST

Method BLASTX g1293563 NCBI GI 262 BLAST score 2.0e-22 E value 197 Match length % identity 36

NCBI Description (U49188) Diff33 gene product [Homo sapiens]

14122 Seq. No.

30039 1.R1040 Contig ID

LIB3051-112-Q1-K1-A8 5'-most EST

14123 Seq. No.

30040 1.R1040 Contig ID k11701208452.h1 5'-most EST

Seq. No. 14124

30041 1.R1040 Contig ID

 $jC-gm\overline{l}e01810055f07a1$ 5'-most EST

BLASTX Method g3850583 NCBI GI 465 BLAST score 2.0e-46 E value 222 Match length 54 % identity

(AC005278) Contains similarity to transcription initiation NCBI Description factor IIE, alpha subunit gb\_X63468 from Homo sapiens.

[Arabidopsis thaliana]

14125 Seq. No.

Contig ID 30045 1.R1040

LIB3051-112-Q1-K1-C1 5'-most EST

14126 Seq. No.

30051 1.R1040 Contig ID

5'-most EST  $LIB30\overline{5}1-112-Q1-K1-C8$ 

Seq. No.

14127 30057 1.R1040 Contig ID

LIB3170-065-Q1-K1-D3 5'-most EST

Seq. No. 14128

30057 2.R1040 Contig ID uaw700662430.hl 5'-most EST

Seq. No.

14129

30063 1.R1040 Contig ID

LIB3051-112-Q1-K1-G2 5'-most EST



Seq. No. 14130

Contig ID 30067\_1.R1040

5'-most EST LIB3051-112-Q1-K1-H1

Seq. No. 14131

Contig ID 30075\_1.R1040

5'-most EST LIB3051-113-Q1-K1-A4

Seq. No. 14132

Contig ID 30077\_1.R1040 5'-most EST awf700836725.h1

Method BLASTX
NCBI GI g4185599
BLAST score 144
E value 4.0e-13
Match length 201

Match length 201 % identity 32

NCBI Description (AB010708) Anthocyanin 5-aromatic acyltransferase [Gentiana

triflora]

Seq. No. 14133

Contig ID 30078\_1.R1040

5'-most EST LIB3170-066-Q1-K1-B3

Seq. No. 14134

Contig ID 30083 1.R1040 5'-most EST asn701138539.h1

Seq. No. 14135

Contig ID 30085 1.R1040

5'-most EST LIB3170-066-Q1-K1-F3

Seq. No. 14136

Contig ID 30086\_1.R1040

5'-most EST uC-gmrominsoy258g06b1

Seq. No. 14137

Contig ID 30086 2.R1040

5'-most EST LIB30 $\overline{5}$ 1-113-Q1-K1-C11

Seq. No. 14138

Contig ID 30087 1.R1040

5'-most EST LIB3170-066-Q1-K1-H3

Method BLASTX
NCBI GI g3880609
BLAST score 120
E value 3.0e-09
Match length 83
% identity 48

NCBI Description (Z82081) similar to Zinc-binding dehydrogenases; cDNA EST EMBL:D73225 comes from this gene; cDNA EST yk489c10.3 comes

from this gene; cDNA EST yk437g7.3 comes from this gene;

cDNA EST yk437g7.5 comes from this gene; cDNA EST yk

Seq. No. 14139

Contig ID 30089 1.R1040



5'-most EST LIB3051-113-Q1-K1-D11

Seq. No. 14140

Contig ID 30094 1.R1040

5'-most EST LIB3170-067-Q1-K1-A4

Seq. No. 14141

Contig ID 30097\_1.R1040

5'-most EST uC-gmronoir060e03b1

Method BLASTX
NCBI GI g1620970
BLAST score 1451
E value 1.0e-161
Match length 349
% identity 82

NCBI Description (Y08887) L-lactate dehydrogenase [Lycopersicon esculentum]

>gi\_1806117\_emb\_CAA71611\_ (Y10602) L-lactate dehydrogenase

[Lycopersicon esculentum]

Seq. No. 14142

Contig ID 30097 2.R1040

5'-most EST uC-gmronoir062a03b1

Method BLASTN
NCBI GI g167066
BLAST score 84
E value 4.0e-39
Match length 136
% identity 90

NCBI Description Hordeum vulgare L-lactate dehydrogenase mRNA, complete cds

Seq. No. 14143

Contig ID 30097\_4.R1040 5'-most EST fC-gmle700557013r2

Method BLASTX
NCBI GI g1620970
BLAST score 170
E value 4.0e-12
Match length 48
% identity 71

NCBI Description (Y08887) L-lactate dehydrogenase [Lycopersicon esculentum]

>gi 1806117 emb CAA71611 (Y10602) L-lactate dehydrogenase

[Lycopersicon esculentum]

Seq. No. 14144

Contig ID 30099\_1.R1040

5'-most EST LIB3051-113-Q1-K1-E9

Method BLASTX
NCBI GI g4580467
BLAST score 423
E value 2.0e-41
Match length 104
% identity 72

NCBI Description (AC006081) putative protein phosphatase; similar to protein

phosphatase 2C from Mesembryanthemum [Arabidopsis thaliana]

Seq. No. 14145

Contig ID 30100\_1.R1040

```
jC-gmst02400049e05a1
5'-most EST
                  BLASTX
Method
                  q2129473
NCBI GI
BLAST score
                  254
E value
                   2.0e-27
                  166
Match length
% identity
                   45
                  arabinogalactan-like protein - loblolly pine >gi_607774
NCBI Description
                   (U09556) arabinogalactan-like protein [Pinus taeda]
                   14146
Seq. No.
                   30100 2.R1040
Contig ID
                   jC-qmst02400056c04d1
5'-most EST
Seq. No.
                   14147
                   30101 1.R1040
Contig ID
                  LIB3109-013-Q1-K1-F3
5'-most EST
                   14148
Seq. No.
                   30103 1.R1040
Contig ID
5'-most EST
                   jC-qmf102220053b01a1
Method
                   BLASTX
                   g2262156
NCBI GI
BLAST score
                   267
                   4.0e-23
E value
Match length
                   165
% identity
                   37
                   (AC002329) hypothetical protein with weak similarity to S.
NCBI Description
                   cerevisiae hypothetical protein PID:g1066493 [Arabidopsis
                   thaliana]
                   14149
Seq. No.
                   30109 1.R1040
Contig ID
                   LIB3051-113-Q1-K1-G7
5'-most EST
                   BLASTN
Method
                   g531828
NCBI GI
BLAST score
                   35
                   6.0e-10
E value
                   120
Match length
% identity
                   81
NCBI Description Cloning vector pSport1, complete cds
                   14150
Seq. No.
                   30114 1.R1040
Contig ID
5'-most EST
                   bth700848135.hl
Method
                   BLASTX
                   q2346978
NCBI GI
BLAST score
                   441
E value
                   2.0e-43
                   179
Match length
% identity
NCBI Description
                   (AB006601) ZPT2-14 [Petunia x hybrida]
```

Seq. No. 14151

Contig ID 30115\_1.R1040

5'-most EST LIB3170-054-Q1-J1-A7

Method BLASTX



```
q3426037
NCBI GI
                  151
BLAST score
                                                                        ....
                  1.0e-09
E value
                  75
Match length
                  41
% identity
                   (AC005168) putative ABC transporter protein [Arabidopsis
NCBI Description
                  thaliana]
                  14152
Seq. No.
                  30116 1.R1040
Contig ID
                   sat701015035.h1
5'-most EST
                  BLASTX
Method
                  g2244785
NCBI GI
                   140
BLAST score
E value
                   8.0e-12
Match length
                   83
                   49
% identity
                  (Z97335) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   14153
Seq. No.
                   30119 1.R1040
Contig ID
                   LIB3051-114-Q1-K1-B3
5'-most EST
                   14154
Seq. No.
Contig ID
                   30120 1.R1040
                   gsv701049853.hl
5'-most EST
                   14155
Seq. No.
                   30121 1.R1040
Contig ID
5'-most EST
                   pcp700995455.hl
                   BLASTX
Method
NCBI GI
                   g2129753
                   299
BLAST score
E value
                   4.0e-27
                   100
Match length
                   67
% identity
                   threonine synthase (EC 4.2.99.2) precursor - Arabidopsis
NCBI Description
                   thaliana (fragment) >gi 1448917 (L41666) threonine synthase
                   [Arabidopsis thaliana]
Seq. No.
                   14156
                   30123 1.R1040
Contig ID
5'-most EST
                   uC-gmropic041e07b1
Method
                   BLASTX
NCBI GI
                   g1923256
BLAST score
                   724
E value
                   1.0e-76
Match length
                   196
% identity
                   (U86782) 26S proteasome-associated pad1 homolog [Homo
NCBI Description
                   sapiens]
                   14157
Seq. No.
                   30124 1.R1040
```

Contig ID

5'-most EST LIB3093-027-Q1-K1-B6

BLASTX Method NCBI GI g2262159

2391



BLAST score 7.0e-14 E value Match length 66 55 % identity

(AC002329) predicted protein similar to S.pombe protein NCBI Description

C5H10.03 [Arabidopsis thaliana]

14158 Seq. No.

30125 1.R1040 Contiq ID 5'-most EST pxt700943346.hl

Method BLASTX NCBI GI g2832625 BLAST score 434 9.0e-46 E value Match length 121 % identity 78

(AL021711) putative protein [Arabidopsis thaliana] NCBI Description

Seq. No.

14159

30127 1.R1040 Contig ID

5'-most EST LIB3170-066-Q1-K1-B5

14160

Seq. No.

30130 1.R1040 Contig ID

LIB3139-003-P1-N1-D9 5'-most EST

BLASTX Method NCBI GI q4432825 BLAST score 378 E value 5.0e-36 134 Match length

% identity 69

(AC006593) putative SOP2p protein [Arabidopsis thaliana] NCBI Description

14161 Seq. No.

30135 1.R1040 Contig ID

LIB3051-114-Q1-K1-G10 5'-most EST

14162 Seq. No.

30135 2.R1040 Contig ID dpv701099732.hl 5'-most EST

14163 Seq. No.

30137 1.R1040 Contig ID

LIB3051-114-Q1-K1-G6 5'-most EST

14164 Seq. No.

30142 1.R1040 Contig ID 5'-most EST g5509350

Seq. No. 14165

30145\_1.R1040 Contig ID  $zhf70\overline{0}956842.h1$ 5'-most EST

BLASTX Method g2499703 NCBI GI BLAST score 585 E value 4.0e-60 Match length 315



% identity PHOSPHOLIPASE D1 (PLD 1) (CHOLINE PHOSPHATASE 1) NCBI Description (PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D1) >gi 1185463 (U38545) phospholipase D1 [Homo sapiens] >gi\_4505873\_ref\_NP\_002653.1\_pPLD1\_ phospholipase D1,
phophatidylcholine-specific (NOTE: redefinition of symbol)

14166 Seq. No.

30145 2.R1040 Contig ID

5'-most EST LIB3170-068-Q1-K1-F6

14167 Seq. No.

30152 1.R1040 Contig ID zpv700762404.h1 5'-most EST

14168 Seq. No.

Contig ID 30158 1.R1040 5'-most EST pxt700942684.h1

BLASTX Method q2623297 NCBI GI 174 BLAST score 5.0e-12 E value 45 Match length

% identity

(AC002409) unknown protein [Arabidopsis thaliana] NCBI Description

>gi 3790583 (AF079180) RING-H2 finger protein RHC1a

[Arabidopsis thaliana]

14169 Seq. No.

Contig ID 30158 2.R1040

LIB3051-115-Q1-K1-D4 5'-most EST

Seq. No. 14170

30161 1.R1040 Contig ID

LIB3170-068-Q1-K1-G6 5'-most EST

Seq. No. 14171

30166 1.R1040 Contig ID

LIB3170-066-Q1-K1-B6 5'-most EST

Seq. No. 14172

30167 1.R1040 Contig ID fde700870847.h1 5'-most EST

14173 Seq. No.

30173 1.R1040 Contig ID ssr700560031.hl 5'-most EST

14174 Seq. No.

30175 1.R1040 Contig ID

5'-most EST LIB3051-115-Q1-K1-G6

Method BLASTX g2435518 NCBI GI 172 BLAST score 3.0e-12 E value Match length 46 % identity 59



```
NCBI Description (AF024504) contains similarity to C3HC4-type zinc fingers [Arabidopsis thaliana]

Seq. No. 14175
Contig ID 30177_1.R1040
5'-most EST eep700866093.h1
Method BLASTX
NCBI GI g3414809
```

NCBI GI g3414809 BLAST score 217 E value 6.0e-17 Match length 355 % identity 3

NCBI Description (AF061529) rjs [Mus musculus]

Seq. No. 14176

Contig ID 30177\_2.R1040

5'-most EST LIB3170-081-Q1-K1-C6

Seq. No. 14177

Contig ID 30178 1.R1040

5'-most EST LIB3051-115-Q1-K1-H5

Seq. No. 14178

Contig ID 30178\_2.R1040

5'-most EST LIB3109-001-Q1-K1-C8

Seq. No. 14179

Contig ID 30183\_1.R1040 5'-most EST fua701041016.h1

Seq. No. 14180

Contig ID 30183 2.R1040

5'-most EST LIB3087-009-Q1-K1-A2

Seq. No. 14181

Contig ID 30184 1.R1040

5'-most EST jC-gmst02400043h02a1

Method BLASTX
NCBI GI g3341691
BLAST score 284
E value 5.0e-25
Match length 127
% identity 48

NCBI Description (AC003672) putative heterogeneous nuclear ribonucleoprotein

Al [Arabidopsis thaliana]

Seq. No. 14182

Contig ID 30185\_1.R1040 5'-most EST uaw700667005.h1

Method BLASTX
NCBI GI g2462760
BLAST score 271
E value 2.0e-23
Match length 116
% identity 47

NCBI Description (AC002292) Hypothetical protein [Arabidopsis thaliana]



Contig ID 30191\_1.R1040

5'-most EST LIB3109-050-Q1-K1-H2

Seq. No. 14184

Contig ID 30192\_1.R1040

5'-most EST LIB3170-055-Q1-K1-H6

Seq. No. 14185

Contig ID 30195\_1.R1040 5'-most EST g5058424

5'-most EST g505842

Seq. No. 14186

Contig ID 30196\_1.R1040 5'-most EST dpv701102546.h1

Method BLASTX
NCBI GI g3779218
BLAST score 680
E value 2.0e-71
Match length 160
% identity 85

NCBI Description (AF030879) protein kinase CPK1 [Solanum tuberosum]

Seq. No. 14187

Contig ID 30197\_1.R1040 5'-most EST sat701003413.h1

Seq. No. 14188

Contig ID 30199 1.R1040

5'-most EST jC-gmle01810088f04a1

Seq. No. 14189

Contig ID 30200\_1.R1040 5'-most EST leu701145140.h1

Seq. No. 14190

Contig ID 30203\_1.R1040

5'-most EST LIB3051-116-Q1-K1-F6

Seq. No. 14191

Contig ID 30204\_1.R1040

5'-most EST LIB3170-068-Q1-K1-G7

Seq. No. 14192

Contig ID 30208 1.R1040

5'-most EST LIB3051-116-Q1-K1-G6

Seq. No. 14193

Contig ID 30209\_1.R1040

5'-most EST LIB3170-068-Q1-K1-H7

Seq. No. 14194

Contig ID 30215 1.R1040

5'-most EST LIB3051-117-Q1-K1-A1

Method BLASTX
NCBI GI g4206789
BLAST score 435



E value 1.0e-42
Match length 237
% identity 39

NCBI Description (AF112864) syntaxin-related protein At-SYR1 [Arabidopsis

thaliana]

Seq. No. 14195

Contig ID 30216\_1.R1040 5'-most EST hrw701058648.h1

Seq. No. 14196

Contig ID 30216\_2.R1040 5'-most EST g5753553

Seq. No. 14197

Contig ID 30218\_1.R1040 5'-most EST zhf700958818.h1

Seq. No. 14198

Contig ID 30222\_1.R1040

5'-most EST LIB3170-066-Q1-K1-H7

Seq. No. 14199

Contig ID 30230\_1.R1040

5'-most EST LIB3051-117-Q1-K1-C5

Seq. No. 14200

Contig ID 30232 1.R1040 5'-most EST kl1701211090.h1

Seq. No. 14201

Contig ID 30232\_2.R1040 5'-most EST asn701139522.h1

Seq. No. 14202

Contig ID 30234\_1.R1040

5'-most EST LIB3051-117-Q1-K1-D8

Method BLASTX
NCBI GI 94218122
BLAST score 144
E value 7.0e-09
Match length 74
% identity 50

NCBI Description (AL035353) putative protein [Arabidopsis thaliana]

Seq. No. 14203

Contig ID 30234\_2.R1040 5'-most EST uC-gmropic102e11b1

Seq. No. 14204

Contig ID 30235\_1.R1040

5'-most EST LIB3170-065-Q1-K1-G8

Method BLASTX
NCBI GI g3157929
BLAST score 240
E value 5.0e-20
Match length 146



Seq. No. 14205

Contig ID 30239 1.R1040

5'-most EST LIB3170-065-Q1-K1-H8

Method BLASTX
NCBI GI g4510376
BLAST score 296
E value 8.0e-27
Match length 90
% identity 61

NCBI Description (AC007017) unknown protein [Arabidopsis thaliana]

Seq. No. 14206

Contig ID 30242\_1.R1040 5'-most EST leu701150355.h1

Method BLASTX
NCBI GI g4140326
BLAST score 281
E value 5.0e-31
Match length 123
% identity 54

NCBI Description (AL031282) dJ283E3.6.1 (PUTATIVE novel protein similar to

many (archae) bacterial, worm and yeast hypothetical

proteins) [Homo sapiens]

Seq. No. 14207

Contig ID 30243\_1.R1040

Method BLASTX
NCBI GI g4539295
BLAST score 171
E value 5.0e-12
Match length 86
% identity 51

NCBI Description (AL049480) putative protein [Arabidopsis thaliana]

Seq. No. 14208

Contig ID 30250 1.R1040

5'-most EST jC-gmle01810064h03a1

Seq. No. 14209

Contig ID 30262 1.R1040 5'-most EST kl1701202731.h1

Method BLASTX
NCBI GI g3702323
BLAST score 217
E value 3.0e-17
Match length 64
% identity 67

NCBI Description (AC005397) unknown protein [Arabidopsis thaliana]

Seq. No. 14210

Contig ID 30262 2.R1040

5'-most EST LIB3052-017-Q1-N1-H2



Contig ID 30264\_1.R1040 5'-most EST zzp700831828.h1

Seq. No. 14212

Contig ID 30267\_1.R1040 5'-most EST q4397475

Seq. No. 14213

Contig ID 30274 1.R1040

5'-most EST LIB3052-017-Q1-N1-G10

Method BLASTN
NCBI GI g1046277
BLAST score 187
E value 1.0e-100
Match length 615
% identity 84

NCBI Description Phaseolus vulgaris embryo-specific acidic transcriptional

activator PvAlf mRNA, complete cds

Seq. No. 14214

Contig ID 30290 1.R1040

5'-most EST LIB3109-032-Q1-K1-A2

Method BLASTX
NCBI GI g2980798
BLAST score 585
E value 3.0e-60
Match length 207
% identity 55

NCBI Description (AL022197) putative protein [Arabidopsis thaliana]

Seq. No. 14215

Contig ID 30300 1.R1040 5'-most EST dpv701103364.h1

Seq. No. 14216

Contig ID 30305\_1.R1040

5'-most EST LIB3052-008-Q1-N1-F3

Method BLASTX
NCBI GI g3461815
BLAST score 270
E value 4.0e-23
Match length 310
% identity 25

NCBI Description (AC004138) hypothetical protein [Arabidopsis thaliana]

Seq. No. 14217

Contig ID 30307 1.R1040

5'-most EST LIB3052-017-Q1-N1-D10

Seq. No. 14218

Contig ID 30317\_1.R1040 5'-most EST awf700843444.h1

Method BLASTX
NCBI GI g4006895
BLAST score 560



1.0e-57 E value 157 Match length % identity 69

(Z99708) putative protein [Arabidopsis thaliana] NCBI Description

14219 Seq. No.

30319 1.R1040 Contig ID

uC-qmflminsoy089d01b1 5'-most EST

Method BLASTX g3337366 NCBI GI 394 BLAST score 4.0e-38 E value 188 Match length 48 % identity

(AC004481) unknown protein [Arabidopsis thaliana] NCBI Description

Seq. No. 14220

30319 2.R1040 Contig ID jsh701070263.hl 5'-most EST

Seq. No. 14221

30321 1.R1040 Contig ID

 $LIB30\overline{5}2-017-Q1-N1-B10$ 5'-most EST

BLASTX Method NCBI GI g3367537 BLAST score 185 1.0e-13 E value Match length 61 61

% identity

(AC004392) Contains similarity to ANK repeat region of NCBI Description

Fowlpox virus BamHI-orf7 protein homolog C18F10.7 gi\_485107 from Caenorhabditis elegans cosmid gb\_U00049. This gene is continued from unannotated gene on BAC F19K23 gb AC000375.

[Arabid

14222 Seq. No.

Contig ID 30379 1.R1040 uaw700662982.h1 5'-most EST

BLASTX Method NCBI GI q1808656 BLAST score 821 E value 1.0e-113 Match length 248 71 % identity

NCBI Description (Y10804) Ubiquitin activating enzyme E1 [Nicotiana tabacum]

14223 Seq. No.

30385 1.R1040 Contig ID 5'-most EST ncj700982209.hl

Seq. No. 14224

30404 1.R1040 Contig ID

5'-most EST LIB3052-016-Q1-N1-B2

14225 Seq. No.

30405 1.R1040 Contig ID

5'-most EST jC-gmro02910075e10a1



BLASTX Method NCBI GI q1313907 BLAST score 864 E value 5.0e-93 267 Match length % identity 67

NCBI Description (D84507) CDPK-related protein kinase [Zea mays]

Seq. No. 14226

Contig ID 30423 1.R1040 5'-most EST gsv701051467.h1

Seq. No. 14227

30438 1.R1040 Contig ID

5'-most EST LIB3052-015-Q1-N1-D2

Method BLASTX NCBI GI g2244760 BLAST score 666 E value 7.0e-70 210 Match length % identity 59

NCBI Description (Z97335) selenium-binding protein [Arabidopsis thaliana]

Seq. No. 14228

30438 2.R1040 Contig ID txt700736656.h1 5'-most EST

Method BLASTX NCBI GI g2244760 BLAST score 263 E value 3.0e-23 Match length 65

% identity 74

NCBI Description (Z97335) selenium-binding protein [Arabidopsis thaliana]

Seq. No. 14229

Contig ID 30441 1.R1040

5'-most EST LIB3055-002-Q1-B1-B7

Method BLASTX NCBI GI g1762428 BLAST score 304 E value 1.0e-27 Match length 114 % identity

NCBI Description (U59467) aromatic rich glycoprotein JP630 [Arabidopsis

thaliana]

Seq. No. 14230

Contig ID 30441 2.R1040 5'-most EST rlr700900194.h1

Method BLASTX NCBI GI g1762584 BLAST score 411 E value 2.0e-40 Match length 123 % identity

(U63373) polygalacturonase isoenzyme 1 beta subunit homolog NCBI Description

[Arabidopsis thaliana]

% identity

32



```
14231
Seq. No.
                  30444 1.R1040
Contig ID
                  vzy700751396.hl
5'-most EST
                  BLASTX
Method
                  g2281105
NCBI GI
                  325
BLAST score
                  7.0e-30
E value
                  185
Match length
                   45
% identity
                  (AC002333) unknown protein [Arabidopsis thaliana]
NCBI Description
                   14232
Seq. No.
                   30447 1.R1040
Contig ID
                   zhf700959118.h1
5'-most EST
                   BLASTX
Method
                   g3522938
NCBI GI
                   170
BLAST score
                                                  Š*
                   8.0e-12
E value
                   64
Match length
                   55
% identity
                  (AC004411) unknown protein [Arabidopsis thaliana]
NCBI Description
                   14233
Seq. No.
                   30451_1.R1040
Contig ID
                   fC-gmle7000739836d1
5'-most EST
                   BLASTN
Method
                   q495658
NCBI GI
                   202
BLAST score
                   1.0e-109
E value
                   393
Match length
                   88
% identity
                  Pisum sativum aspartate carbamoyltransferase (pyrB1) mRNA,
NCBI Description
                   complete cds
                   14234
Seq. No.
                   30455_1.R1040
Contig ID
                   k1170\overline{1}213560.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4510373
                   236
BLAST score
                   1.0e-32
E value
Match length
                   152
                   45
% identity
                   (AC007017) putative harpin-induced protein [Arabidopsis
NCBI Description
                   thaliana]
                   14235
Seq. No.
                   30463 1.R1040
Contig ID
                   seb700654120.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4406775
                   309
BLAST score
                   8.0e-28
E value
Match length
                   250
```

NCBI Description (AC006836) unknown protein [Arabidopsis thaliana]



```
14236
Seq. No.
                   30477 1.R1040
Contig ID
5'-most EST
                   g4306022
                   14237
Seq. No.
                   30495 1.R1040
Contig ID
                   LIB3052-014-Q1-N1-E9
5'-most EST
                   14238
Seq. No.
                   30496 1.R1040
Contig ID
                   LIB30\overline{5}2-014-Q1-N1-F1
5'-most EST
                   BLASTX
Method
                   g4249380
NCBI GI
BLAST score
                   213
E value
                   6.0e-17
Match length
                   115
% identity
                   43
                   (AC005966) ESTs gb_Z37637, gb_AA042498 and gb_AA042269 come
NCBI Description
                   from this gene. [Arabidopsis Thaliana]
Seq. No.
                   14239
                   30499 1.R1040
Contig ID
                   fC-gmro700849362d1
5'-most EST
                   BLASTN
Method
NCBI GI
                   g170023
BLAST score
                   44
                   2.0e-15
E value
Match length
                   59
                   97
% identity
NCBI Description Glycine max maturation-associated protein (MAT9) mRNA,
                   complete cds
                   14240
Seq. No.
                   30501 1.R1040
Contig ID
                   leu701154431.h1
5'-most EST
                   BLASTX
Method
                   g3220021
NCBI GI
                   411
BLAST score
                   1.0e-107
E value
                   299
Match length
% identity
                   64
                  (U57828) lipase homolog [Arabidopsis thaliana]
NCBI Description
                   14241
Seq. No.
                   30501 2.R1040
Contig ID
                   r1r70\overline{0}899638.h1
5'-most EST
                   BLASTX
Method
                   q3482914
NCBI GI
                    332
BLAST score
E value
                    5.0e-31
Match length
                    112
```

thaliana]

NCBI Description

% identity

Seq. No.

14242

58

(AC003970) Similar to nodulins and lipase [Arabidopsis



```
30533 1.R1040
Contig ID
                  LIB3052-014-Q1-N1-C8
5'-most EST
                   14243
Seq. No.
                   30534 1.R1040
Contig ID
                  LIB3109-047-Q1-K1-F11
5'-most EST
                   14244
Seq. No.
                   30534 2.R1040
Contig ID
                   LIB3106-113-Q1-K1-C7
5'-most EST
                   14245
Seq. No.
                   30534 3.R1040
Contig ID
                   hrw701061781.hl
5'-most EST
                   14246
Seq. No.
                   30535 1.R1040
Contig ID
                   zpv700760556.h1
5'-most EST
                   14247
Seq. No.
                   30536_1.R1040
Contig ID
                   uC-gm\overline{f}lminsoy029e06b1
5'-most EST
                   BLASTX
Method
                   g4006888
NCBI GI
                   628
BLAST score
                   1.0e-65
E value
                   178
Match length
                   66
% identity
                  (Z99708) putative protein [Arabidopsis thaliana]
NCBI Description
                   14248
Seq. No.
                   30544 1.R1040
Contig ID
                   k11701205474.h1
5'-most EST
                   BLASTX
Method
                   q2224901
NCBI GI
                    231
BLAST score
                   7.0e-19
E value
                    88
Match length
                    55
% identity
NCBI Description (U67134) PcMYB1 protein [Petroselinum crispum]
                    14249
Seq. No.
                    30551 1.R1040
Contig ID
                    LIB30\overline{5}2-013-Q1-N1-F5
 5'-most EST
                    14250
Seq. No.
                    30561 1.R1040
 Contig ID
                    fua701038140.hl
 5'-most EST
```

BLASTX Method q2760844 NCBI GI 1837 BLAST score 0.0e + 00E value 471 Match length 77 % identity

NCBI Description (AC003105) hypothetical protein [Arabidopsis thaliana]

14251 Seq. No.

E value

% identity

Match length

1.0e-40

120

71



```
Contig ID
                  30571 1.R1040
5'-most EST
                  LIB3052-013-Q1-N1-E11
                  14252
Seq. No.
Contig ID
                  30583_1.R1040
5'-most EST
                  jC-gmro02800038c01a1
                  14253
Seq. No.
                  30587 1.R1040
Contig ID
                  wvk700684511.hl
5'-most EST
Method
                  BLASTX
NCBI GI
                  q3063691
BLAST score
                  380
E value
                  3.0e-45
Match length
                  292
% identity
                  40
NCBI Description (AL022537) putative protein [Arabidopsis thaliana]
Seq. No.
                  14254
                  30587 3.R1040
Contig ID
5'-most EST
                  vwf700678973.hl
                  14255
Seq. No.
                  30587_4.R1040
Contig ID
5'-most EST
                  txt700735595.h1
                  14256
Seq. No.
                  30593 1.R1040
Contig ID
5'-most EST
                  jC-qmst02400066b03a2
Method
                  BLASTX
NCBI GI
                  g2832686
BLAST score
                  544
E value
                  2.0e-55
                  232
Match length
% identity
                  53
NCBI Description (AL021712) putative protein [Arabidopsis thaliana]
                  14257
Seq. No.
                  30596 1.R1040
Contig ID
5'-most EST
                  LIB3052-012-Q1-N1-H12
Method
                  BLASTX
NCBI GI
                  q2809246
BLAST score
                  515
E value
                  3.0e-52
Match length
                  206
% identity
                  47
NCBI Description (AC002560) F2401.15 [Arabidopsis thaliana]
                  14258
Seq. No.
                  30610 1.R1040
Contig ID
5'-most EST
                  LIB3052-012-Q1-N1-G7
Method
                  BLASTX
NCBI GI
                  q4490738
BLAST score
                  238
```



```
NCBI Description (AL035708) putative protein [Arabidopsis thaliana]

Seq. No. 14259
Contig ID 30610_2.R1040
5'-most EST g5677823
```

Contig ID 30618 1.R1040

5'-most EST LIB3052-012-Q1-N1-G1

Seq. No. 14261

Contig ID 30621 1.R1040

5'-most EST LIB3139-094-P1-N1-D11

Method BLASTX
NCBI GI g4097880
BLAST score 1909
E value 0.0e+00
Match length 368

% identity 99

NCBI Description (U70866) polyprotein [Bean pod mottle virus]

Seq. No. 14262

Contig ID 30622\_1.R1040

5'-most EST LIB3052-012-Q1-N1-G3

Seq. No. 14263

Contig ID 30627 1.R1040 5'-most EST asn701131676.h1

Method BLASTX
NCBI GI g4544428
BLAST score 476
E value 1.0e-47
Match length 138
% identity 68

NCBI Description (AC006955) unknown protein [Arabidopsis thaliana]

Seq. No. 14264

Contig ID 30637 1.R1040

5'-most EST LIB3052-012-Q1-N1-E7

Seq. No. 14265

Contig ID 30642\_1.R1040 5'-most EST awf700841903.h1

Method BLASTX
NCBI GI g2983690
BLAST score 187
E value 5.0e-14
Match length 128
% identity 38

NCBI Description (AE000730) hypothetical protein [Aquifex aeolicus]

Seq. No. 14266

Contig ID 30712\_1.R1040

5'-most EST LIB3109-057-Q1-K1-A3

Method BLASTN
NCBI GI g2924257
BLAST score 547

```
0.0e + 00
E value
                  1152
Match length
                  88
% identity
NCBI Description Tobacco chloroplast genome DNA
Seq. No.
                  14267
Contig ID
                 30713 1.R1040
5'-most EST
                zhf700958269.h1
Method
                 BLASTX
NCBI GI
                 g3116122
BLAST score
                 176
                 4.0e-12
E value
Match length
                  314
                  22
% identity
NCBI Description (AL023287) hypothetical protein [Schizosaccharomyces pombe]
Seq. No.
                  14268
                  30724 1.R1040
Contig ID
5'-most EST
                  g5606324
                  14269
Seq. No.
                  30730 1.R1040
Contig ID
5'-most EST
                  trc700568526.h1
Method
                  BLASTX
NCBI GI
                  q1805654
BLAST score
                  466
E value
                  2.0e-77
Match length
                  175
```

% identity 84 NCBI Description (X99972) calmodulin-stimulated calcium-ATPase [Brassica

oleracea]

14270 Seq. No.

30741 1.R1040 Contig ID

5'-most EST LIB3052-009-Q1-N1-E10

Seq. No. 14271

Contig ID 30749 1.R1040 uaw700663601.h1 5'-most EST

Seq. No. 14272

30765\_1.R1040 Contig ID

5'-most EST LIB3107-066-Q1-K1-D1

Method BLASTX NCBI GI g3721864 BLAST score 297 E value 1.0e-26 Match length 147 % identity 45

NCBI Description (AB016068) Hs Ste24p [Homo sapiens]

Seq. No. 14273

30765 2.R1040 Contig ID 5'-most EST kl1701207342.h1

Seq. No. 14274

Contig ID 30766 1.R1040



```
LIB3052-008-Q1-N1-E11
5'-most EST
Method
                  BLASTX
NCBI GI
                  q3292830
BLAST score
                  412
E value
                  6.0e-40
Match length
                  203
% identity
                  50
NCBI Description (AL031018) putative protein [Arabidopsis thaliana]
Seq. No.
                  14275
                  30771 1.R1040
Contig ID
5'-most EST
                  uC-gmronoir0001b07b1
                  BLASTX
Method
NCBI GI
                  g4455227
BLAST score
                  164
E value
                  3.0e-25
Match length
                  74
% identity
                  80
NCBI Description (AL035440) SNF8 like protein [Arabidopsis thaliana].
Seq. No.
                  14276
                  30771 2.R1040
Contig ID
5'-most EST
                  wrg700788220.h1
Seq. No.
                  14277
                  30772 1.R1040
Contig ID
5'-most EST
                  LIB3052-008-Q1-N1-G10
Method
                  BLASTX
NCBI GI
                  q3121844
BLAST score
                  216
E value
                  2.0e-17
Match length
% identity
                  68
                  PHOSPHATIDATE CYTIDYLYLTRANSFERASE (CDP-DIGLYCERIDE
NCBI Description
                  SYNTHETASE) (CDP-DIGLYCERIDE PYROPHOSPHORYLASE)
                   (CDP-DIACYLGLYCEROL SYNTHASE) (CDS) (CTP:PHOSPHATIDATE
                  CYTIDYLYLTRANSFERASE) (CDP-DAG SYNTHASE)
                  >gi 1652668 dbj BAA17588 (D90907) phosphatidate
                  cytidylyltransferase [Synechocystis sp.]
Seq. No.
                  14278
Contig ID
                  30774 1.R1040
5'-most EST
                  jC-qmle01810068b01a1
                  BLASTX
Method
NCBI GI
                  g3319357
BLAST score
                  931
                  1.0e-101
E value
Match length
                  262
```

72 % identity NCBI Description (AF077407) contains similarity to phosphoenolpyruvate

synthase (ppsA) (GB:AE001056) [Arabidopsis thaliana]

Seq. No. 14279 Contig ID

30776 1.R1040 leu701156150.h1 5'-most EST

Method BLASTN g1498327 NCBI GI



```
BLAST score 360
E value 0.0e+00
Match length 425
% identity 98
NCBI Description Glycine
Seq. No. 14280
Contig ID 30776_2
```

NCBI Description Glycine max actin (Soy70) gene, partial cds

Contig ID 30776\_2.R1040 5'-most EST uC-gmropic034a06b1

Method BLASTN
NCBI GI g1498337
BLAST score 179
E value 4.0e-96
Match length 215
% identity 96

NCBI Description Glycine max actin (Soy119) gene, partial cds

 Seq. No.
 14281

 Contig ID
 30779\_1.R1040

 5'-most EST
 gsv701052659.h1

 Method
 BLASTX

 NCBI GI
 g3582334

BLAST score 352
E value 3.0e-33
Match length 101
% identity 63

NCBI Description (AC005496) hypothetical protein [Arabidopsis thaliana]

Seq. No. 14282

Contig ID 30793\_1.R1040 5'-most EST awf700838767.h1

Method BLASTN
NCBI GI g2347089
BLAST score 104
E value 4.0e-51
Match length 224
% identity 87

NCBI Description Phaseolus vulgaris low molecular weight heat shock protein

PvHSP17-19 (Pvhsp17-19) mRNA, partial cds

Seq. No. 14283

Contig ID 30797\_1.R1040 5'-most EST gsv701055796.h1

Seq. No. 14284

Contig ID 30816 1.R1040 5'-most EST jsh701070147.h1

Method BLASTX
NCBI GI g2499945
BLAST score 1721
E value 0.0e+00
Match length 474
% identity 72

NCBI Description URIDINE 5'-MONOPHOSPHATE SYNTHASE (UMP SYNTHASE) (OROTATE

PHOSPHORIBOSYLTRANSFERASE AND OROTIDINE 5'-PHOSPHATE

DECARBOXYLASE >gi\_1076363\_pir\_\_S46440 orotate
phosphoribosyltransferase (EC 2.4.2.10) /



orotidine-5'-phosphate decarboxylase (EC 4.1.1.23) - Arabidopsis thaliana >gi\_443818\_emb\_CAA50686\_ (X71842) pyrE-F [Arabidopsis thaliana]

Seq. No. 14285

Contig ID 30829 1.R1040

5'-most EST LIB3052-007-Q1-B1-F10

Seq. No. 14286

Contig ID 30849 1.R1040

5'-most EST LIB3106-014-Q1-K1-H11

Seq. No. 14287

Contig ID 30853\_1.R1040 5'-most EST gsv701056241.h1

Method BLASTX
NCBI GI g3757520
BLAST score 238
E value 6.0e-20
Match length 93
% identity 59

NCBI Description (AC005167) unknown protein [Arabidopsis thaliana]

Seq. No. 14288

Contig ID 30860 1.R1040

5'-most EST LIB3139-015-P1-N1-A4

Method BLASTX
NCBI GI 94314388
BLAST score 587
E value 4.0e-64
Match length 169
% identity 73

NCBI Description (AC006232) hypothetical protein [Arabidopsis thaliana]

Seq. No. 14289

Contig ID 30864\_1.R1040 5'-most EST kl1701204412.h2

Seq. No. 14290

Contig ID 30884 1.R1040 5'-most EST ncj700982689.h1

Seq. No. 14291

Contig ID 30896\_1.R1040 5'-most EST jsh701065477.h1

Method BLASTX
NCBI GI 94427003
BLAST score 624
E value 7.0e-65
Match length 198
% identity 61

NCBI Description (AF127664) NBD-like protein [Arabidopsis thaliana]

Seq. No. 14292

Contig ID 30896 2.R1040 5'-most EST kll701208182.h1



```
Seq. No.
                  14293
                  30899 1.R1040
Contig ID
5'-most EST
                  hrw701059473.hl
Method
                  BLASTX
NCBI GI
                  g1524370
BLAST score
                  673
E value
                  2.0e-70
                  195
Match length
                  68
% identity
NCBI Description (X92491) TOM20 [Solanum tuberosum]
Seq. No.
                  14294
                  30899 2.R1040
Contig ID
5'-most EST
                  jC-gmf102220092d07d1
Method
                  BLASTN
NCBI GI
                  g1524369
BLAST score
                  52
                  3.0e-20
E value
Match length
                  84
                  90
% identity
NCBI Description S.tuberosum mRNA for TOM20 protein
                  14295
Seq. No.
Contig ID
                  30901 1.R1040
5'-most EST
                  LIB3138-130-Q1-N1-D8
Seq. No.
                  14296
Contig ID
                  30911 1.R1040
5'-most EST
                  rca701000063.h1
                  14297
Seq. No.
                  30911 3.R1040
Contig ID
5'-most EST
                  zzp700834337.h1
Method
                  BLASTX
                  g1176658
NCBI GI
BLAST score
                  198
E value
                  4.0e-15
Match length
                  69
                  55
% identity
NCBI Description
                  HYPOTHETICAL 200.6 KD PROTEIN B0228.2 IN CHROMOSOME II
                  >gi 726363 (U23168) No definition line found
                  [Caenorhabditis elegans]
Seq. No.
                  14298
Contig ID
                  30925 1.R1040
5'-most EST
                  jC-qmle01810073c03a1
Method
                  BLASTX
NCBI GI
                  g4139041
BLAST score
                  171
E value
                  2.0e-11
Match length
                  327
% identity
                  11
```

NCBI Description (AF072274) resistance protein candidate RGC20 [Lactuca

sativa]

14299 Seq. No.

Contig ID 30925 3.R1040



```
LIB3170-047-Q1-J1-B5
5'-most EST
                  14300
Seq. No.
                  30925 4.R1040
Contig ID
5'-most EST
                  sat701004637.h1
Seq. No.
                  14301
                  30932 1.R1040
Contig ID
                  kl1701204681.hl
5'-most EST
Seq. No.
                  14302
Contig ID
                  30938 1.R1040
5'-most EST
                  fua701037725.hl
                  14303
Seq. No.
Contig ID
                  30943 1.R1040
5'-most EST
                  LIB3052-002-Q1-B1-E8
Method
                  BLASTN
                  g2108285
NCBI GI
BLAST score
                  60
                  9.0e-25
E value
Match length
                  213
                  88
% identity
NCBI Description Cicer arietinum L. partial leg gene and promoter sequence
Seq. No.
                  14304
                  30956_1.R1040
Contig ID
5'-most EST
                  qsv701045885.h1
Method
                  BLASTX
NCBI GI
                  g2842494
                  547
BLAST score
                  4.0e-56
E value
Match length
                  125
                  84
% identity
NCBI Description (AL021749) prohibitin-like protein [Arabidopsis thaliana]
                  >gi 4097688 (U66591) prohibitin 1 [Arabidopsis thaliana]
                  >gi 4097694 (U66594) prohibitin 1 [Arabidopsis thaliana]
Seq. No.
                  14305
Contig ID
                  30995 1.R1040
5'-most EST
                  LIB3106-115-Q1-K1-B7
Seq. No.
                  14306
                  30997 1.R1040
Contig ID
5'-most EST
                  hyd700727807.h1
                  14307
Seq. No.
Contig ID
                  31010 1.R1040
```

5'-most EST LIB3052-001-Q1-B1-E8

Method BLASTX NCBI GI g1113941 BLAST score 458 E value 4.0e-51 Match length 140

% identity

NCBI Description (U40713) Pv42p [Phaseolus vulgaris]



31010 2.R1040 Contig ID uaw700666002.h1 5'-most EST

Method BLASTN NCBI GI g1113940 BLAST score 166 2.0e-88 E value 242 Match length % identity

NCBI Description Phaseolus vulgaris Pv42p mRNA, complete cds

Seq. No.

14309

Contig ID

31014 1.R1040

5'-most EST

uC-gmrominsoy045e03b1

Seq. No.

14310

Contig ID

31018 1.R1040

5'-most EST

LIB3106-108-Q1-K1-H10

Method BLASTX NCBI GI q4206206 BLAST score 479 8.0e-48 E value Match length 183 % identity 54

NCBI Description (AF071527) putative M-type thioredoxin [Arabidopsis

thaliana] >gi\_4263039 gb\_AAD15308 (AC005142) putative

M-type thioredoxin [Arabidopsis thaliana]

Seq. No. 14311

31023 1.R1040 Contig ID

5'-most EST LIB3052-001-Q1-B1-C12

Seq. No. 14312

31027 1.R1040 Contig ID 5'-most EST sat701006176.hl

Seq. No. 14313

31028 1.R1040 Contig ID 5'-most EST ncj700984810.hl

Seq. No.

14314

Contig ID

31035 1.R1040

5'-most EST

LIB3052-001-Q1-B1-A12

Method BLASTX NCBI GI q2352492 BLAST score 546 E value 5.0e-56 Match length 138 % identity 72

NCBI Description

(AF005047) transport inhibitor response 1 [Arabidopsis

thaliana] >gi\_2352494 (AF005048) transport inhibitor

response 1 [Arabidopsis thaliana]

Seq. No. 14315

Contig ID 31042 1.R1040 kmv700741672.h1 5'-most EST

Method BLASTX



```
g4567263
NCBI GI
BLAST score
                  250
                  2.0e-21
E value
Match length
                  58
                  83
% identity
NCBI Description
                  (AC006841) putative cell division inhibitor [Arabidopsis
                  thaliana]
Seq. No.
                  14316
                  31042 2.R1040
Contig ID
                  LIB3052-001-Q1-B1-B1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g4567263
BLAST score
                  191
E value
                  2.0e-14
Match length
                  46
% identity
NCBI Description
                 (AC006841) putative cell division inhibitor [Arabidopsis
                  thalianal
Seq. No.
                  14317
Contig ID
                  31063 1.R1040
                  LIB3052-003-Q1-N1-B10
5'-most EST
                  BLASTX
Method
NCBI GI
                  g2842490
BLAST score
                  204
                  1.0e-15
E value
Match length
                  58
% identity
                  64
NCBI Description (AL021749) heat-shock protein [Arabidopsis thaliana]
Seq. No.
                  14318
Contig ID
                  31064 1.R1040
5'-most EST
                  LIB3093-037-Q1-K1-D7
                  14319
Seq. No.
                  31083 1.R1040
Contig ID
5'-most EST
                  kl1701206444.h1
Method
                  BLASTX
NCBI GI
                  g3548815
BLAST score
                  238
E value
                  1.0e-19
Match length
                  128
% identity
                  45
                  (AC005313) similar to axoneme-associated protein mst101
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  14320
Contig ID
                  31098_1.R1040
                  LIB3074-037-Q1-K1-H12
5'-most EST
Method
                  BLASTN
NCBI GI
                  q2264310
BLAST score
                  35
E value
                  6.0e-10
Match length
                  87
% identity
                  85
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:
```

NCBI GI

E value

BLAST score



## MKP11, complete sequence [Arabidopsis thaliana]

```
14321
Seq. No.
Contig ID
                   31099 1.R1040
5'-most EST
                  LIB3106-065-P1-K1-F1
                  14322
Seq. No.
Contig ID
                  31137 1.R1040
                  LIB3053-014-Q1-N1-G12
5'-most EST
Method
                  BLASTX
                  g2952433
NCBI GI
BLAST score
                  514
                  5.0e-52
E value
                  168
Match length
                   60
% identity
NCBI Description (AF051135) putative ubiquitin activating enzyme E1
                   [Arabidopsis thaliana]
Seq. No.
                  14323
Contig ID
                  31139 1.R1040
5'-most EST
                  LIB3138-060-Q1-N1-H6
Method
                  BLASTX
NCBI GI
                  g1907076
BLAST score
                  333
E value
                   4.0e-31
Match length
                  98
% identity
                   65
NCBI Description
                  (Y07867) pirin [Homo sapiens] >gi_1907078_emb_CAA69195_
                   (Y07868) pirin [Homo sapiens]
                  >gi_4505823_ref_NP_003653.1_pPIR_ pirin
Seq. No.
                   14324
Contig ID
                   31139 2.R1040
5'-most EST
                  wvk700683220.h1
                  14325
Seq. No.
                  31150 1.R1040
Contig ID
5'-most EST
                  wvk700680072.h2
Method
                  BLASTX
                   q4033838
NCBI GI
BLAST score
                   212
E value
                   6.0e-17
Match length
                  103
% identity
                  56
NCBI Description (Y18550) sigma-like factor [Arabidopsis thaliana]
                  14326
Seq. No.
Contig ID
                  31153 1.R1040
5'-most EST
                  LIB3053-014-Q1-N1-E3
                  14327
Seq. No.
                  31157 1.R1040
Contig ID
5'-most EST
                  pcp700991075.hl
Method
                  BLASTX
```

g3894197

2.0e-73



```
Match length 193
% identity 70
NCBI Description (AC
```

NCBI Description (AC005662) hypothetical protein [Arabidopsis thaliana]

Seq. No. 14328 Contig ID 31159

Contig ID 31159\_1.R1040 5'-most EST seb700651839.h1

Method BLASTX
NCBI GI g4454051
BLAST score 446
E value 4.0e-44
Match length 136
% identity 66

NCBI Description (AL035394) putative polygalacturonase [Arabidopsis

thaliana]

Seq. No. 14329

Contig ID 31165\_1.R1040

5'-most EST LIB3055-004-Q1-N1-F2

Seq. No. 14330

Contig ID 31169 1.R1040

5'-most EST LIB3053-014-Q1-N1-C8

Method BLASTX
NCBI GI g1931641
BLAST score 305
E value 8.0e-28
Match length 147
% identity 48

NCBI Description (U95973) unknown protein [Arabidopsis thaliana]

Seq. No. 14331

Contig ID 31174\_1.R1040 5'-most EST dpv701103238.h1

Seq. No. 14332

Contig ID 31178\_1.R1040 5'-most EST pmv700889280.h1

Seq. No. 14333

Contig ID 31183\_1.R1040 5'-most EST crh700854773.h1

Method BLASTX
NCBI GI g3786008
BLAST score 183
E value 1.0e-13
Match length 117
% identity 36

NCBI Description (AC005499) unknown protein [Arabidopsis thaliana]

Seq. No. 14334

Contig ID 31185\_1.R1040 5'-most EST leu701157302.h1

Method BLASTX NCBI GI g1922242 BLAST score 217 E value 4.0e-17



Match length 68 % identity 63

NCBI Description (Y10084) hypothetical protein [Arabidopsis tHaliana]

Seq. No. 14335

Contig ID 31185 2.R1040 5'-most EST leu701149979.h1

Seq. No.

Contig ID 31186\_1.R1040 5'-most EST epx701107341.h1

14336

14337

Seq. No.

Contig ID 31190\_1.R1040 5'-most EST fua701041942.h1 Method BLASTX

NCBI GI g2827661 BLAST score 528 E value 1.0e-53 Match length 154 % identity 69

NCBI Description (AL021637) hyuC-like protein [Arabidopsis thaliana]

Seq. No. 14338

Contig ID 31199 1.R1040

5'-most EST LIB3053-013-Q1-N1-H3

Seq. No. 14339

Contig ID 31202\_1.R1040 5'-most EST smc700747812.h1

Method BLASTX
NCBI GI g3033375
BLAST score 496
E value 9.0e-50
Match length 210
% identity 45

NCBI Description (AC004238) putative berberine bridge enzyme [Arabidopsis

thaliana]

Seq. No. 14340

Contig ID 31203\_1.R1040 5'-most EST uC-gmronoir033a01b1

Method BLASTX
NCBI GI 94490317
BLAST score 307
E value 2.0e-53
Match length 269
% identity 45

NCBI Description (AL035678) putative protein [Arabidopsis thaliana]

Seq. No. 14341

Contig ID 31206 1.R1040

5'-most EST LIB3053-013-Q1-N1-E3

Seq. No. 14342

Contig ID 31208\_1.R1040

5'-most EST LIB3106-046-Q1-K1-B2



```
14343
Seq. No.
                  31232 1.R1040
Contig ID
                  LIB3107-016-Q1-K1-F3
5'-most EST
                  14344
Seq. No.
                  31249 1.R1040
Contig ID
5'-most EST
                  zzp700832740.h1
                  14345
Seq. No.
                   31259 1.R1040
Contig ID
                  LIB3053-012-Q1-N1-H8
5'-most EST
                   14346
Seq. No.
                   31260 1.R1040
Contig ID
                   g4304305
5'-most EST
                   BLASTX
Method
                   g4263818
NCBI GI
                   556
BLAST score
                   9.0e-57
E value
                   183
Match length
                   57
% identity
                  (AC006067) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   14347
                   31260 2.R1040
Contig ID
                   epx70\overline{1}107171.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4263818
                   375
BLAST score
E value
                   7.0e-36
                   124
Match length
                   57
% identity
                   (AC006067) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   14348
                   31260 3.R1040
Contig ID
                   LIB3139-033-P1-N1-E3
5'-most EST
Method
                   BLASTX
                   g4263818
NCBI GI
BLAST score
                   192
                   2.0e-14
E value
Match length
                   72
                   46
% identity
                   (AC006067) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   14349
                   31266 1.R1040
Contig ID
                   LIB3074-031-Q1-K1-C5
5'-most EST
                   14350
Seq. No.
```

Contig ID 31267 1.R1040

5'-most EST LIB3053-012-Q1-N1-B12

Seq. No. 14351

Contig ID 31268\_1.R1040

5'-most EST LIB3139-004-P1-N1-G1



Method BLASTX
NCBI GI g2828293
BLAST score 366
E value 9.0e-35
Match length 172
% identity 68

NCBI Description (AL021687) putative protein [Arabidopsis thaliana]

Seq. No. 14352

Contig ID 31269 1.R1040

5'-most EST LIB3053-012-Q1-N1-B5

Seq. No. 14353

Contig ID 31272\_1.R1040
5'-most EST g5508961
Method BLASTX
NCBI GI g2190012
BLAST score 450
E value 2.0e-44
Match length 145

Match length 145 % identity 61

NCBI Description (AB004242) din1 [Raphanus sativus]

Seq. No. 14354

Contig ID 31272\_2.R1040 5'-most EST wvk700684777.h1

Method BLASTX
NCBI GI g2129729
BLAST score 180
E value 3.0e-13
Match length 49
% identity 71

NCBI Description senescence-associated protein sen1 - Arabidopsis thaliana

>gi\_1046270 (U26945) senescence-associated protein

[Arabidopsis thaliana] >gi\_3367595\_emb\_CAA20047\_ (AL031135) senescence-associated protein sen1 [Arabidopsis thaliana] >gi\_3805843\_emb\_CAA21463\_ (AL031986) senescence-associated

protein sen1 [Arabidopsis thaliana]

Seq. No. 14355

Contig ID 31272 3.R1040

5'-most EST LIB3093-045-Q1-K1-B11

Seq. No. 14356

Contig ID 31273\_1.R1040

5'-most EST LIB3170-024-Q1-J1-F11

Method BLASTX
NCBI GI g1150932
BLAST score 374
E value 1.0e-35
Match length 107
% identity 71

NCBI Description (X88864) cyclin [Medicago sativa]

Seq. No. 14357

Contig ID 31273 2.R1040 5'-most EST wvk700680291.h2

E value

Match length

% identity

114



```
14358
Seq. No.
                  31279 1.R1040
Contig ID
                  LIB3053-012-Q1-N1-A8
5'-most EST
                  BLASTX
Method
                  g4322346
NCBI GI
                  302
BLAST score
                  2.0e-27
E value
                  132
Match length
                  43
% identity
                  (AF081825) sodium-dependent high-affinity dicarboxylate
NCBI Description
                  transporter [Rattus norvegicus]
                  14359
Seq. No.
                  31281 1.R1040
Contig ID
                  LIB3109-034-Q1-K1-F3
5'-most EST
                  BLASTX
Method
                  g3242785
NCBI GI
BLAST score
                  768
                  1.0e-151
E value
                   344
Match length
                  74
% identity
                  (AF055355) respiratory burst oxidase protein C [Arabidopsis
NCBI Description
                   thaliana]
                   14360
Seq. No.
                   31281 2.R1040
Contig ID
                   uC-gmropic056d11b1
5'-most EST
                   BLASTX
Method
                   g3242785
NCBI GI
                   921
BLAST score
                   2.0e-99
E value
                   243
Match length
                   72
% identity
                   (AF055355) respiratory burst oxidase protein C [Arabidopsis
NCBI Description
                   thaliana]
                   14361
Seq. No.
                   31282 1.R1040
Contig ID
5'-most EST
                   zsq701126519.hl
                   BLASTX
Method
                   g4104931
NCBI GI
BLAST score
                   664
                   2.0e-69
E value
Match length
                   261
                   56
% identity
                  (AF042196) auxin response factor 8 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   14362
                   31282 2.R1040
Contig ID
                   bth700849333.h1
5'-most EST
                   BLASTX
Method
                   g4104931
NCBI GI
                   219
BLAST score
                   1.0e-17
```



Contig ID 31283\_1.R1040 5'-most EST sat701004681.h1

Method BLASTX
NCBI GI g3668086
BLAST score 917
E value 6.0e-99
Match length 260
% identity 71

NCBI Description (AC004667) unknown protein [Arabidopsis thaliana]

NCBI Description (AF042196) auxin response factor 8 [Arabidopsis thaliana]

Seq. No. 14364

Contig ID 31298 1.R1040 5'-most EST kll701212377.h1

Seq. No. 14365

Contig ID 31308\_1.R1040

5'-most EST LIB3053-011-Q1-N1-D12

Seq. No. 14366

Contig ID 31316\_1.R1040 5'-most EST wrg700788760.h2

Seq. No. 14367

Contig ID 31318\_1.R1040 5'-most EST smc700744220.h1

Seq. No. 14368

Contig ID 31330\_1.R1040

5'-most EST LIB3053-011-Q1-N1-C10

Method BLASTX
NCBI GI g1354849
BLAST score 538
E value 4.0e-55
Match length 157
% identity 61

NCBI Description (U57350) epoxide hydrolase [Nicotiana tabacum]

Seq. No. 14369

Contig ID 31342\_1.R1040

5'-most EST LIB3138-019-Q1-N1-H3

Method BLASTX
NCBI GI g4512018
BLAST score 921
E value 1.0e-99
Match length 209
% identity 82

NCBI Description (AF106660) mRNA binding protein precursor [Lycopersicon

esculentum]

Seq. No. 14370

Contig ID 31343 1.R1040 5'-most EST g5677490

Seq. No. 14371



```
31343 2.R1040
Contig ID
                  leu701155240.h1
5'-most EST
                   14372
Seq. No.
                   31348 1.R1040
Contig ID
                  k1170\overline{1}206961.h1
5'-most EST
                  BLASTX
Method
                   g3559807
NCBI GI
                   420
BLAST score
                   4.0e-41
E value
                   148
Match length
                   64
% identity
                  (Y15628) HCF136 protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   14373
                   31352 1.R1040
Contig ID
                   LIB3053-010-Q1-N1-F6
5'-most EST
                   BLASTX
Method
                   g3063696
NCBI GI
                   202
BLAST score
                   2.0e-20
E value
                   116
Match length
                   50
% identity
                   (AL022537) putative protein [Arabidopsis thaliana]
NCBI Description
                   14374
Seq. No.
                   31353 1.R1040
Contig ID
                   LIB3053-010-Q1-N1-F9
5'-most EST
                   14375
Seq. No.
                   31357 1.R1040
Contig ID
                   pcp700995376.hl
5'-most EST
                   BLASTX
Method
                   q3063451
NCBI GI
                   427
BLAST score
                   8.0e-42
E value
                   114
Match length
% identity
                   (AC003981) F22013.13 [Arabidopsis thaliana]
NCBI Description
                   14376
Seq. No.
                   31357 2.R1040
Contig ID
                   LIB3053-010-Q1-N1-C7
5'-most EST
                   14377
Seq. No.
                   31358 1.R1040
Contig ID
 5'-most EST
                   uC-qmflminsoy054e05b1
                    14378
 Seq. No.
                    31359 1.R1040
 Contig ID
                   wrq700787215.h2
 5'-most EST
                   BLASTX
 Method
                    q4455349
 NCBI GI
```

2421

577

275

49

4.0e-59

BLAST score

Match length

% identity

E value

5'-most EST

BLAST score

Method

NCBI GI

g4284726

BLASTX

317

g731675



```
Seq. No.
                  14379
                  31359 2.R1040
Contig ID
5'-most EST
                  LIB3107-002-Q1-K1-G2
                  BLASTX
Method
NCBI GI
                  g4455349
BLAST score
                  158
                  1.0e-10
E value
                  74
Match length
                  46
% identity
NCBI Description (AL035524) putative protein [Arabidopsis thaliana]
                  14380
Seq. No.
                  31366 1.R1040
Contig ID
5'-most EST
                  LIB3138-031-Q1-N1-B1
Method
                  BLASTX
NCBI GI
                  q1514643
BLAST score
                  610
                  3.0e-63
E value
Match length
                  194
% identity
                  29
NCBI Description (Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza]
Seq. No.
                  14381
Contig ID
                  31378 1.R1040
5'-most EST
                  rlr700898137.h1
Seq. No.
                  14382
Contig ID
                  31380 1.R1040
5'-most EST
                  eep700866819.h1
Method
                  BLASTX
NCBI GI
                  g4262237
                  377
BLAST score
                  5.0e-36
E value
Match length
                  142
% identity
NCBI Description (AC006200) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  14383
Contig ID
                  31383 1.R1040
5'-most EST
                  LIB3053-009-Q1-N1-H10
Method
                  BLASTX
NCBI GI
                  q2956690
BLAST score
                  160
                  1.0e-10
E value
                  56
Match length
                  34
% identity
NCBI Description (AJ223306) PSBY [Arabidopsis thaliana] >gi_3414928
                  (AF079800) PsbY precursor [Arabidopsis thaliana]
Seg. No.
                  14384
Contig ID
                  31384 1.R1040
```

NCBI Description (AL035524) putative protein [Arabidopsis thaliana]



E value 5.0e-29 Match length 87 % identity 64

NCBI Description HYPOTHETICAL 80.7 KD PROTEIN IN ERG7-NMD2 INTERGENIC REGION

>gi\_626631\_pir\_\_S46811 hypothetical protein YHR074w - yeast
(Saccharomyces cerevisiae) >gi 500832 (U10556) Yhr074wp

[Saccharomyces cerevisiae]

Seq. No. 14385

Contig ID 31385 1.R1040

5'-most EST uC-gmrominsoy189b09b1

Method BLASTX
NCBI GI g3915165
BLAST score 644
E value 2.0e-67
Match length 210
% identity 59

NCBI Description TRYPTOPHAN SYNTHASE BETA CHAIN 2 PRECURSOR >gi\_2792520

(AF042320) tryptophan synthase beta subunit [Camptotheca acuminata] >gi\_2801771 (AF042321) tryptophan synthase beta

[Camptotheca acuminata]

Seq. No. 14386

Contig ID 31387 1.R1040

5'-most EST LIB3053-009-Q1-N1-H8

Method BLASTX
NCBI GI g2947064
BLAST score 294
E value 2.0e-26
Match length 122
% identity 44

NCBI Description (AC002521) unknown protein [Arabidopsis thaliana]

Seq. No. 14387

Contig ID 31393 1.R1040 5'-most EST g5606102 Method BLASTX NCBI GI g3176690 BLAST score 849 3.0e-91 E value Match length 188 89 % identity

NCBI Description (AC003671) Similar to ubiquitin ligase gb D63905 from S.

cerevisiae. EST gb R65295 comes from this gene.

[Arabidopsis thaliana]

Seq. No. 14388

Contig ID 31393\_2.R1040 5'-most EST wrg700789538.h2

Method BLASTX
NCBI GI g3176690
BLAST score 1358
E value 1.0e-151
Match length 316
% identity 84

NCBI Description (AC003671) Similar to ubiquitin ligase gb\_D63905 from S.

cerevisiae. EST gb R65295 comes from this gene.



## [Arabidopsis thaliana]

Seq. No. 14389

Contig ID 31395\_1.R1040

5'-most EST LIB3055-004-Q1-N1-H2

Method BLASTN
NCBI GI g431956
BLAST score 132
E value 1.0e-67
Match length 400

% identity 87

NCBI Description  $\mbox{P.sativum}$  mRNA for thioredoxin  $\mbox{M}$ 

Seq. No. 14390

Contig ID 31404\_1.R1040 5'-most EST g4291989

Seq. No. 14391

Contig ID 31406\_1.R1040

5'-most EST LIB3055-013-Q1-N1-D7

Method BLASTX
NCBI GI g3970652
BLAST score 295
E value 9.0e-27
Match length 97
% identity 54

NCBI Description (X77499) amino acid permease [Arabidopsis thaliana]

1

Seq. No. 14392

Contig ID 31409\_1.R1040

5'-most EST LIB3106-041-Q1-K1-F12

Method BLASTX
NCBI GI g2832625
BLAST score 461
E value 5.0e-46
Match length 125
% identity 70

NCBI Description (AL021711) putative protein [Arabidopsis thaliana]

Seq. No. 14393

Contig ID 31421\_1.R1040 5'-most EST txt700731920.h1

Seq. No. 14394

Contig ID 31422\_1.R1040 5'-most EST g4313446

Seq. No. 14395

Contig ID 31427\_2.R1040 5'-most EST pxt700943844.h1

Seq. No. 14396

Contig ID 31432\_1.R1040 5'-most EST gsv701055659.h1

Seq. No. 14397

Contig ID 31442\_1.R1040

Contig ID

14404

31485 1.R1040



```
5'-most EST
                  kl1701204309.h2
Method
                  BLASTX
NCBI GI
                  q4098244
BLAST score
                  180
                  5.0e-13
E value
                  57
Match length
% identity
                  68
NCBI Description (U76409) homeobox 1 protein [Lycopersicon esculentum]
                  14398
Seq. No.
                  31448 1.R1040
Contig ID
                  uaw700664445.hl
5'-most EST
Method
                  BLASTX
NCBI GI
                  q2673917
BLAST score
                  1459
E value
                  1.0e-162
Match length
                  372
% identity
                  45
NCBI Description (AC002561) putative ATP-dependent RNA helicase [Arabidopsis
                  thaliana]
                  14399
Seq. No.
                  31458 1.R1040
Contig ID
5'-most EST
                  LIB3170-047-Q1-J1-C6
Seq. No.
                  14400
                  31470 1.R1040
Contig ID
5'-most EST
                  vzy700754145.h1
Seq. No.
                  14401
                  31475 1.R1040
Contig ID
5'-most EST
                  g5676874
Method
                  BLASTX
                  g3080425
NCBI GI
BLAST score
                  481
E value
                  2.0e-48
Match length
                  146
% identity
NCBI Description (AL022604) putative protein [Arabidopsis thaliana]
Seq. No.
                  14402
                  31481 1.R1040
Contig ID
5'-most EST
                  ssr700557796.h1
                  14403
Seq. No.
Contig ID
                  31482 1.R1040
                  rca701000712.hl
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3859597
BLAST score
                  149
E value
                  5.0e-09
Match length
                  112
                  39
% identity
NCBI Description (AF104919) No definition line found [Arabidopsis thaliana]
```



```
smc700745347.hl
5'-most EST
                   BLASTX
Method
                   q4539386
NCBI GI
BLAST score
                   565
                   1.0e-57
E value
Match length
                   362
% identity
                   (AL035526) extensin-like protein [Arabidopsis thaliana]
NCBI Description
                   14405
Seq. No.
                   31485 2.R1040
Contig ID
                   jC-gm\overline{l}e01810044a08a1
5'-most EST
                   14406
Seq. No.
                   31485 3.R1040
Contig ID
5'-most EST
                   LIB3053-007-Q1-N1-E9
                   14407
Seq. No.
                   31485 4.R1040
Contig ID
                   sat701014058.hl
5'-most EST
                   14408
Seq. No.
                   31495 1.R1040
Contig ID
                   LIB3092-004-Q1-K1-D6
5'-most EST
                   BLASTX
Method
                   g4063751
NCBI GI
BLAST score
                   306
E value
                   1.0e-27
                   195
Match length
% identity
                   (AC005851) putative white protein [Arabidopsis thaliana]
NCBI Description
                   >gi 4510409 gb_AAD21495.1_ (AC006929) putative white
                   protein [Arabidopsis thaliana]
                   14409
Seq. No.
                   31496 1.R1040
Contig ID
                   awf700843423.hl
 5'-most EST
                   BLASTX
Method
                   g4220486
NCBI GI
                   339
 BLAST score
                   2.0e-31
 E value
                   216
Match length
 % identity
                   (AC006069) unknown protein [Arabidopsis thaliana]
 NCBI Description
                    14410
 Seq. No.
                    31497_1.R1040
 Contig ID
                   xzy700966778.hl
 5'-most EST
                    BLASTX
 Method
                    q3184282
 NCBI GI
 BLAST score
                    500
```

1.0e-50 E value 144 Match length 66 % identity

NCBI Description (AC004136) hypothetical protein [Arabidopsis thaliana]

14411 Seq. No.

```
31500 1.R1040
Contig ID
                   ncj700982693.hl
5'-most EST
                   14412
Seq. No.
Contig ID
                   31502 1.R1040
                   LIB3072-061-Q1-K1-H5
5'-most EST
                   14413
Seq. No.
                   31503 1.R1040
Contig ID
                   g4290849
5'-most EST
Method
                   BLASTX
                   g3785977
NCBI GI
BLAST score
                   181
                   4.0e-13
E value
                   112
Match length
% identity
                   38
                   (AC005560) putative growth regulator protein [Arabidopsis
NCBI Description
                   thaliana]
                   14414
Seq. No.
Contig ID
                    31505 1.R1040
5'-most EST
                   qsv701044173.hl
                    14415
Seq. No.
                    31516 1.R1040
Contig ID
                    \verb"jC-gm\overline{l}e01810022e08a1"
5'-most EST
```

14416 Seq. No. Contig ID

31516 2.R1040  $g4294\overline{4}28$ 5'-most EST

14417 Seq. No.

31516 3.R1040 Contig ID g4395664 5'-most EST BLASTX Method g1890317 NCBI GI 179 BLAST score 8.0e-27 E value 80

Match length 74 % identity

(Y11791) peroxidase ATP26a [Arabidopsis thaliana] NCBI Description

14418 Seq. No.

31516 4.R1040 Contig ID 5'-most EST ssr700560731.hl

BLASTX Method q1935909 NCBI GI 1905 BLAST score E value 0.0e + 00Match length 461 % identity

(U77345) lethal leaf-spot 1 [Zea mays] NCBI Description

14419 Seq. No.

31516 7.R1040 Contig ID hrw701059968.hl 5'-most EST

BLASTX Method



```
g1935909
NCBI GI
BLAST score
                  216
E value
                  3.0e-17
                  87
Match length
                  69
% identity
NCBI Description (U77345) lethal leaf-spot 1 [Zea mays]
Seq. No.
                  14420
                  31516 9.R1040
Contig ID
5'-most EST
                  zsg701125810.h1
Seq. No.
                  14421
                  31517 1.R1040
Contig ID
                  LIB3053-007-Q1-N1-G5
5'-most EST
                  BLASTX
Method
NCBI GI
                  g3201969
BLAST score
                  624
E value
                  7.0e-65
Match length
                  171
% identity
                  63
NCBI Description (AF068332) submergence induced protein 2A [Oryza sativa]
Seq. No.
                  14422
                  31517 2.R1040
Contig ID
5'-most EST
                  wrg700789449.h2
                  BLASTX
Method
NCBI GI
                  g3201969
BLAST score
                  253
                  7.0e-22
E value
Match length
                  73
% identity
                  60
NCBI Description
                 (AF068332) submergence induced protein 2A [Oryza sativa]
Seq. No.
                  14423
                  31520 1.R1040
Contig ID
5'-most EST
                  wrg700788463.h1
Seq. No.
                  14424
                  31521 1.R1040
Contig ID
5'-most EST
                  LIB3065-006-Q1-N1-D6
                  14425
Seq. No.
                  31522 1.R1040
Contig ID
                  pcp700991760.hl
5'-most EST
Seq. No.
                  14426
Contig ID
                  31525 1.R1040
5'-most EST
                  jC-gmf102220055e12d1
```

Contig ID 31526 1.R1040

5'-most EST LIB3053-007-Q1-N1-H12

BLASTX Method g3548802 NCBI GI BLAST score 557 3.0e-57 E value Match length 165



% identity (AC005313) axi 1-like protein [Arabidopsis thaliana] NCBI Description >qi 4335769 gb AAD17446 (AC006284) putative axil protein [Nicotiana tabacum] [Arabidopsis thaliana] 14428 Seq. No. 31528 1.R1040 Contig ID  $jC-gm\overline{l}e01810049h08a1$ 5'-most EST BLASTX Method g1653230 NCBI GI 257 BLAST score 6.0e-22 E value 107 Match length % identity 50 NCBI Description (D90912) hypothetical protein [Synechocystis sp.] 14429 Seq. No. 31538 1.R1040 Contig ID uC-gmflminsoy075g02b1 5'-most EST BLASTX Method g2651310 NCBI GI 388 BLAST score 2.0e-37 E value 106 Match length % identity 59 (ACO02336) putative PTR2-B peptide transporter [Arabidopsis NCBI Description thaliana] 14430 Seq. No. 31538 2.R1040 Contig ID leu701144915.h1 5'-most EST BLASTX Method q2651310 NCBI GI BLAST score 1503 1.0e-167 E value Match length 564 % identity (AC002336) putative PTR2-B peptide transporter [Arabidopsis NCBI Description thaliana] 14431 Seq. No. 31538 3.R1040 Contig ID LIB3109-035-Q1-K1-G2 5'-most EST Seq. No. 14432 31538 4.R1040 Contig ID LIB3094-060-Q1-K1-B3 5'-most EST Seq. No. 14433 31538 5.R1040 Contig ID

hyd700727204.h1 5'-most EST

BLASTX Method g2651310 NCBI GI BLAST score 159 5.0e-11 E value 40 Match length 65 % identity



```
(AC002336) putative PTR2-B peptide transporter [Arabidopsis
NCBI Description
                  thaliana]
                  14434
Seq. No.
                  31540 1.R1040
Contig ID
                  jC-gmro02910060d03a1
5'-most EST
                  BLASTX
Method
                  g2264373
NCBI GI
                  789
BLAST score
                  5.0e-84
E value
                  288
Match length
                   56
% identity
NCBI Description (AC002354) putative NAM/no apical meristem protein
                   [Arabidopsis thaliana]
                   14435
Seq. No.
                   31542 1.R1040
Contig ID
                   LIB3138-006-Q1-N1-A2
5'-most EST
                   BLASTX
Method
                   g3860264
NCBI GI
                   1566
BLAST score
                   1.0e-175
E value
                   372
Match length
                   79
% identity
NCBI Description (AC005824) unknown protein [Arabidopsis thaliana]
                   14436
Seq. No.
                   31543 1.R1040
Contig ID
                   bth700845117.hl
5'-most EST
                   BLASTX
Method
                   g3402711
NCBI GI
                   186
BLAST score
                   2.0e-13
E value
                   159
Match length
% identity
                   (AC004261) putative RNA-binding protein [Arabidopsis
NCBI Description
                   thaliana]
                   14437
Seq. No.
                   31543 2.R1040
Contig ID
                   q4313491
5'-most EST
                   BLASTX
Method
                   g3402711
NCBI GI
                   152
BLAST score
E value
                   1.0e-09
                   73
Match length
 % identity
                   (AC004261) putative RNA-binding protein [Arabidopsis
NCBI Description
                   thaliana]
 Seq. No.
                   14438
                   31543 3.R1040
 Contig ID
                   V4L-02-Q1-B1-G5
 5'-most EST
 Seq. No.
                   14439
```

2430

31550 1.R1040

epx701109672.h1

Contig ID

5'-most EST

Seq. No.

Contig ID

14446

31570 1.R1040



```
14440
Seq. No.
                  31559 1.R1040
Contig ID
5'-most EST
                  fC-qmse700754455b1
Seq. No.
                  14441
                  31563 1.R1040
Contig ID
5'-most EST
                  pcp700994055.h1
Seq. No.
                  14442
                  31563 2.R1040
Contig ID
5'-most EST
                  leu701147464.h1
Method
                  BLASTX
NCBI GI
                  g4417286
BLAST score
                  143
E value
                  8.0e-09
Match length
                  80
                  39
% identity
NCBI Description (AC007019) putative shikimate kinase [Arabidopsis thaliana]
                  14443
Seq. No.
Contig ID
                  31567 1.R1040
5'-most EST
                  LIB3106-043-Q1-K1-D12
Method
                  BLASTX
NCBI GI
                  g2244810
BLAST score
                  537
E value
                  6.0e-55
Match length
                  135
% identity
                  78
NCBI Description (Z97336) CCAAT-binding transcription factor subunit
                  A(CBF-A) [Arabidopsis thaliana]
Seq. No.
                  14444
                  31567 2.R1040
Contig ID
                  taw700659368.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q2244810
BLAST score
                  521
                  1.0e-52
E value
                  122
Match length
% identity
                  86
NCBI Description (Z97336) CCAAT-binding transcription factor subunit
                  A(CBF-A) [Arabidopsis thaliana]
Seq. No.
                  14445
                  31567 3.R1040
Contig ID
5'-most EST
                  ncj700977785.h1
Method
                  BLASTX
NCBI GI
                  g2398529
BLAST score
                  296
                  4.0e-27
E value
Match length
                  63
% identity
NCBI Description (Y13724) Transcription factor [Arabidopsis thaliana]
```

Match length

% identity

107 41



```
fde700874625.hl
5'-most EST
                   BLASTX
Method
                   g2832643
NCBI GI
                   672
BLAST score
                   2.0e-70
E value
Match length
                   160
% identity
NCBI Description (AL021710) hypothetical protein [Arabidopsis thaliana]
                   14447
Seq. No.
                   31572 1.R1040
Contig ID
                   k1170\overline{1}209591.h1
5'-most EST
                   BLASTX
Method
                   q4469025
NCBI GI
                   299
BLAST score
                   4.0e-27
E value
Match length
                   97
% identity
NCBI Description (AL035602) putative protein [Arabidopsis thaliana]
                   14448
Seq. No.
                   31577 1.R1040
Contig ID
                   ssr700555567.hl
5'-most EST
                   14449
Seq. No.
                   31579 1.R1040
Contig ID
                   LIB3053-006-Q1-N1-G10
5'-most EST
                   BLASTX
Method
                   q1652467
NCBI GI
BLAST score
                    181
                    3.0e-13
E value
                    53
Match length
 % identity
                    62
                   (D90905) hypothetical protein [Synechocystis sp.]
NCBI Description
                    14450
 Seq. No.
                    31580 1.R1040
 Contig ID
                    wrg70\overline{0}787839.h2
 5'-most EST
                    BLASTX
Method
                    g1071912
 NCBI GI
                    726
 BLAST score
                    8.0e-77
 E value
                    170
 Match length
                    83
 % identity
                    cysteine synthase (EC 4.2.99.8) cpACS1 - Arabidopsis
 NCBI Description
                    thaliana >gi_572517_emb_CAA57344_ (X81698) cysteine
                    synthase [Arabidopsis thaliana]
                    14451
 Seq. No.
                    31588 1.R1040
 Contig ID
 5'-most EST
                    leu701144368.hl
                    BLASTX
 Method
                    g1871577
 NCBI GI
                    193
 BLAST score
                    1.0e-14
 E value
```

NCBI GI

E value

BLAST score

Match length

% identity

a2842494

5.0e-60

581



```
NCBI Description (Y11553) putative 21kD protein precursor [Medicago sativa]
Seq. No.
                  14452
                  31588 2.R1040
Contig ID
                  LIB3106-094-Q1-K1-H1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g1871577
BLAST score
                  188
E value
                  4.0e-14
Match length
                  85
% identity
                  45
                  (Y11553) putative 21kD protein precursor [Medicago sativa]
NCBI Description
                  14453
Seq. No.
Contig ID
                  31590 1.R1040
5'-most EST
                  rlr700902291.h1
Method
                  BLASTX
NCBI GI
                  g509810
BLAST score
                  1149
E value
                  1.0e-126
Match length
                  444
                  52
% identity
                  (L08468) envelope Ca2+-ATPase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  14454
Contig ID
                  31595_1.R1040
5'-most EST
                  pcp700994567.h2
Method
                  BLASTX
NCBI GI
                  g2244757
BLAST score
                  181
E value
                  3.0e-13
Match length
                  110
% identity
                  (Z97335) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  14455
                  31600 1.R1040
Contig ID
5'-most EST
                  pmv700893371.h1
Method
                  BLASTX
NCBI GI
                  q4097690
BLAST score
                  813
E value
                  5.0e-87
Match length
                  188
% identity
                  89
                  (U66592) prohibitin 2 [Arabidopsis thaliana] >gi 4099801
NCBI Description
                   (U89791) prohibitin-like protein [Arabidopsis thaliana]
                  >gi 4204301 (AC003027) prohibitin 2 [Arabidopsis thaliana]
                  14456
Seq. No.
                  31600_2.R1040
Contig ID
5'-most EST
                  uaw700664470.h1
Method
                  BLASTX
```



NCBI Description (AL021749) prohibitin-like protein [Arabidopsis thaliana] >gi\_4097688 (U66591) prohibitin 1 [Arabidopsis thaliana] >gi\_4097694 (U66594) prohibitin 1 [Arabidopsis thaliana]

Seq. No. 14457

Contig ID 31600\_3.R1040 5'-most EST pmv700893277.h1

Method BLASTX
NCBI GI g2842494
BLAST score 307
E value 5.0e-28
Match length 99
% identity 61

NCBI Description (AL021749) prohibitin-like protein [Arabidopsis thaliana] >gi\_4097688 (U66591) prohibitin 1 [Arabidopsis thaliana]

>gi 4097694 (U66594) prohibitin 1 [Arabidopsis thaliana]

Seq. No.

14458

Contig ID 31613 1.R1040

5'-most EST uC-gmrominsoy246b05b1

Method BLASTX
NCBI GI g4101570
BLAST score 249
E value 2.0e-20
Match length 359
% identity 27

NCBI Description (AF004843) stamina pistilloidia [Pisum sativum]

Seq. No.

Contig ID 31613\_2.R1040 5'-most EST sat701012874.h1

Seq. No. 14460

Contig ID 31618\_1.R1040 5'-most EST pmv700891373.h1

Method BLASTX
NCBI GI g1431629
BLAST score 406
E value 1.0e-39
Match length 163
% identity 42

NCBI Description (X99348) pectinacetylesterase precursor [Vigna radiata]

Seq. No.

14461

Contig ID 31621\_1.R1040

5'-most EST LIB3106-023-Q1-K1-G8

Seq. No. 14462

Contig ID 31621\_2.R1040 5'-most EST smc700745714.h1

Seq. No. 14463

Contig ID 31623\_1.R1040

5'-most EST jC-gmro02910007b09d1

Method BLASTX NCBI GI g4406787 BLAST score 359

```
E value 5.0e-34
Match length 98
% identity 77
```

NCBI Description (AC006532) NADH dehydrogenase [Arabidopsis thaliana]

 Seq. No.
 14464

 Contig ID
 31631\_1.R1040

 5'-most EST
 g4313342

 Method
 BLASTX

 NCBI GI
 g148071

 BLAST score
 247

E value 2.0e-20 Match length 106 % identity 43

NCBI Description (M54881) thioredoxin [Escherichia coli]

Seq. No. 14465

Contig ID 31636 1.R1040

5'-most EST uC-gmflminsoy072g02b1

Method BLASTX
NCBI GI g4006908
BLAST score 184
E value 1.0e-13
Match length 148
% identity 32

NCBI Description (Z99708) putative protein [Arabidopsis thaliana]

Seq. No. 14466

Contig ID 31646\_1.R1040

5'-most EST uC-gmflminsoy043d10b1

Method BLASTX
NCBI GI g3080365
BLAST score 235
E value 2.0e-19
Match length 123
% identity 42

NCBI Description (AL022580) putative protein [Arabidopsis thaliana]

Seq. No. 14467

Contig ID 31646\_2.R1040 5'-most EST djj700606002.h2

Seq. No.

Contig ID 31648\_1.R1040 5'-most EST jex700905245.h1

14468

Method BLASTX
NCBI GI g4455284
BLAST score 502
E value 1.0e-50
Match length 158
% identity 61

NCBI Description (AL035527) beta-glucosidase-like protein [Arabidopsis

thaliana]

Seq. No. 14469

Contig ID 31654\_1.R1040 5'-most EST ncj700982263.h1



14470 Seq. No. 31659 1.R1040 Contig ID  $fde70\overline{0}871104.h1$ 5'-most EST 14471 Seq. No. 31662 1.R1040 Contig ID zsq701127468.hl 5'-most EST BLASTX Method g4155128 NCBI GI 225 BLAST score 4.0e-18 E value 119 Match length 40 % identity (AE001491) putative 3-HYDROXYACID DEHYDROGENASE NCBI Description [Helicobacter pylori J99] 14472 Seq. No. 31664 1.R1040 Contig ID zhf700953664.h1 5'-most EST BLASTX Method q3193287 NCBI GI 507 BLAST score 4.0e-54 E value Match length 136 71 % identity (AF069298) Arabidopsis predicted protein of unknown NCBI Description function T10P11.19 (GB:AC002330) [Arabidopsis thaliana] 14473 Seq. No. 31668 1.R1040 Contig ID LIB3053-004-Q1-N1-H7 5'-most EST BLASTX Method g4559384 NCBI GI 385 BLAST score 5.0e-37 E value 102 Match length 75 % identity (AC006526) unknown protein [Arabidopsis thaliana] NCBI Description 14474 Seq. No. 31669 1.R1040 Contig ID LIB3109-016-Q1-K1-C9 5'-most EST BLASTX Method g3128209 NCBI GI 1188 BLAST score 1.0e-131 E value 277 Match length

50 % identity

(AC004077) unknown protein [Arabidopsis thaliana] NCBI Description

14475 Seq. No.

31670 1.R1040 Contig ID

LIB3053-004-Q1-N1-H9 5'-most EST

BLASTX Method g3236249 NCBI GI BLAST score 518



```
1.0e-84
E value
Match length
                  230
% identity
                  (AC004684) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  14476
Seq. No.
                  31671 1.R1040
Contig ID
                  jC-gmle01810087e12a1
5'-most EST
                   14477
Seq. No.
                   31674 1.R1040
Contig ID
                   jC-gm\overline{l}e01810075c03a1
5'-most EST
                   BLASTN
Method
                   g20672
NCBI GI
BLAST score
                   406
E value
                   0.0e + 00
                   899
Match length
% identity
                   87
NCBI Description Pea cap mRNA for carbonic anhydrase (EC 4.2.1.1)
                   14478
Seq. No.
                   31674 2.R1040
Contig ID
                   LIB3139-062-P1-N1-D2
5'-most EST
                   BLASTX
Method
                   g2829902
NCBI GI
BLAST score
                   520
E value
                   7.0e-53
                   158
Match length
                   67
% identity
                   (AC002311) Putative sulphate transporter protein#protein
NCBI Description
                   [Arabidopsis thaliana]
                   14479
Seq. No.
                   31674 3.R1040
Contig ID
                   fC-gmst700890552h1
5'-most EST
                   BLASTN
Method
                   g169056
NCBI GI
                   180
BLAST score
                   2.0e-96
E value
                   355
Match length
                   88
% identity
NCBI Description P.sativum carbonic anhydrase mRNA, complete cds
                   14480
Seq. No.
                   31674 4.R1040
Contig ID
                   rca701001685.h1
 5'-most EST
                   BLASTN
Method
                   g20672
NCBI GI
BLAST score
                   192
E value
                   1.0e-104
Match length
                   347
                   89
 % identity
 NCBI Description Pea cap mRNA for carbonic anhydrase (EC 4.2.1.1)
 Seq. No.
                    14481
```

2437

31674 5.R1040

LIB3053-002-Q1-B1-D4

Contig ID

5'-most EST



Method BLASTX
NCBI GI g115471
BLAST score 502
E value 1.0e-101
Match length 236
% identity 80

NCBI Description CARBONIC ANHYDRASE, CHLOROPLAST PRECURSOR (CARBONATE DEHYDRATASE) >gi\_100078\_pir\_\_S10200 carbonate dehydratase (EC 4.2.1.1) precursor - garden pea >gi\_20673\_emb\_CAA36792\_(X52558) precursor peptide (AA -104 to 224) [Pisum sativum]

Seq. No. 14482

Contig ID 31674 6.R1040

5'-most EST LIB3092-022-Q1-K1-B9

Method BLASTN
NCBI GI g169056
BLAST score 39
E value 1.0e-12
Match length 130
% identity 88

NCBI Description P.sativum carbonic anhydrase mRNA, complete cds

Seq. No.

14483 31674 7.R1040

Contig ID 5'-most EST

35-V4L-01-Q1-E1-A12

Method BLASTN
NCBI GI g20672
BLAST score 89
E value 2.0e-42
Match length 204

% identity 87

NCBI Description Pea cap mRNA for carbonic anhydrase (EC 4.2.1.1)

Seq. No. 14484

Contig ID 31678 1.R1040

5'-most EST uC-gmflminsoy027d05b1

Seq. No. 14485

Contig ID 31680\_1.R1040

5'-most EST LIB3139-013-P1-N1-A1

Method BLASTX
NCBI GI g1934730
BLAST score 777
E value 1.0e-82
Match length 198
% identity 74

NCBI Description (U95036) germin-like protein [Arabidopsis thaliana]

Seq. No.

14486

Contig ID 31680\_2.R1040 5'-most EST tku700646383.h1

Method BLASTX
NCBI GI g1934730
BLAST score 380
E value 1.0e-36
Match length 94
% identity 74



NCBI Description (U95036) germin-like protein [Arabidopsis thaliana]

Seq. No.

14487

Contig ID

31687 2.R1040

5'-most EST

uC-gmrominsoy136a11b1

Method NCBI GI BLASTX

BLAST score

g2342690

E value

535 1.0e-54

Match length % identity

215 43

NCBI Description

(AC000106) Similar to Homo copine I (gb U83246).

[Arabidopsis thaliana]

Seq. No.

14488

Contig ID 5'-most EST

31689 1.R1040 pmv700890791.h1

Seq. No.

14489

Contig ID

31689 2.R1040

5'-most EST

LIB3106-078-P1-K1-E8

Seq. No.

14490

Contig ID 5'-most EST

31690 1.R1040 pxt700943729.h1

Method

BLASTX

NCBI GI

q3885338

BLAST score

535

E value

3.0e-54

Match length

228

% identity

46

NCBI Description

(AC005623) unknown protein [Arabidopsis thaliana]

Seq. No.

14491

Contig ID

31701 1.R1040

5'-most EST

uC-gmflminsoy049b01b1

Method NCBI GI BLASTX

q1707998

BLAST score

2472

E value

0.0e+00518

Match length

91

% identity NCBI Description

SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL PRECURSOR

(SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE)

(SHMT) >gi 481944 pir S40218 glycine

hydroxymethyltransferase (EC 2.1.2.1) - potato >gi 438247 emb CAA81082 (Z25863) glycine hydroxymethyltransferase [Solanum tuberosum]

Seq. No.

14492

Contig ID

31706 1.R1040

5'-most EST

awf700839836.h1

Method

BLASTX

NCBI GI

q4567281

BLAST score

E value

359

Match length

1.0e-33 141



% identity NCBI Description (AC006841) unknown protein [Arabidopsis thaliana]

14493 Seq. No.

31708 2.R1040 Contig ID crh700853714.h15'-most EST

14494 Seq. No.

31716 1.R1040 Contig ID

 $jC-gm\overline{l}e01810052h11a1$ 5'-most EST

BLASTX Method q461595 NCBI GI BLAST score 366 7.0e-49 E value 215 Match length % identity 60

ATP SYNTHASE B' CHAIN PRECURSOR (SUBUNIT II) NCBI Description

>gi\_479533\_pir\_\_S34473 H+-transporting ATP synthase (EC 3.6.1.34) chain 9 - spinach >gi\_394755\_emb\_CAA50520

(X71397) CF(o) II ATP synthase subunit 9 [Spinacia oleracea]

14495 Seq. No.

31716 2.R1040 Contig ID taw700657780.hl 5'-most EST

BLASTX Method g461595 NCBI GI 260 BLAST score 2.0e-22 E value 119 Match length 56 % identity

ATP SYNTHASE B' CHAIN PRECURSOR (SUBUNIT II) NCBI Description

>gi\_479533\_pir\_\_S34473 H+-transporting ATP synthase (EC
3.6.1.34) chain 9 - spinach >gi\_394755\_emb\_CAA50520\_

(X71397) CF(o) II ATP synthase subunit 9 [Spinacia oleracea]

14496 Seq. No.

31721 1.R1040 Contig ID fde700875909.h1 5'-most EST

BLASTX Method q2621798 NCBI GI 395 BLAST score 4.0e-38 E value 132 Match length % identity

(AE000850) transcriptional regulator [Methanobacterium NCBI Description

thermoautotrophicum]

14497 Seq. No.

31725 1.R1040 Contig ID pcp700992789.h1 5'-most EST

Method BLASTX g728867 NCBI GI 538 BLAST score 3.0e-56 E value Match length 222 % identity 51

NCBI Description ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR



>gi\_99694\_pir\_\_S21961 proline-rich protein APG Arabidopsis thaliana >gi\_22599\_emb\_CAA42925\_ (X60377) APG

[Arabidopsis thaliana]

Seq. No. 14498

Contig ID 31729 1.R1040

5'-most EST jC-gmle01810084g06a1

Method BLASTX
NCBI GI g3063445
BLAST score 443
E value 1.0e-43
Match length 207
% identity 48

NCBI Description (AC003981) F22013.7 [Arabidopsis thaliana]

Seq. No. 14499

Contig ID 31729 2.R1040

5'-most EST jC-gmle01810084g06d1

Seq. No. 14500

Contig ID 31738\_1.R1040 5'-most EST smc700750229.h1

Method BLASTX
NCBI GI g2194137
BLAST score 388
E value 2.0e-37
Match length 119
% identity 66

NCBI Description (AC002062) ESTs gb R29947, gb H76702 come from this gene.

[Arabidopsis thaliana]

Seq. No. 14501

Contig ID 31739\_1.R1040

5'-most EST LIB3053-004-Q1-N1-A11

Seq. No. 14502

Contig ID 31743\_1.R1040

5'-most EST jC-gmle01810043a08a1

Method BLASTX
NCBI GI g3176709
BLAST score 249
E value 4.0e-21
Match length 121
% identity 43

NCBI Description (AC002392) putative anthranilate

N-hydroxycinnamoyl/benzoyltransferase [Arabidopsis

thaliana]

Seq. No. 14503

Contig ID 31744 1.R1040 5'-most EST g5677587

Seq. No.

14504

Contig ID 31744 2.R1040

5'-most EST LIB3053-006-Q1-N1-F5

Seq. No. 14505

BLAST score

E value

839 4.0e-90



```
31747 1.R1040
Contig ID
                   pmv700891371.hl
5'-most EST
                   14506
Seq. No.
                   31756 1.R1040
Contig ID
                   LIB3053-003-Q1-N1-D10
5'-most EST
                   BLASTX
Method
                   g2108252
NCBI GI
                   463
BLAST score
                   3.0e-46
E value
                   113
Match length
                   40
% identity
                   (Y10228) P-glycoprotein-2 [Arabidopsis thaliana]
NCBI Description
                   >gi_2108254_emb_CAA71276_ (Y10227) P-glycoprotein-2
                   [Arabidopsis thaliana] >gi_4538925_emb_CAB39661.1
                   (AL049483) P-glycoprotein-2 (pgp2) [Arabidopsis thaliana]
                   14507
Seq. No.
                   31765 1.R1040
Contig ID
                   LIB31\overline{3}8-028-Q1-N1-G1
5'-most EST
                   BLASTX
Method
                   g1652868
NCBI GI
                   204
BLAST score
                   7.0e-16
E value
                   82
Match length
                   50
% identity
                   (D90909) hypothetical protein [Synechocystis sp.]
NCBI Description
                   14508
Seq. No.
                   31769 1.R1040
Contig ID
                   jC-gm\overline{l}e01810086c01a1
5'-most EST
                   BLASTX
Method
                   g404688
NCBI GI
                   1084
BLAST score
                   1.0e-118
E value
                    343
Match length
                    57
% identity
                   (L19074) cytochrome P450 [Catharanthus roseus]
NCBI Description
                    14509
 Seq. No.
                    31769 2.R1040
 Contig ID
                    fde700870785.h1
 5'-most EST
                    BLASTX
Method
                    q2760837
 NCBI GI
                    223
 BLAST score
                    3.0e-27
 E value
                    125
 Match length
                    50
 % identity
                   (AC003105) putative cytochrome P450 [Arabidopsis thaliana]
 NCBI Description
                    14510
 Seq. No.
                    31775 1.R1040
 Contig ID
                    pcp700992825.h1
 5'-most EST
                    BLASTX
 Method
                    g4544399
 NCBI GI
```



Match length 203 % identity

(AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis NCBI Description

thaliana]

Seq. No. Contig ID

14511 31779 1.R1040

5'-most EST

LIB3053-003-Q1-N1-B10

Method BLASTX NCBI GI g2911077 BLAST score 147 E value 2.0e-09 40

Match length % identity 70

NCBI Description (AL021960) gibberellin 20-oxidase - like protein

[Arabidopsis thaliana]

Seq. No.

14512

Contig ID

31780 1.R1040

5'-most EST

LIB3053-002-Q1-B1-H3

Method BLASTX NCBI GI g2642448 BLAST score 167 1.0e-11 E value Match length 129 % identity 12

(AC002391) hypothetical protein [Arabidopsis thaliana] NCBI Description

>gi 3169187 (AC004401) hypothetical protein [Arabidopsis

thaliana]

Seq. No.

14513

Contig ID

31788 1.R1040

5'-most EST

LIB3109-018-Q1-K1-F3

Seq. No.

14514

Contig ID 5'-most EST

31788 2.R1040 pxt700943529.h1

Seq. No.

14515

Contig ID

31788 3.R1040

5'-most EST

bth700845955.h1

Seq. No.

14516

Contig ID

31791 1.R1040

5'-most EST

LIB3053-003-Q1-N1-A8

Method BLASTN NCBI GI g1946221 BLAST score 158 E value 2.0e-83 Match length 375 87 % identity

NCBI Description M.domestica mRNA for knotted1-like homeobox protein

Seq. No.

14517

Contig ID 5'-most EST

31795 1.R1040 wrg700787120.h2

Method

BLASTX



NCBI GI g2288981 BLAST score 386 4.0e-37 E value 156 Match length 35 % identity

NCBI Description (AC002335) calcium binding protein isolog [Arabidopsis thaliana] >gi 3763938 (AC004450) putative calcium binding

protein [Arabidopsis thaliana]

Seq. No. 14518

Contig ID 31801 1.R1040

5'-most EST jC-qmf102220053a08a1

Method BLASTX NCBI GI g1871184 BLAST score 178 E value 9.0e-13 95 Match length % identity 45

(U90439) unknown protein [Arabidopsis thaliana] NCBI Description

Seq. No.

14519

Contig ID

31802 1.R1040

5'-most EST

jC-gmst02400067a02d1

Seq. No.

14520

Contig ID

31802 2.R1040

5'-most EST q5677815

Seq. No.

14521

Contig ID

31803 1.R1040

5'-most EST

uC-gmrominsoy244g06b1

Seq. No.

14522

Contig ID

31805 1.R1040

5'-most EST

LIB3139-052-P1-N1-B2

Seq. No.

14523

Contig ID 5'-most EST 31810 1.R1040

Method

kl1701207771.h1 BLASTX

NCBI GI

g2984225

BLAST score

441

E value

5.0e-43

Match length

242

% identity

40

NCBI Description

(AE000766) enolase-phosphatase E-1 [Aquifex aeolicus]

Seq. No.

14524

Contig ID

31813 1.R1040

5'-most EST

zzp700835142.h1

Seq. No.

14525

Contig ID

31814 1.R1040

5'-most EST

LIB3053-002-Q1-B1-D8

Method

BLASTX

NCBI GI

BLAST score

g2204236

655

```
9.0e-69
E value
                  139
Match length
                  93
% identity
NCBI Description (Y13861) enoyl-ACP reductase [Nicotiana tabacum]
                  14526
Seq. No.
                  31817 1.R1040
Contig ID
                  LIB3053-002-Q1-B1-E12
5'-most EST
                  BLASTX
Method
                  g1707857
NCBI GI
BLAST score
                  813
                  1.0e-107
E value
                  249
Match length
                  78
% identity
NCBI Description (Y09291) obtusifoliol 14-alpha-demethylase [Triticum
                  aestivum]
Seq. No.
                   14527
                   31820 1.R1040
Contig ID
                   jsh701064206.h1
5'-most EST
                   BLASTX
Method
                   q1652860
NCBI GI
BLAST score
                   212
                   2.0e-16
E value
                   142
Match length
                   37
% identity
NCBI Description (D90909) hypothetical protein [Synechocystis sp.]
                   14528
Seq. No.
                   31824 1.R1040
Contig ID
                   pxt700944664.hl
5'-most EST
                   14529
Seq. No.
                   31825 1.R1040
Contig ID
                   sat701013638.hl
5'-most EST
                   BLASTX
Method
                   g3947733
NCBI GI
                   257
BLAST score
                   3.0e-22
E value
                   107
Match length
 % identity
                   45
                   (AJ009719) NL25 [Solanum tuberosum]
 NCBI Description
                   14530
 Seq. No.
                   31826 1.R1040
 Contiq ID
 5'-most EST
                   rca701002360.h1
                   14531
 Seq. No.
                   31843 1.R1040
 Contig ID
 5'-most EST
                   uC-gmropic088c08b1
 Method
                   BLASTX
                    q3341679
 NCBI GI
                    1789
 BLAST score
                    0.0e+00
 E value
                    445
 Match length
 % identity
                    76
 NCBI Description (AC003672) dynamin-like protein phragmoplastin 12
```



## [Arabidopsis thaliana]

Seq. No. 14532

Contig ID 31843\_2.R1040

5'-most EST LIB3106-103-Q1-K1-E3

Method BLASTX
NCBI GI g3341679
BLAST score 377
E value 6.0e-51
Match length 185
% identity 58

NCBI Description (AC003672) dynamin-like protein phragmoplastin 12

[Arabidopsis thaliana]

Seq. No. 14533

Contig ID 31843\_3.R1040 5'-most EST seb700651011.h1

Method BLASTX
NCBI GI g2129826
BLAST score 322
E value 1.0e-29
Match length 96
% identity 66

NCBI Description dynamin-like protein phragmoplastin 5 - soybean >gi\_1218004

(U36430) SDL5A [Glycine max]

Seq. No. 14534

Contig ID 31846\_1.R1040

5'-most EST uC-gmrominsoy099b07b1

Method BLASTX
NCBI GI g2980760
BLAST score 242
E value 3.0e-20
Match length 65
% identity 66

NCBI Description (AL022198) putative protein [Arabidopsis thaliana]

Seq. No. 14535

Contig ID 31846\_2.R1040 5'-most EST wrg700792275.h1

Method BLASTX
NCBI GI g2642430
BLAST score 240
E value 2.0e-20
Match length 63
% identity 68

NCBI Description (AC002391) putative AP2 domain containing protein

[Arabidopsis thaliana]

Seq. No. 14536

Contig ID 31849 1.R1040

5'-most EST LIB3053-002-Q1-B1-B11

Method BLASTX
NCBI GI g4455307
BLAST score 175
E value 1.0e-12
Match length 70



% identity

NCBI Description (AL035528) methionyl-tRNA synthetase-like protein

[Arabidopsis thaliana]

Seq. No.

14537

Contig ID

31853 2.R1040

5'-most EST

LIB3053-001-Q1-B1-F6

Method NCBI GI BLAST score BLASTX q4309698 562

E value Match length

5.0e-58 130

% identity NCBI Description

(AC006266) putative glucosyltransferase [Arabidopsis

thaliana]

Seq. No.

14538

Contig ID

31854 1.R1040

5'-most EST

jC-qmle01810040d03a1

Method NCBI GI BLASTX g1351239

BLAST score

443

E value Match length 1.0e-43 111

% identity

69

NCBI Description

THIOREDOXIN M-TYPE PRECURSOR (TRX-M) >gi\_481594\_pir\_\_\$38909

thioredoxin m precursor - garden pea

>gi\_431957\_emb\_CAA53900\_ (X76269) thioredoxin m [Pisum

sativuml

Seq. No.

14539

Contig ID

31854 2.R1040

5'-most EST

LIB3053-001-Q1-B1-F7

Method NCBI GI BLASTX g4206206

BLAST score

252

E value

2.0e-21 108

Match length % identity

44

NCBI Description

(AF071527) putative M-type thioredoxin [Arabidopsis thaliana] >gi\_4263039 gb\_AAD15308 (AC005142) putative

M-type thioredoxin [Arabidopsis thaliana]

Seq. No.

14540

Contig ID

31862 1.R1040

5'-most EST

LIB3106-050-Q1-K1-E9

Method NCBI GI BLASTX g399212

BLAST score

E value

148

Match length

6.0e-09 93

% identity

22 NCBI Description ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA HOMOLOG

CD4A PRECURSOR >gi\_100189\_pir\_\_A35905 CD4A protein - tomato >gi\_170433 (M32603) ATP-dependent protease (CD4A)

[Lycopersicon esculentum]



```
14541
Seq. No.
                  31862 2.R1040
Contig ID
                  epx701107314.h1
5'-most EST
Seq. No.
                  14542
                  31868 1.R1040
Contig ID
                  wvk700681054.hl
5'-most EST
                  14543
Seq. No.
                  31870 1.R1040
Contig ID
5'-most EST
                  pmv700889619.h1
                  14544
Seq. No.
                  31871 1.R1040
Contig ID
                  jC-gmst02400007e04d1
5'-most EST
Method
                  BLASTX
                  q4417271
NCBI GI
                  1872
BLAST score
                  0.0e + 00
E value
                   409
Match length
% identity
                   (AC007019) putative cellulose synthase catalytic subunit
NCBI Description
                   [Arabidopsis thaliana]
                   14545
Seq. No.
                   31871 3.R1040
Contig ID
                   zsg701123864.h1
5'-most EST
                   BLASTX
Method
                   q3135611
NCBI GI
                   319
BLAST score
                   1.0e-35
E value
Match length
                   126
                   63
% identity
                  (AF062485) cellulose synthase [Arabidopsis thaliana]
NCBI Description
                   14546
Seq. No.
                   31873 1.R1040
Contig ID
                   ssr700554569.hl
5'-most EST
                   14547
Seq. No.
                   31874 1.R1040
Contig ID
                   jC-gmf102220077e11a1
5'-most EST
                   BLASTX
Method
                   g3068705
NCBI GI
                   367
BLAST score
                   2.0e-34
E value
                   229
Match length
                   39
% identity
                   (AF049236) unknown [Arabidopsis thaliana]
NCBI Description
```

NCBI Description

Seq. No. 14548

Contig ID 31874 2.R1040 5'-most EST LIB3106-106-Q1-K1-B12

Method BLASTX

NCBI GI g3068705 BLAST score 201 E value 4.0e-15



Match length 201 % identity 30

(AF049236) unknown [Arabidopsis thaliana] NCBI Description

Seq. No.

14549

Contig ID 31874 3.R1040 5'-most EST zhf700964756.h1

Seq. No.

14550

Contig ID 5'-most EST

31874 4.R1040 leu701152465.h1

Seq. No.

14551

Contig ID 5'-most EST

31875 1.R1040 LIB3053-001-Q1-B1-E7

Method

BLASTX

NCBI GI BLAST score

g2252830 527

E value Match length 1.0e-53 136

73

% identity

(AF013293) weak similarity to receptor protein kinase NCBI Description

[Arabidopsis thaliana]

Seq. No.

14552

Contig ID

31878 1.R1040

5'-most EST

jC-gmle01810004e03d1

Method NCBI GI BLAST score E value

BLASTX q3355480 161 2.0e-14

Match length % identity

59

(AC004218) Medicago nodulin N21-like protein [Arabidopsis NCBI Description

thaliana]

Seq. No.

14553

85

Contig ID 5'-most EST

31881 1.R1040 pcp700992459.h1

Method NCBI GI BLAST score BLASTX g4006878 411

E value Match length 3.0e-40

% identity

138

NCBI Description (Z99707) MAP3K-like protein kinase [Arabidopsis thaliana]

Seq. No. 14554

Contig ID

31885 1.R1040

5'-most EST

LIB3053-001-Q1-B1-B12

Method NCBI GI BLAST score BLASTX g2317905 264

E value Match length 6.0e-23 63

81

% identity

NCBI Description (U89959) bZIP-like protein [Arabidopsis thaliana]



Seq. No. 14555

Contig ID 31886 1.R1040

5'-most EST LIB31 $\overline{3}$ 9-043-P1-N1-B5

Method BLASTX
NCBI GI g4455159
BLAST score 1564
E value 1.0e-175
Match length 363
% identity 79

NCBI Description (AL021687) putative protein [Arabidopsis thaliana]

Seq. No.

14556

Contig ID 31886 2.R1040 5'-most EST vzy700756263.h1

Seq. No.

14557

Contig ID 31897\_1.R1040 5'-most EST asn701134441.h1

Method BLASTX
NCBI GI g2062175
BLAST score 926
E value 1.0e-100
Match length 423
% identity 52

NCBI Description (AC001645) hypothetical protein [Arabidopsis thaliana]

Seq. No. 14558

Contig ID 31899 1.R1040

5'-most EST LIB3053-001-Q1-B1-A3

Seq. No. 14559

Contig ID 31900\_1.R1040
5'-most EST g5342499
Method BLASTX
NCBI GI g4490305
BLAST score 731
E value 5.0e-77

Match length 220 % identity 64

NCBI Description (AL035678) putative protein [Arabidopsis thaliana]

Seq. No. 14560

Contig ID 31900\_2.R1040 5'-most EST uC-gmropic013g11b1

Method BLASTX
NCBI GI g4490305
BLAST score 182
E value 3.0e-13
Match length 74
% identity 57

NCBI Description (AL035678) putative protein [Arabidopsis thaliana]

Seq. No. 14561

Contig ID 31900\_3.R1040 5'-most EST smc700747915.h1

E value

Match length

% identity

4.0e-32

88 73



```
14562
Seq. No.
Contig ID
                   31909 1.R1040
5'-most EST
                   q5606130
Method
                   BLASTX
NCBI GI
                   g4337192
BLAST score
                   399
E value
                   2.0e-38
Match length
                   158
% identity
                   54
NCBI Description (AC006403) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   14563
                   31909 2.R1040
Contig ID
5'-most EST
                   taw700659113.h1
Seq. No.
                   14564
                   31911 1.R1040
Contig ID
5'-most EST
                   jsh70\overline{1}064107.h1
                   BLASTX
Method
NCBI GI
                   a3643602
BLAST score
                   814
E value
                   5.0e-87
Match length
                   245
% identity
                   63
NCBI Description
                  (AC005395) putative tonoplast intrinsic protein
                   [Arabidopsis thaliana]
                   14565
Seq. No.
                   31912 1.R1040
Contig ID
5'-most EST
                   LIB3053-001-Q1-B1-D5
Seq. No.
                   14566
Contig ID
                   31932 1.R1040
5'-most EST
                   jC-gmro02910019g05d1
Seq. No.
                   14567
                   31967 1.R1040
Contig ID
5'-most EST
                   gsv701044878.h1
Seq. No.
                   14568
                   31970 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400009h05a1
Seq. No.
                   14569
Contig ID
                   31976 1.R1040
5'-most EST
                   jC-gmf102220055d01d1
Seq. No.
                   14570
                   31986 1.R1040
Contig ID
5'-most EST
                   LIB3170-077-Q1-J1-H3
Method
                   BLASTX
NCBI GI
                   g2769642
                   343
BLAST score
```

NCBI Description (297215) nine-cis-epoxycarotenoid dioxygenase [Lycopersicon



## esculentum]

Seq. No. 14571 31998 1.R1040 Contig ID 5'-most EST jC-gmro02910025d07a1

Seq. No. 14572

31999 1.R1040 Contig ID

5'-most EST jC-gmro02910074h02d1

14573 Seq. No.

31999 2.R1040 Contig ID

5'-most EST jC-gmle01810008h05d1

Seq. No. 14574

Contig ID 32001 1.R1040

5'-most EST uC-gmrominsoy219d07b1

Method BLASTX NCBI GI g4510371 BLAST score 421 E value 3.0e-41 Match length 203 % identity

(AC007017) putative harpin-induced protein [Arabidopsis NCBI Description

thaliana]

14575 Seq. No.

32001 2.R1040 Contig ID

5'-most EST uC-gmrominsoy315d01b1

Method BLASTX NCBI GI g4510371 BLAST score 205 4.0e-16 E value Match length 96

% identity

(AC007017) putative harpin-induced protein [Arabidopsis NCBI Description

thaliana]

Seq. No. 14576

32001 3.R1040 Contig ID 5'-most EST gsv701056521.h1

Method BLASTX NCBI GI g4510371 BLAST score 292 E value 2.0e-26 Match length 120 % identity

NCBI Description (AC007017) putative harpin-induced protein [Arabidopsis

thaliana]

Seq. No. 14577

Contig ID 32001 4.R1040 5'-most EST dpv701101884.h1

14578 Seq. No.

32009 1.R1040 Contig ID

5'-most EST LIB3055-013-Q1-N1-G12



```
Method
                  BLASTX
NCBI GI
                  g3402719
                  135
BLAST score
E value
                  3.0e-17
                  90
Match length
                  53
% identity
NCBI Description
                  (AC004261) unknown protein [Arabidopsis thaliana]
                  14579
Seq. No.
                  32010 1.R1040
Contiq ID
5'-most EST
                  pmv700895143.h1
                  BLASTX
Method
NCBI GI
                  g3786016
BLAST score
                  247
E value
                  9.0e-31
Match length
                  121
% identity
```

NCBI Description (AC005499) putative elongation factor [Arabidopsis

thaliana]

 Seq. No.
 14580

 Contig ID
 32013\_1.R1040

 5'-most EST
 zsg701130031.h1

 Mothed
 BLASTY

Method BLASTX
NCBI GI g2791276
BLAST score 310
E value 3.0e-28
Match length 77
% identity 79

NCBI Description (Z95327) Cleavage Stimulation Factor (CF-1, Polyadenylation

Factor) 64 kD subunit [Homo sapiens]

Seq. No. 14581

Contig ID 32018 1.R1040

5'-most EST LIB3107-041-Q1-K1-E5

Method BLASTX
NCBI GI 94559382
BLAST score 230
E value 9.0e-19
Match length 198
% identity 30

NCBI Description (AC006526) putative DNA binding protein [Arabidopsis

thaliana]

Seq. No. 14582

Contig ID 32019 1.R1040

5'-most EST LIB3107-009-01-K1-G6

Seq. No. 14583

Contig ID 32019\_2.R1040 5'-most EST wvk700680408.h1

Seq. No. 14584

Contig ID 32019\_3.R1040 5'-most EST uC-gmropic073b01b1

Seq. No. 14585



```
32021 1.R1040
Contig ID
5'-most EST
                  zsq701128655.hl
                  BLASTX
Method
                  q3643608
NCBI GI
                  335
BLAST score
                  4.0e-31
E value
                  106
Match length
                   62
% identity
NCBI Description (AC005395) hypothetical protein [Arabidopsis thaliana]
                   14586
Seq. No.
                   32024 1.R1040
Contig ID
                   LIB3055-013-Q1-N1-G10
5'-most EST
                   BLASTX
Method
                   q4185137
NCBI GI
                   1592
BLAST score
                   1.0e-178
E value
                   357
Match length
% identity
                   (AC005724) SecY homolog [Arabidopsis thaliana]
NCBI Description
                   14587
Seq. No.
                   32029 1.R1040
Contig ID
                   LIB3065-019-Q1-N1-H3
5'-most EST
                   BLASTN
Method
                   g12147
NCBI GI
                   391
BLAST score
                   0.0e + 00
E value
                   648
Match length
                   93
% identity
                   Pea chloroplast genes for ATP synthetase subunits beta and
NCBI Description
                   epsilon (atpB and atpE)
                   14588
Seq. No.
                   32029 3.R1040
Contig ID
                   uC-gmflminsoy003b07b1
 5'-most EST
                   BLASTN
Method
                   q4063569
NCBI GI
                   97
BLAST score
                   5.0e-47
E value
                   201
Match length
                   88
 % identity
                   Tropaeolum tricolor ATP synthase beta subunit (atpB) gene,
 NCBI Description
                   chloroplast gene encoding chloroplast protein, partial cds
 Seq. No.
                   14589
                   32030 1.R1040
 Contig ID
                   LIB3055-013-Q1-N1-F10
 5'-most EST
 Method
                   BLASTX
 NCBI GI
                   q3549657
                   196
 BLAST score
                    4.0e-15
 E value
                   100
 Match length
```

40 % identity

(AL031394) putative protein [Arabidopsis thaliana] NCBI Description

14590 Seq. No.

BLAST score

E value Match length 181 1.0e-12

151



```
Contig ID
                   32033 1.R1040
                  LIB3055-013-Q1-N1-F2
5'-most EST
                  14591
Seq. No.
Contig ID
                  32038 1.R1040
5'-most EST
                  leu701148817.h1
                  BLASTX
Method
NCBI GI
                  q2979542
BLAST score
                  480
E value
                  2.0e-48
Match length
                  115
                  74
% identity
                  (AC003680) putative Ser/Thr kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  14592
Contig ID
                  32041 1.R1040
5'-most EST
                  LIB3109-016-Q1-K1-H9
                  14593
Seq. No.
Contig ID
                  32042 1.R1040
5'-most EST
                  g4293828
                  14594
Seq. No.
Contig ID
                  32042 2.R1040
                  LIB3107-082-Q1-K1-D1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2497492
BLAST score
                  212
E value
                  7.0e-32
Match length
                  150
% identity
                   57
                  URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP
NCBI Description
                  KINASE) >gi 1653646 dbj BAA18558 (D90915) uridine
                  monophosphate kinase [Synechocystis sp.]
                  14595
Seq. No.
Contig ID
                  32053 1.R1040
5'-most EST
                  wrq70\overline{0}786118.h2
                  BLASTX
Method
                  g1001404
NCBI GI
BLAST score
                  161
                   2.0e-10
E value
Match length
                  138
% identity
NCBI Description
                 (D63999) hypothetical protein [Synechocystis sp.]
Seq. No.
                  14596
                   32063 1.R1040
Contig ID
5'-most EST
                  pxt700944871.h1
Method
                  BLASTX
NCBI GI
                  g3695388
```

% identity 41 NCBI Description (AF096371) No definition line found [Arabidopsis thaliana]



```
Seq. No.
Contig ID
                  32069 1.R1040
5'-most EST
                  LIB3055-008-Q1-N1-C7
Method
                  BLASTX
NCBI GI
                  q2541876
BLAST score
                  472
E value
                  4.0e-47
Match length
                  237
% identity
                  43
NCBI Description
                  (D26015) CND41, chloroplast nucleoid DNA binding protein
                  [Nicotiana tabacum]
                  14598
Seq. No.
Contig ID
                  32072 1.R1040
5'-most EST
                  ejt700606213.h1
Method
                  BLASTX
                  q4056494
NCBI GI
BLAST score
                  583
                  3.0e-60
E value
Match length
                  144
                  76
% identity
                  (AC005896) putative protein translocase [Arabidopsis
NCBI Description
                  thaliana]
                  14599
Seq. No.
Contig ID
                  32072 2.R1040
5'-most EST
                  jC-gmro02910010f05a1
Method
                  BLASTX
NCBI GI
                  q4056494
BLAST score
                  571
                  7.0e-59
E value
Match length
                  158
% identity
                  70
NCBI Description
                  (AC005896) putative protein translocase [Arabidopsis
                  thaliana]
Seq. No.
                  14600
                  32072 3.R1040
Contig ID
5'-most EST
                  LIB3093-015-Q1-K2-C12
Method
                  BLASTX
NCBI GI
                  g4056494
BLAST score
                  374
E value
                  5.0e-36
Match length
                  90
% identity
NCBI Description
                  (AC005896) putative protein translocase [Arabidopsis
                  thaliana]
                  14601
Seq. No.
Contig ID
                  32078 1.R1040
                  pmv700892438.h1
```

5'-most EST Method BLASTX

g3121739 NCBI GI BLAST score 253 E value 8.0e-22 Match length 125 % identity 28





ANGIO-ASSOCIATED MIGRATORY CELL PROTEIN NCBI Description >gi\_2134759\_pir\_\_I39383 angio-associated migratory cell protein - human >gi\_870803 (M95627) angio-associated migratory cell protein [Homo sapiens] >gi\_4557229\_ref\_NP\_001078.1\_pAAMP\_ angio-associated, migratory cell protein 14602 Seq. No. 32083 1.R1040 Contig ID txt700734511.h1 5'-most EST BLASTX Method g3065835 NCBI GI 253 BLAST score 9.0e-22 E value 100 Match length % identity (AF058800) putative methyltransferase [Arabidopsis NCBI Description thaliana] 14603 Seq. No. 32084\_1.R1040 Contig ID LIB3093-018-Q1-K1-B8 5'-most EST BLASTX Method g4539444 NCBI GI 475 BLAST score 3.0e-47E value 238 Match length 43 % identity (AL049523) hypothetical protein [Arabidopsis thaliana] NCBI Description 14604 Seq. No. 32086 1.R1040 Contig ID jC-gmle01810085f04a1 5'-most EST BLASTX Method q2497977 NCBI GI 557 BLAST score 8.0e-57 E value 272 Match length % identity 46 HYPOTHETICAL 30.2 KD PROTEIN IN CAPB 3'REGION >gi\_1513082 NCBI Description (U62986) ATPase [Pseudomonas fragi] 14605 Seq. No. 32086 3.R1040 Contig ID LIB3138-051-Q1-N1-G3 5'-most EST BLASTX Method g1709101 NCBI GI 209 BLAST score 1.0e-16 E value 108 Match length

% identity 44

MRP PROTEIN HOMOLOG >gi\_1001155\_dbj\_BAA10297\_ (D64001) put. NCBI Description ATPase [Synechocystis sp.]

14606 Seq. No.

32096 1.R1040 Contig ID

LIB3167-029-P1-K1-G6 5'-most EST



```
14607
Seq. No.
                  32098 1.R1040
Contig ID
                  LIB3107-026-Q1-K1-E11
5'-most EST
                  14608
Seq. No.
                  32098 2.R1040
Contig ID
                  kmv700743382.h1
5'-most EST
                  BLASTX
Method
                  g461999
NCBI GI
                  1675
BLAST score
                  0.0e + 00
E value
                   345
Match length
                   95
% identity
                  ELONGATION FACTOR G, CHLOROPLAST PRECURSOR (EF-G)
NCBI Description
                   14609
Seq. No.
                   32110 1.R1040
Contig ID
                   LIB3055-012-Q1-N1-E5
5'-most EST
                   14610
Seq. No.
                   32112 1.R1040
Contig ID
                   zsg701117710.h2
5'-most EST
                   BLASTX
Method
                   g4455332
NCBI GI
BLAST score
                   261
                   1.0e-22
E value
Match length
                   87
                   54
% identity
                   (AL035525) putative protein [Arabidopsis thaliana]
NCBI Description
                   14611
Seq. No.
                   32113 1.R1040
Contiq ID
                   leu701149273.hl
5'-most EST
                   BLASTX
Method
                   g3929333
NCBI GI
                   709
BLAST score
                   1.0e-107
E value
                   424
Match length
                   49
% identity
                   CYTOCHROME P450 76B1 (7-ETHOXYCOUMARIN O-DEETHYLASE) (ECOD)
NCBI Description
                   (PHENYLUREA DEALKYLASE) >gi_2370230_emb_CAA71054_ (Y09920)
                   7-ethoxycoumarin O-deethylase [Helianthus tuberosus]
                   14612
Seq. No.
                   32113 2.R1040
Contig ID
                   zhf700959116.h1
 5'-most EST
                   BLASTX
Method
                   q4008006
NCBI GI
                   635
BLAST score
                   7.0e-99
 E value
                   274
Match length
```

% identity

(AF084034) receptor-like protein kinase [Arabidopsis NCBI Description

thaliana]

14613

Seq. No.

Match length

% identity

```
32113 3.R1040
Contig ID
                   vwf700678139.hl
5'-most EST
                   BLASTX
Method
                   q4008006
NCBI GI
                   379
BLAST score
                   1.0e-36
E value
Match length
                   91
                   86
% identity
                  (AF084034) receptor-like protein kinase [Arabidopsis
NCBI Description
                   thaliana]
                   14614
Seq. No.
                   32119_1.R1040
Contig ID
                   LIB3055-012-Q1-N1-F6
5'-most EST
Seq. No.
                   14615
                   32125 1.R1040
Contig ID
                   leu701156113.hl
5'-most EST
                   BLASTX
Method
                   g3643608
NCBI GI
BLAST score
                   362
                   8.0e-47
E value
                   203
Match length
                   50
% identity
NCBI Description (AC005395) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   14616
                   32125 4.R1040
Contig ID
                   jex700907439.hl
5'-most EST
                   BLASTX
Method
                   q3643608
NCBI GI
                   158
BLAST score
                   6.0e-11
E value
                   39
Match length
                   69
% identity
                   (AC005395) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   14617
Seq. No.
                   32125 5.R1040
Contig ID
                   ncj70\overline{0}984166.h1
 5'-most EST
                   BLASTX
Method
                   g4415908
NCBI GI
                    142
BLAST score
                    1.0e-08
 E value
                    75
 Match length
                    39
 % identity
                   (ACO06282) unknown protein [Arabidopsis thaliana]
 NCBI Description
                    14618
 Seq. No.
                    32125 6.R1040
 Contig ID
 5'-most EST
                    vzy700751125.hl
                    BLASTX
 Method
                    q3643608
 NCBI GI
                    269
 BLAST score
                    5.0e-24
 E value
```



NCBI Description (AC005395) hypothetical protein [Arabidopsis thaliana]

Seq. No. 14619

Contig ID 32128\_1.R1040 5'-most EST hrw701060081.h2

Method BLASTX
NCBI GI g3953471
BLAST score 397
E value 3.0e-38
Match length 175
% identity 51

NCBI Description (AC002328) F2202.16 [Arabidopsis thaliana]

Seq. No. 14620

Contig ID 32129\_1.R1040 5'-most EST hrw701058727.h1

Seq. No. 14621

Contig ID 32146\_1.R1040 5'-most EST uC-gmropic040f03b1

Method BLASTX
NCBI GI g3402279
BLAST score 1222
E value 1.0e-135
Match length 247
% identity 91

NCBI Description (AJ000999) putative beta-subunit of K+ channels [Solanum

tuberosum]

Seq. No. 14622

Contig ID 32146 2.R1040 5'-most EST ncj700978917.h1

Method BLASTN
NCBI GI g2832782
BLAST score 92
E value 2.0e-44
Match length 176
% identity 88

NCBI Description Egeria densa mRNA for potassium channel beta subunit

Seq. No. 14623

Contig ID 32148\_1.R1040

5'-most EST LIB3109-012-Q1-K1-A2

Seq. No. 14624

Contig ID 32148\_2.R1040

5'-most EST LIB3170-079-Q1-K1-B7

Seq. No. 14625

Contig ID 32153\_1.R1040

5'-most EST LIB3055-012-Q1-N1-C3

Seq. No. 14626

Contig ID 32160\_2.R1040

5'-most EST uC-gmflminsoy034f04b1

Method BLASTX NCBI GI g1865677



BLAST score 665 E value 6.0e-70 Match length 168 % identity 78

NCBI Description (Y08568) trehalose-6-phosphate synthase [Arabidopsis

thaliana]

Seq. No. 14627

Contig ID 32163\_1.R1040

5'-most EST LIB3106-064-Q1-K1-B8

Method BLASTX
NCBI GI g2695931
BLAST score 394
E value 4.0e-38
Match length 96
% identity 78

NCBI Description (AJ222779) hypothetical protein [Hordeum vulgare]

Seq. No. 14628

Contig ID 32166 1.R1040

5'-most EST LIB3106-051-Q1-K1-G5

Method BLASTX
NCBI GI g2459435
BLAST score 237
E value 6.0e-20
Match length 78
% identity 56

NCBI Description (AC002332) putative serine carboxypeptidase [Arabidopsis

thaliana]

Seq. No. 14629

Contig ID 32168\_1.R1040 5'-most EST hyd700729809.h1

Method BLASTX
NCBI GI g130718
BLAST score 444
E value 7.0e-44
Match length 192
% identity 43

NCBI Description ACID PHOSPHATASE PRECURSOR 1 >gi\_170370 (M83211) acid

phosphatase type 1 [Lycopersicon esculentum] >gi\_170372 (M67474) acid phosphatase type 5 [Lycopersicon esculentum] >gi\_445121\_prf\_\_1908427A acid phosphatase 1 [Lycopersicon

esculentum]

Seq. No. 14630

Contig ID 32169\_1.R1040 5'-most EST gsv701056223.h1

Seq. No. 14631

Contig ID 32172 1.R1040

5'-most EST jC-gmst02400026g01d1

Seq. No. 14632

Contig ID 32176\_1.R1040 5'-most EST uC-gmropic075h12b1



```
14633
Seq. No.
                  32186 1.R1040
Contig ID
                  LIB3055-011-Q1-N1-E4
5'-most EST
Method
                  BLASTX
                  q3298540
NCBI GI
                  382
BLAST score
                  1.0e-37
E value
                  113
Match length
% identity
                   (AC004681) unknown protein [Arabidopsis thaliana]
NCBI Description
                  14634
Seq. No.
                  32187 1.R1040
Contig ID
                  wvk700682893.hl
5'-most EST
                  BLASTX
Method
                   g1168408
NCBI GI
BLAST score
                   1620
                   0.0e + 00
E value
                   357
Match length
                   89
% identity
                   FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME 1
NCBI Description
                   >gi_2118268_pir__S58168 fructose-bisphosphate aldolase (EC
                   4.1.2.13) - garden pea >gi_927507_emb_CAA61946_ (X89828)
                   fructose-1,6-bisphosphate aldolase [Pisum sativum]
                   14635
Seq. No.
                   32187 2.R1040
Contig ID
                   g5606535
5'-most EST
                   BLASTN
Method
                   g927506
NCBI GI
                   109
BLAST score
                   4.0e-54
E value
                   250
Match length
                   89
% identity
                  P.sativum mRNA for fructose-1, 6-biphosphate aldolase
NCBI Description
                   (clone aldcyt1)
                   14636
Seq. No.
                   32191 1.R1040
Contig ID
5'-most EST
                   LIB3109-022-Q1-K1-A5
                   BLASTX
Method
                   q2754849
NCBI GI
                   1762
BLAST score
                   0.0e + 00
E value
Match length
                   401
 % identity
                   (AF039000) putative serine-glyoxylate aminotransferase
NCBI Description
                    [Fritillaria agrestis]
 Seq. No.
                   14637
                   32191 2.R1040
 Contig ID
                   jC-gmf102220052c01a1
 5'-most EST
```

Method BLASTX
NCBI GI g3288821
BLAST score 376
E value 8.0e-36
Match length 113



```
% identity
                  (AF063901) alanine:glyoxylate aminotransferase;
NCBI Description
                  transaminase [Arabidopsis thaliana]
Seq. No.
                  14638
                  32191 3.R1040
Contig ID
                  jC-gmro02910017d08d1
5'-most EST
                  14639
Seq. No.
                  32191 9.R1040
Contig ID
                  ncj700984383.hl
5'-most EST
                  BLASTX
Method
                  g3288821
NCBI GI
                   209
BLAST score
                   7.0e-19
E value
Match length
                   56
% identity
                   77
                   (AF063901) alanine:glyoxylate aminotransferase;
NCBI Description
                   transaminase [Arabidopsis thaliana]
                   14640
Seq. No.
                   32192 1.R1040
Contig ID
                   uC-gmronoir060a03b1
5'-most EST
                   BLASTX
Method
                   g4544399
NCBI GI
BLAST score
                   179
                   5.0e-13
E value
                   73
Match length
                   47
% identity
                   (AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis
NCBI Description
                   thaliana]
                   14641
Seq. No.
                   32197_1.R1040
Contig ID
                   jC-gm\overline{f}102220081h07a1
5'-most EST
                   14642
Seq. No.
                   32198_1.R1040
Contig ID
                   LIB3056-009-Q1-N1-E7
5'-most EST
                   BLASTX
Method
                   g1431629
NCBI GI
                   738
BLAST score
                   2.0e-78
E value
                   183
Match length
                   73
 % identity
                   (X99348) pectinacetylesterase precursor [Vigna radiata]
NCBI Description
                   14643
 Seq. No.
                   32199 2.R1040
 Contig ID
                   rca701001083.hl
 5'-most EST
 Method
                   BLASTX
                   q3264757
 NCBI GI
                   1724
 BLAST score
                   0.0e + 00
 E value
                   427
 Match length
 % identity
                   76
 NCBI Description (AF071888) zeaxanthin epoxidase [Prunus armeniaca]
```



220

thaliana]

75

Match length

NCBI Description

% identity

```
14644
Seq. No.
                  32199 3.R1040
Contig ID
                  LIB3107-034-Q1-K1-G5
5'-most EST
Method
                  BLASTX
                  q2129941
NCBI GI
                  178
BLAST score
                  5.0e-13
E value
                  41
Match length
                  80
% identity
                  zeaxanthin epoxidase precursor - curled-leaved tobacco
NCBI Description
                  >gi_1370274_emb_CAA65048_ (X95732) zeaxanthin epoxidase
                   [Nicotiana plumbaginifolia]
                   14645
Seq. No.
                   32203 1.R1040
Contig ID
                   uaw700661832.hl
5'-most EST
                   BLASTX
Method
                   q2462748
NCBI GI
                   1309
BLAST score
                   1.0e-145
E value
                   271
Match length
                   90
% identity
                   (AC002292) putative Clathrin Coat Assembly protein
NCBI Description
                   [Arabidopsis thaliana]
                   14646
Seq. No.
                   32207 1.R1040
Contig ID
                   fde700874892.hl
5'-most EST
                   BLASTX
Method
                   q4049399
NCBI GI
                   639
BLAST score
                   1.0e-66
E value
                   288
Match length
                   43
% identity
                   (Y09581) FRO2 [Arabidopsis thaliana]
NCBI Description
                   14647
Seq. No.
                   32215 1.R1040
Contig ID
5'-most EST
                   LIB3167-004-P1-K1-E11
                   14648
 Seq. No.
                   32229 1.R1040
 Contig ID
                   LIB3139-045-P1-N1-F11
 5'-most EST
                   14649
 Seq. No.
                   32232 1.R1040
 Contig ID
                   q5607002
 5'-most EST
 Method
                   BLASTX
                   q421826
 NCBI GI
 BLAST score
                   891
                   5.0e-96
 E value
```

2464

chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana

>gi\_298036\_emb\_CAA50712\_ (X71878) CP29 [Arabidopsis



```
14650
Seq. No.
                   32232 2.R1040
Contig ID
                   jC-gm\overline{l}e01810043f11a1
5'-most EST
                   14651
Seq. No.
                   32235 1.R1040
Contig ID
                   LIB3055-010-Q1-N1-A2
5'-most EST
                   14652
Seq. No.
                   32240 1.R1040
Contig ID
                   LIB3055-011-Q1-N1-A2
5'-most EST
                   BLASTX
Method
                   g1709039
NCBI GI
BLAST score
                   326
E value
                   2.0e-30
Match length
                   136
% identity
                   48
                   MIS5 PROTEIN >gi_829086_dbj_BAA06729_ (D31960) unknown
NCBI Description
                   [Schizosaccharomyces pombe]
Seq. No.
                   14653
                   32243_1.R1040
Contig ID
                   uC-gmflminsoy053d04b1
5'-most EST
                   BLASTX
Method
                   g2827158
NCBI GI
                   251
BLAST score
E value
                   7.0e-21
Match length
                   224
                   30
% identity
                   (AF032666) rsec5 [Rattus norvegicus]
NCBI Description
                   14654
Seq. No.
                   32247 1.R1040
Contig ID
                   LIB3139-016-P1-N1-C3
5'-most EST
                   BLASTX
Method
                   g2462832
NCBI GI
                   453
BLAST score
                   6.0e-45
E value
                   134
Match length
% identity
                   63
                   (AF000657) similar to Bacillus CotA [Arabidopsis thaliana]
NCBI Description
                   14655
Seq. No.
                   32248 1.R1040
Contig ID
                   jex70\overline{0}908410.h1
5'-most EST
                   BLASTX
Method
                   q2668492
NCBI GI
BLAST score
                   192
                    2.0e-14
E value
Match length
                    64
                    55
 % identity
```

NCBI Description

(D89981) metal-transporting P-type ATPase [Arabidopsis

thaliana]

Seq. No. 14656

Contig ID 32248\_2.R1040



LIB3093-035-Q1-K1-D2 5'-most EST BLASTX Method g2668492 NCBI GI 509 BLAST score 2.0e-51E value 202 Match length 52 % identity (D89981) metal-transporting P-type ATPase [Arabidopsis NCBI Description thaliana] 14657 Seq. No. 32253 1.R1040 Contig ID eep700864802.hl 5'-most EST Seq. No. 14658 32261 1.R1040 Contig ID LIB3107-060-Q1-K1-D1 5'-most EST BLASTX Method g1532163 NCBI GI 225 BLAST score 3.0e-18 E value 91 Match length 48 % identity (U63815) similar to glutaredoxin encoded by GenBank NCBI Description Accession Number Z49699; localized according to blastn similarity to EST sequences; therefore, the coding span corresponds only to an area of similarity since the initation codon and stop c 14659 Seq. No. 32261 2.R1040 Contig ID  $eep70\overline{0}867748.h1$ 5'-most EST 14660 Seq. No. 32280 1.R1040 Contig ID 5'-most EST LIB3055-010-Q1-N1-F4 14661 Seq. No. Contig ID 32282 1.R1040  $q5606\overline{2}54$ 5'-most EST BLASTX Method q4538911 NCBI GI 339 BLAST score E value 1.0e-31 Match length 113 58 % identity NCBI Description (AL049482) hypothetical protein [Arabidopsis thaliana] Seq. No. 14662 32282 2.R1040 Contig ID LIB3055-010-Q1-N1-C2 5'-most EST BLASTX Method

Method BLASTX
NCBI GI 94538911
BLAST score 345
E value 7.0e-37
Match length 152
% identity 56



NCBI Description (AL049482) hypothetical protein [Arabidopsis thaliana]

14663 Seq. No.

32283 1.R1040 Contig ID g5753386 5'-most EST

14664 Seq. No.

32284 1.R1040 Contig ID uC-gmropic063g12b1 5'-most EST

Method BLASTX g3292824 NCBI GI 734 BLAST score 3.0e-81 E value 225 Match length % identity 75

(AL031018) putative protein [Arabidopsis thaliana] NCBI Description

14665 Seq. No.

32287 1.R1040 Contig ID

LIB3055-010-Q1-N1-C9 5'-most EST

14666 Seq. No.

32292 1.R1040 Contig ID dpv701101032.hl 5'-most EST

14667 Seq. No.

32294 1.R1040 Contig ID

LIB3055-010-Q1-N1-D5 5'-most EST

BLASTX Method g2980789 NCBI GI 379 BLAST score 3.0e-43E value 204 Match length

50 % identity

NCBI Description (AL022197) hypothetical protein [Arabidopsis thaliana]

14668 Seq. No.

32302 1.R1040 Contig ID

LIB3055-010-Q1-N1-A8 5'-most EST

14669 Seq. No.

32308 1.R1040 Contig ID fC-gmle700559641f2 5'-most EST

BLASTX Method NCBI GI g1432058 377 BLAST score 3.0e-36 E value 141 Match length % identity

(U58540) WRKY2 [Petroselinum crispum] NCBI Description

Seq. No. 14670

32312 1.R1040 Contig ID g5688<del>3</del>98 5'-most EST Method BLASTX g2213643 NCBI GI 244 BLAST score



E value 1.0e-20 Match length 70 % identity 67

NCBI Description (U57338) glossyl homolog [Oryza sativa]

Seq. No. 14671

Contig ID 32322\_1.R1040 5'-most EST zzp700834168.h1

Method BLASTN
NCBI GI g3249564
BLAST score 198
E value 1.0e-107
Match length 610
% identity 83

NCBI Description Vernicia fordii aquaporin mRNA, complete cds

Seq. No.

14672

Contig ID

32322 2.R1040

5'-most EST

LIB3170-013-Q1-J1-D3

Method BLASTN
NCBI GI g3249564
BLAST score 93
E value 1.0e-44
Match length 189
% identity 87

NCBI Description Vernicia fordii aquaporin mRNA, complete cds

Seq. No. 14673

Contig ID 32322\_4.R1040
5'-most EST g4292371
Method BLASTN
NCBI GI g3249564
BLAST score 54
E value 2.0e-21

E value 2.06
Match length 106
% identity 88

NCBI Description Vernicia fordii aquaporin mRNA, complete cds

Seq. No. 14674

32331 1.R1040 Contig ID 5'-most EST g5666629 Method BLASTX NCBI GI g2739375 BLAST score 217 E value 3.0e-17 Match length 98 % identity 53

NCBI Description (AC002505) unknown protein [Arabidopsis thaliana]

Seq. No. 14675

Contig ID 32335\_2.R1040 5'-most EST zhf700956364.h1

Method BLASTX
NCBI GI g4263791
BLAST score 1912
E value 0.0e+00
Match length 490

% identity (AC006068) putative receptor protein kinase [Arabidopsis NCBI Description thaliana] 14676 Seq. No. Contig ID 32341 1.R1040  $k1170\overline{1}207087.h1$ 5'-most EST Seq. No. 14677 32343 1.R1040 Contig ID LIB3055-009-Q1-N1-G10 5'-most EST Method BLASTX NCBI GI g1666171 BLAST score 420 E value 4.0e-43 Match length 108 % identity NCBI Description (Y09105) unknown [Nicotiana plumbaginifolia] 14678

 Seq. No.
 14678

 Contig ID
 32344\_1.R1040

 5'-most EST
 g5678164

 Method
 BLASTX

 NCBI GI
 g1001355

 BLAST score
 163

 E value
 6.0e-11

Match length 86 % identity 37

NCBI Description (D64006) auxin-induced protein [Synechocystis sp.]

Seq. No. 14679

Contig ID 32346\_1.R1040 5'-most EST jex700905235.h1

Seq. No. 14680

Contig ID 32350\_1.R1040

5'-most EST LIB3106-115-Q1-K1-D3

Method BLASTX
NCBI GI g3046696
BLAST score 660
E value 2.0e-69
Match length 167
% identity 72

NCBI Description (AL022224) CTP synthase like protein [Arabidopsis thaliana]

Seq. No. 14681

Contig ID 32352 1.R1040

5'-most EST LIB3 $\overline{0}6-062-Q1-K1-E7$ 

Seq. No. 14682

Contig ID 32352 2.R1040

5'-most EST LIB3055-009-Q1-N1-D2

Seq. No. 14683

Contig ID 32355\_1.R1040 5'-most EST fde700874312.h1

Method BLASTX



NCBI GI g399307 BLAST score 462 E value 1.0e-45 Match length 143 % identity 62

NCBI Description PRENYL TRANSFERASE >gi\_99282\_pir\_A40433 prephytoene pyrophosphatase dehydrogenase (crtE) homolog - Cyanophora paradoxa >gi\_336639 (M37111) prephytoene pyrophosphate dehydrogenase [Cyanophora paradoxa] >gi\_1016130 (U30821)

prenyl transferase [Cyanophora paradoxa]

Seq. No. 14684

Contig ID 32355\_3.R1040

5'-most EST LIB3138-035-Q1-N1-G9

Seq. No. 14685

Contig ID 32360\_1.R1040 5'-most EST wvk700686689.h1

Seq. No. 14686

Contig ID 32364\_1.R1040

5'-most EST LIB3055-010-Q1-N1-E9

Seq. No. 14687

Contig ID 32367\_1.R1040 5'-most EST ssr700554673.h1

Method BLASTX
NCBI GI g3402713
BLAST score 273
E value 5.0e-24
Match length 128
% identity 52

NCBI Description (AC004261) hypothetical protein [Arabidopsis thaliana]

Seq. No. 14688

Contig ID 32370\_1.R1040 5'-most EST asn701141520.h1

Seq. No. 14689

Contig ID 32376\_1.R1040 5'-most EST wvk700680051.h2

Method BLASTX
NCBI GI g3929647
BLAST score 509
E value 1.0e-51
Match length 134
% identity 73

NCBI Description (AJ004881) Immutans protein [Arabidopsis thaliana]

Seq. No. 14690

Contig ID 32377\_1.R1040 5'-most EST leu701149695.h1

Seq. No. 14691

Contig ID 32391\_1.R1040 5'-most EST leu701145466.h1



```
14692
Seq. No.
                  32393 1.R1040
Contig ID
                  LIB3092-050-Q1-K1-A2
5'-most EST
                  BLASTX
Method
                  q4559334
NCBI GI
                  935
BLAST score
                  1.0e-103
E value
                  253
Match length
% identity
                  (AC007087) unknown protein [Arabidopsis thaliana]
NCBI Description
                   14693
Seq. No.
                   32400 1.R1040
Contig ID
                  LIB3139-118-P1-N1-E9
5'-most EST
                  BLASTX
Method
                  g2244910
NCBI GI
                   172
BLAST score
                   3.0e-12
E value
                   61
Match length
                   52
% identity
                  (Z97339) unnamed protein product [Arabidopsis thaliana]
NCBI Description
                   14694
Seq. No.
                   32400 2.R1040
Contig ID
                   LIB3107-032-Q1-K1-A3
5'-most EST
                   BLASTX
Method
                   g2244910
NCBI GI
                   186
BLAST score
                   7.0e-14
E value
                   68
Match length
                   53
% identity
                  (Z97339) unnamed protein product [Arabidopsis thaliana]
NCBI Description
                   14695
Seq. No.
                   32402 1.R1040
Contig ID
                   pcp700991340.hl
5'-most EST
                   BLASTX
Method
                   a1075616
NCBI GI
                   490
BLAST score
                   3.0e-49
E value
                   257
Match length
 % identity
                   carboxyl-terminal processing proteinase precursor -
NCBI Description
                   Synechocystis sp. (PCC 6803) >gi_493215 (L25250) protease
                    [Synechocystis sp.] >gi_1001562_dbj_BAA10189_ (D64000)
                   carboxyl-terminal processing protease [Synechocystis sp.]
                   14696
 Seq. No.
                    32404 1.R1040
 Contig ID
```

bth700847129.h1 5'-most EST

14697 Seq. No.

32406 1.R1040 Contig ID uaw700666865.hl 5'-most EST

Method BLASTX g3096945 NCBI GI 370 BLAST score



E value 2.0e-35
Match length 98
% identity 73

NCBI Description (AL023094) putative auxin-regulated protein [Arabidopsis

thaliana]

Seq. No. 14698

Contig ID 32409 1.R1040

5'-most EST jC-gmle01810080b11a1

Method BLASTX
NCBI GI g2262105
BLAST score 578
E value 1.0e-59
Match length 138
% identity 75

NCBI Description (AC002343) unknown protein [Arabidopsis thaliana]

Seq. No. 14699

Contig ID 32410 1.R1040 5'-most EST gsv701047902.h1

Method BLASTX
NCBI GI g1336084
BLAST score 610
E value 1.0e-63
Match length 123
% identity 91

NCBI Description (U56635) Arabidopsis thaliana glutamate dehydrogenase 2

(GDH2) mRNA, complete cds. [Arabidopsis thaliana]

Seq. No. 14700

Contig ID 32411 1.R1040

5'-most EST LIB3055-008-Q1-N1-H11

Method BLASTX
NCBI GI g3600054
BLAST score 405
E value 1.0e-39
Match length 129
% identity 56

NCBI Description (AF080120) No definition line found [Arabidopsis thaliana]

Seq. No. 14701

Contig ID 32413 1.R1040

5'-most EST LIB3055-008-Q1-N1-H2

Method BLASTX
NCBI GI g1419090
BLAST score 1072
E value 1.0e-125
Match length 296
% identity 74

NCBI Description (X94968) 37kDa chloroplast inner envelope membrane

polypeptide precursor [Nicotiana tabacum]

Seq. No. 14702

Contig ID 32415\_1.R1040

5'-most EST LIB3073-019-Q1-K1-D11

Method BLASTX NCBI GI g1173194



BLAST score 4.0e-55 E value Match length 161 % identity 56 NCBI Description

30S RIBOSOMAL PROTEIN S13, CHLOROPLAST PRECURSOR (CS13) >gi\_2119093\_pir\_\_S59594 ribosomal protein S13 precursor, chloroplast - Arabidopsis thaliana >gi\_16767\_emb\_CAA79013 (Z17611) chloroplast 30S ribosomal protein S13 [Arabidopsis thaliana] >gi\_662869 emb\_CAA88028\_ (Z47986) chloroplast ribosomal protein S13 [Arabidopsis thaliana]

>gi\_1107483\_emb\_CAA63021\_ (X91955) 30S ribosomal protein
S13 [Arabidopsis thaliana] >gi\_1515107\_emb\_CAA60413\_ (X86734) plastid ribosomal protein S13 [Arabidopsis]

thaliana]

Seq. No. 14703

Contig ID 32418 1.R1040

5'-most EST LIB3170-065-Q1-K1-D6

Method BLASTX NCBI GI q2827633 BLAST score 152 E value 1.0e-09 Match length 135 % identity 36

NCBI Description (AL021636) putative protein [Arabidopsis thaliana]

Seq. No. 14704

Contig ID 32433 1.R1040 rca700997242.h1 5'-most EST

Method BLASTN q3769670 NCBI GI BLAST score 197 E value 1.0e-106 Match length 613 % identity 84

NCBI Description Pisum sativum Tic22 mRNA, nuclear mRNA encoding chloroplast

protein, complete cds

14705 Seq. No.

Contig ID 32435 1.R1040 5'-most EST V4R-01-Q1-B1-A3

Seq. No. 14706

Contig ID 32442 1.R1040

5'-most EST LIB3055-008-Q1-N1-D6

Method BLASTX NCBI GI g1946368 BLAST score 522 E value 2.0e-65 Match length 190 % identity 72

NCBI Description (U93215) unknown protein [Arabidopsis thaliana]

Seq. No. 14707

Contig ID 32444 1.R1040

5'-most EST uC-gmrominsoy058g09b1

Method BLASTX



```
NCBI GI g4559334
BLAST score 361
E value 2.0e-34
Match length 92
% identity 72
```

NCBI Description (AC007087) unknown protein [Arabidopsis thaliana]

Seq. No. 14708

Contig ID 32444\_2.R1040 5'-most EST fua701041086.h1

Seq. No. 14709

Contig ID 32453 1.R1040

5'-most EST LIB3055-008-Q1-N1-B5

Seq. No. 14710

Contig ID 32456\_1.R1040 5'-most EST zsg701130491.h1

Seq. No. 14711

Contig ID 32462\_1.R1040 5'-most EST kl1701213091.h1

Seq. No. 14712

Contig ID 32463\_1.R1040 5'-most EST jex700903487.h1

Method BLASTX
NCBI GI 93600060
BLAST score 194
E value 1.0e-14
Match length 96
% identity 36

NCBI Description (AF080120) contains similarity to protein kinases (Pfam:

pkinase.hmm, score: 24.94) [Arabidopsis thaliana]

Seq. No. 14713

Contig ID 32468 1.R1040

5'-most EST LIB3055-008-Q1-N1-A10

Seq. No. 14714

Contig ID 32469 1.R1040

5'-most EST LIB3055-008-Q1-N1-A12

Seq. No. 14715

Contig ID 32469\_2.R1040 5'-most EST dpv701100435.h1

Method BLASTX
NCBI GI 94467153
BLAST score 379
E value 3.0e-36
Match length 96
% identity 71

NCBI Description (AL035540) putative thaumatin-like protein [Arabidopsis

thaliana]

Seq. No. 14716

Contig ID 32470 1.R1040



```
uaw700664369.h1
5'-most EST
                   BLASTX
Method
                   a3033384
NCBI GI
                   945
BLAST score
                   1.0e-102
E value
                   256
Match length
                   72
% identity
NCBI Description (AC004238) putative CTP synthase [Arabidopsis thaliana]
                   14717
Seq. No.
                   32473 1.R1040
Contig ID
                   leu701152944.h1
5'-most EST
                   BLASTX
Method
                   q4539003
NCBI GI
                   160
BLAST score
                   8.0e-11
E value
                   106
Match length
                   39
% identity
NCBI Description (AL049481) putative protein [Arabidopsis thaliana]
                   14718
Seq. No.
                   32475 1.R1040
Contig ID
                   jC-gmst02400014a09a1
5'-most EST
Seq. No.
                   14719
                   32488 1.R1040
Contig ID
                   uC-gmrominsoy317h12b1
5'-most EST
                   14720
 Seq. No.
                   32495 1.R1040
Contig ID
                   jC-gmro02910064e02a1
5'-most EST
                   BLASTX
Method
                   q1669341
NCBI GI
 BLAST score
                   543
                   2.0e-55
 E value
 Match length
                   203
% identity
                   53
                   (D45066) AOBP (ascorbate oxidase promoter-binding protein)
NCBI Description
                    [Cucurbita maxima]
                    14721
 Seq. No.
                    32500 1.R1040
 Contig ID
                   LIB3056-010-Q1-N1-F8
 5'-most EST
 Method
                   BLASTX
                    g1711517
 NCBI GI
 BLAST score
                    176
                    1.0e-12
 E value
```

96 Match length 38 % identity

SIGNAL RECOGNITION PARTICLE 72 KD PROTEIN (SRP72) NCBI Description >gi 508584 (L32975) signal recognition particle 72 kDa

subunit [Schistosoma mansoni]

14722 Seq. No.

32501 1.R1040 Contig ID jex700905731.hl 5'-most EST

BLASTN Method



```
g169362
      NCBI GI
                        98
      BLAST score
                        2.0e-47
      E value
      Match length
                        256
      % identity
                        90
      NCBI Description P.vulgaris PVPR3 protein mRNA, complete cds
                        14723
      Seq. No.
                        32503 1.R1040
      Contig ID
                        jC-gmf102220058f02a1
      5'-most EST
                         14724
      Seq. No.
                         32503 2.R1040
      Contig ID
                        pmv700892679.h1
      5'-most EST
      Seq. No.
                         14725
                         32515 1.R1040
      Contig ID
                         fde700871335.hl
      5'-most EST
                         BLASTX
      Method
                         q2911078
      NCBI GI
      BLAST score
                         181
                         3.0e-13
      E value
                         86
      Match length
                         49
      % identity
      NCBI Description (AL021960) putative protein [Arabidopsis thaliana]
                         14726
      Seq. No.
                         32527 1.R1040
      Contig ID
                         LIB3055-007-Q1-N1-B8
      5'-most EST
                         14727
      Seq. No.
                         32528 1.R1040
      Contig ID
                         vzy70\overline{0}752957.h1
      5'-most EST
                         BLASTX
      Method
                         g4559339
      NCBI GI
                         879
      BLAST score
                         1.0e-179
E value
                         473
      Match length
      % identity
                         (AC007087) putative ATP-dependent RNA helicase [Arabidopsis
      NCBI Description
                         thaliana]
                         14728
     Seq. No.
                         32534 1.R1040
       Contig ID
                         LIB3055-007-Q1-N1-C3
       5'-most EST
                         BLASTX
      Method
                         g3980396
       NCBI GI
                         474
       BLAST score
       E value
                         1.0e-47
                         114
       Match length
```

% identity 75

(AC004561) putative C-4 sterol methyl oxidase [Arabidopsis NCBI Description

thaliana]

14729 Seq. No.

32535 1.R1040 Contig ID

LIB3055-007-Q1-N1-C4 5'-most EST

NCBI Description

```
14730
Seq. No.
                   32538 1.R1040
Contig ID
                   ncj70\overline{0}978173.h1
5'-most EST
                   BLASTX
Method
                   g3702327
NCBI GI
BLAST score
                   315
                   7.0e-29
E value
                   107
Match length
                   50
% identity
NCBI Description (AC005397) unknown protein [Arabidopsis thaliana]
                   14731
Seq. No.
                   32542 1.R1040
Contig ID
                   ssr700558945.h1
5'-most EST
                   BLASTX
Method
                   g4049341
NCBI GI
                   652
BLAST score
                   3.0e-68
E value
                   145
Match length
                   86
% identity
                   (AL034567) putative protein [Arabidopsis thaliana]
NCBI Description
                   14732
Seq. No.
                   32542 2.R1040
Contig ID
                   uaw700665979.h1
5'-most EST
                   BLASTN
Method
                   q4049332
NCBI GI
                   38
BLAST score
                   4.0e-12
E value
                   70
Match length
                   89
% identity
                   Arabidopsis thaliana DNA chromosome 4, BAC clone F8B4
NCBI Description
                    (ESSAII project)
                   14733
Seq. No.
                   32547 1.R1040
Contig ID
                   epx701108149.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q2832700
BLAST score
                   142
                   1.0e-08
E value
                    95
Match length
                    42
% identity
                   (AL021713) unknown protein [Arabidopsis thaliana]
NCBI Description
                    14734
Seq. No.
                    32548 1.R1040
Contig ID
                   ncj70\overline{0}988084.h1
5'-most EST
Method
                   BLASTX
                    g3298538
NCBI GI
                    326
BLAST score
                    4.0e-30
E value
                    95
Match length
 % identity
                    65
```

(AC004681) hypothetical protein [Arabidopsis thaliana]



```
14735
Seq. No.
                  32548 2.R1040
Contig ID
                  wrg70\overline{0}786122.h2
5'-most EST
                  14736
Seq. No.
                  32554 1.R1040
Contig ID
                  vwf700674436.h1
5'-most EST
                  BLASTX
Method
                  g2764941
NCBI GI
                  392
BLAST score
                   7.0e-38
E value
                   91
Match length
                   74
% identity
                   (X98255) transcriptionally stimulated by gibberellins;
NCBI Description
                   expressed in meristematic region, and style [Arabidopsis
                   thaliana]
                   14737
Seq. No.
                   32556 1.R1040
Contig ID
                   pxt700944130.h1
5'-most EST
                   BLASTX
Method
                   g3335362
NCBI GI
                   160
BLAST score
                   1.0e-10
E value
Match length
                   65
                   52
% identity
                   (AC003028) putative ribosomal protein S31 [Arabidopsis
NCBI Description
                   thaliana]
                   14738
Seq. No.
                   32575 1.R1040
Contig ID
5'-most EST
                   LIB3055-007-Q1-N1-A12
                   14739
Seq. No.
                   32585 1.R1040
Contig ID
5'-most EST
                   LIB3138-002-Q1-N1-F8
Method
                   BLASTX
                   q3395439
NCBI GI
BLAST score
                   245
                   2.0e-20
E value
                   74
Match length
                   66
% identity
                   (AC004683) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   14740
Seq. No.
                   32585 2.R1040
Contig ID
                   LIB3107-008-Q1-K1-B2
5'-most EST
                   14741
Seq. No.
                   32590 1.R1040
Contig ID
                   uC-gmrominsoy210f11b1
5'-most EST
                   BLASTX
Method
                   g2649345
NCBI GI
                   439
BLAST score
                   3.0e-43
E value
```

132

58

Match length

% identity

(AE001019) tryptophan synthase, subunit beta (trpB-1) NCBI Description [Archaeoglobus fulgidus] 14742 Seq. No. 32591 1.R1040 Contig ID jex700904323.h1 5'-most EST BLASTX Method g4469008 NCBI GI BLAST score 382 7.0e-37 E value 126 Match length 53 % identity (AL035602) UDP rhamnose--anthocyanidin-3-glucoside NCBI Description rhamnosyltransferase-like protein [Arabidopsis thaliana] 14743 Seq. No. 32593 1.R1040 Contig ID LIB3055-006-Q1-N1-D4 5'-most EST 14744 Seq. No. 32597 1.R1040 Contig ID LIB3055-006-Q1-N1-D9 5'-most EST BLASTX Method g2947063 NCBI GI BLAST score 342 6.0e-32 E value 191 Match length 43 % identity (AC002521) putative Ser/Thr protein kinase [Arabidopsis NCBI Description thaliana] 14745 Seq. No. 32602 1.R1040 Contig ID 5'-most EST fC-qmse700676135f2 BLASTX Method NCBI GI q4544473 BLAST score 503 6.0e-51 E value 157 Match length % identity 42 NCBI Description (AC006580) putative mei2 protein [Arabidopsis thaliana] 14746 Seq. No. 32608 1.R1040 Contig ID

txt700734859.h1 5'-most EST

BLASTX Method NCBI GI g3334133 BLAST score 245 1.0e-20 E value Match length 93 53 % identity

NCBI Description CYTOCHROME P450 89A2 (CYPLXXXIX) (ATH 6-1) >gi\_1432145

(U61231) cytochrome P450 [Arabidopsis thaliana]

Seq. No.

32612 1.R1040 Contig ID

5'-most EST LIB3109-018-Q1-K1-C3



Method BLASTX
NCBI GI g2736147
BLAST score 581
E value 6.0e-60
Match length 149
% identity 66

NCBI Description (AF021804) fatty acid hydroxylase Fahlp [Arabidopsis thaliana] >gi\_3132481 (AC003096) fatty acid hydroxylase,

FAH1 [Arabidopsis thaliana]

Seq. No. 14748

Contig ID 32612\_2.R1040

5'-most EST jC-gmf102220053g02a1

Method BLASTX
NCBI GI g2736147
BLAST score 325
E value 4.0e-30
Match length 101
% identity 57

NCBI Description (AF021804) fatty acid hydroxylase Fahlp [Arabidopsis

thaliana] >gi\_3132481 (AC003096) fatty acid hydroxylase,

FAH1 [Arabidopsis thaliana]

Seq. No. 14749

Contig ID 32617\_1.R1040

5'-most EST LIB3139-118-P1-N1-G5

Method BLASTX
NCBI GI g2554767
BLAST score 472
E value 4.0e-47
Match length 173
% identity 50

NCBI Description Chain A, EndoEXOCELLULASE: CELLOBIOSE FROM THERMOMONOSPORA

>gi\_2554768\_pdb\_1JS4\_B Chain B, EndoEXOCELLULASE:CELLOBIOSE
FROM THERMOMONOSPORA >gi\_2554821\_pdb\_4TF4\_A Chain A,

EndoEXOCELLULASE: CELLOPENTAOSE FROM THERMOMONOSPORA

>gi\_2554822\_pdb\_4TF4\_B Chain B,

EndoEXOCELLULASE: CELLOPENTAOSE FROM THERMOMONOSPORA

>gi\_2554825\_pdb\_3TF4\_A Chain A,

EndoEXOCELLULASE: CELLOTRIOSE FROM THERMOMONOSPORA

>gi\_2554826\_pdb\_3TF4\_B Chain B,

EndoEXOCELLULASE: CELLOTRIOSE FROM THERMOMONOSPORA >gi\_2554833\_pdb\_1TF4\_A Chain A, EndoEXOCELLULASE FROM

THERMOMONOSPORA >gi 2554834 pdb 1TF4 B Chain B,

EndoEXOCELLULASE FROM THERMOMONOSPORA

Seq. No. 14750

Contig ID 32619\_1.R1040

5'-most EST LIB3055-006-Q1-N1-C9 Method BLASTX

NCBI GI g629592
BLAST score 231
E value 4.0e-19

Match length 91 % identity 47

NCBI Description hypothetical protein - rape



```
Seq. No. 14751
```

Contig ID 32627\_1.R1040

5'-most EST LIB3167-023-P4-K4-B1

Method BLASTX
NCBI GI g3064039
BLAST score 299
E value 9.0e-27
Match length 142
% identity 38

NCBI Description (AF054445) major latex protein homolog [Mesembryanthemum

crystallinum]

Seq. No. 14752

Contig ID 32632\_1.R1040 5'-most EST zhf700954645.h1

Method BLASTX
NCBI GI g2065019
BLAST score 499
E value 3.0e-50
Match length 210
% identity 30

NCBI Description (Y09823) hypothetical protein [Arabidopsis thaliana]

Seq. No. 14753

Contig ID 32632\_2.R1040

5'-most EST LIB3107-041-Q1-K1-C1

Seq. No. 14754

Contig ID 32634\_1.R1040

5'-most EST LIB30 $\overline{9}$ 3-033-Q1-K1-B4

Method BLASTX
NCBI GI g3885328
BLAST score 688
E value 2.0e-72
Match length 175
% identity 71

NCBI Description (AC005623) putative serine/threonine protein kinase

[Arabidopsis thaliana]

Seq. No. 14755

Contig ID 32634\_2.R1040

5'-most EST uC-gmrominsoy192c07b1

Method BLASTX
NCBI GI g3885328
BLAST score 436
E value 5.0e-43
Match length 118
% identity 66

NCBI Description (AC005623) putative serine/threonine protein kinase

[Arabidopsis thaliana]

Seq. No. 14756

Contig ID 32638\_1.R1040 5'-most EST smc700749117.h1

Seq. No. 14757

Contig ID 32640\_1.R1040



uC-gmrominsoy144c11b1 5'-most EST BLASTX Method g4185141 NCBI GI 837 BLAST score 1.0e-89 E value 334 Match length % identity 51 (AC005724) putative calmodulin-binding protein [Arabidopsis NCBI Description thaliana] 14758 Seq. No. 32640\_2.R1040 Contig ID V4L-01-Q1-B1-C4 5'-most EST Seq. No. 14759 32640 3.R1040 Contig ID LIB3055-006-Q1-N1-B5 5'-most EST 14760 Seq. No. 32640 4.R1040 Contig ID LIB3139-083-P1-N1-D1 5'-most EST BLASTX Method g4539298 NCBI GI 188 BLAST score 4.0e-14 E value 78 Match length 44 % identity (AL049480) putative calmodulin-binding protein [Arabidopsis NCBI Description thaliana] 14761 Seq. No. 32643 1.R1040 Contig ID zzp700833726.h1 5'-most EST Method BLASTX q3493647 NCBI GI BLAST score 447 E value 5.0e-44109 Match length % identity (AF082531) transcription activator [Pimpinella brachycarpa] NCBI Description 14762 Seq. No. 32643 2.R1040 Contig ID 5'-most EST wvk700686419.h1 Method BLASTN g3493646 NCBI GI BLAST score 85 7.0e-40 E value 209 Match length % identity 85 Pimpinella brachycarpa transcription activator (MADS1) NCBI Description

mRNA, complete cds 14763

Seq. No.

32649 1.R1040 Contig ID

uC-gmrominsoy067d07b1 5'-most EST

% identity

NCBI Description

60



```
Seq. No.
                  32650 1.R1040
Contig ID
                  LIB3055-005-Q1-N1-H12
5'-most EST
                  14765
Seq. No.
                   32653 1.R1040
Contig ID
                  LIB3055-005-Q1-N1-H5
5'-most EST
                   14766
Seq. No.
                   32659 1.R1040
Contig ID
                   uC-gmrominsoy243d04b1
5'-most EST
                   14767
Seq. No.
                   32667 1.R1040
Contig ID
                   g4290475
5'-most EST
                   BLASTX
Method
                   q1706958
NCBI GI
                   2117
BLAST score
                   0.0e + 00
E value
                   686
Match length
                   79
% identity
                   (U58284) cellulose synthase [Gossypium hirsutum]
NCBI Description
                   14768
Seq. No.
                   32667 2.R1040
Contig ID
                   jC-gmst02400049a06a1
5'-most EST
                   BLASTN
Method
                   q3511284
NCBI GI
                   66
BLAST score
                   1.0e-28
E value
                   98
Match length
                   92
% identity
                   Populus alba x Populus tremula cellulose synthase (cell)
NCBI Description
                   mRNA, complete cds
                   14769
Seq. No.
                   32668 1.R1040
Contig ID
                   LIB3055-005-Q1-N1-F7
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3367596
                   581
BLAST score
                   6.0e-60
E value
                   237
Match length
 % identity
                   54
                   (AL031135) putative protein [Arabidopsis thaliana]
NCBI Description
 Seq. No.
                    14770
                    32670 1.R1040
 Contig ID
                    zhf700960460.h1
 5'-most EST
 Method
                   BLASTX
                    q4263821
 NCBI GI
                    412
 BLAST score
                    1.0e-69
 E value
                    243
 Match length
```

(AC006067) hypothetical protein [Arabidopsis thaliana]



```
14771
Seq. No.
                  32670 2.R1040
Contig ID
                  crh700852078.hl
5'-most EST
Method
                  BLASTX
                  q4263821
NCBI GI
                  211
BLAST score
                  1.0e-16
E value
                  91
Match length
% identity
                  (AC006067) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  14772
Seq. No.
                   32670 3.R1040
Contig ID
                   k11701206680.h1
5'-most EST
Method
                  BLASTX
                   g4263821
NCBI GI
BLAST score
                   216
                   2.0e-17
E value
                   83
Match length
                   58
% identity
NCBI Description (AC006067) hypothetical protein [Arabidopsis thaliana]
                   14773
Seq. No.
                   32672 1.R1040
Contig ID
                   zhf700958224.h1
5'-most EST
                   BLASTX
Method
                   g2789660
NCBI GI
                   1086
BLAST score
                   1.0e-119
E value
                   261
Match length
                   77
% identity
                  (AF040102) p105 [Arabidopsis thaliana]
NCBI Description
                   14774
Seq. No.
                   32675 1.R1040
Contig ID
5'-most EST
                   jex700905955.hl
                   14775
Seq. No.
                   32677 1.R1040
Contig ID
5'-most EST
                   LIB3055-005-Q1-N1-F1
                   14776
Seq. No.
                   32682 1.R1040
Contig ID
                   pxt700943519.hl
5'-most EST
Method
                   BLASTX
                   q2809246
NCBI GI
                   499
BLAST score
                   3.0e-50
E value
Match length
                   143
                   64
 % identity
                   (AC002560) F2401.15 [Arabidopsis thaliana]
NCBI Description
                   14777
 Seq. No.
```

32687 1.R1040 Contig ID

LIB3055-005-Q1-N1-E4 5'-most EST

14778 Seq. No.



Contig ID 32691\_1.R1040 5'-most EST LIB3092-047-Q1-K1-B3

Seq. No. 14779

Contig ID 32691\_2.R1040

5'-most EST LIB $30\overline{5}6-001-Q1-B1-B10$ 

Seq. No. 14780

Contig ID 32698\_1.R1040

5'-most EST LIB3055-005-Q1-N1-C4

Method BLASTX
NCBI GI g1362005
BLAST score 306
E value 8.0e-28
Match length 159
% identity 48

NCBI Description secY protein homolog precursor - Arabidopsis thaliana

Seq. No. 14781

Contig ID 32702 1.R1040

5'-most EST LIB3055-005-Q1-N1-C9

Seq. No. 14782

Contig ID 32702\_2.R1040 5'-most EST fde700870680.h1

Seq. No. 14783

Contig ID 32703\_1.R1040 5'-most EST rlr700897822.h1

Method BLASTX
NCBI GI g2315451
BLAST score 229
E value 2.0e-18
Match length 144
% identity 30

NCBI Description (AF016448) No definition line found [Caenorhabditis

elegans]

Seq. No. 14784

Contig ID 32704\_1.R1040 5'-most EST taw700655703.h1

Method BLASTX
NCBI GI g1001430
BLAST score 184
E value 2.0e-13
Match length 103
% identity 39

NCBI Description (D63999) ORF1 [Synechocystis sp.]

Seq. No. 14785

Contig ID 32706\_1.R1040 5'-most EST asn701141076.h1

Method BLASTX
NCBI GI g4093157
BLAST score 443
E value 2.0e-43
Match length 228



```
% identity
                   (AF087936) phytochrome-associated protein 2 [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   14786
                   32706 2.R1040
Contig ID
                   rrt700645990.h1
5'-most EST
                   BLASTX
Method
                   q4093157
NCBI GI
BLAST score
                   336
E value
                   8.0e-42
Match length
                   245
% identity
                   (AF087936) phytochrome-associated protein 2 [Arabidopsis
NCBI Description
                   thaliana]
                   14787
Seq. No.
                   32708 1.R1040
Contig ID
                   uC-gmrominsoy210b08b1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3176686
BLAST score
                   891
                   3.0e-96
E value
Match length
                   208
% identity
                   76
                   (AC003671) Similar to high affinity potassium transporter,
NCBI Description
                   HAK1 protein gb_U22945 from Schwanniomyces occidentalis.
                   [Arabidopsis thaliana]
                   14788
Seq. No.
                   32716 1.R1040
Contig ID
                   jex70\overline{0}909296.h1
5'-most EST
                   BLASTN
Method
                   g4164158
NCBI GI
                   265
BLAST score
                   1.0e-147
E value
                   701
Match length
                   84
% identity
NCBI Description Passiflora edulis mRNA for ethylene receptor, complete cds
                   14789
Seq. No.
                   32724 1.R1040
Contig ID
                   g4288<del>9</del>31
5'-most EST
                   14790
Seq. No.
                   32727 1.R1040
Contig ID
                   vwf700679653.hl
5'-most EST
```

BLASTX Method NCBI GI g1565225 754 BLAST score E value 8.0e-80 238 Match length % identity

NCBI Description

(X95572) salt-tolerance protein [Arabidopsis thaliana]

Seq. No.

14791

Contig ID

32727\_2.R1040



```
dpv701100333.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q1565225
BLAST score
                  582
E value
                  7.0e-60
                  164
Match length
                  71
% identity
                  (X95572) salt-tolerance protein [Arabidopsis thaliana]
NCBI Description
                  14792
Seq. No.
                   32727 3.R1040
Contig ID
                  LIB3139-119-P1-N1-H6
5'-most EST
                  BLASTX
Method
                   g1565225
NCBI GI
BLAST score
                   433
E value
                   1.0e-42
                   97
Match length
                   80
% identity
                  (X95572) salt-tolerance protein [Arabidopsis thaliana]
NCBI Description
                   14793
Seq. No.
                   32727 4.R1040
Contig ID
                   uC-gmflminsoy082e04b1
5'-most EST
                   BLASTX
Method
                   g1565225
NCBI GI
BLAST score
                   259
                   4.0e-22
E value
Match length
                   149
% identity
                   43
                   (X95572) salt-tolerance protein [Arabidopsis thaliana]
NCBI Description
                   14794
Seq. No.
                   32727 7.R1040
Contiq ID
                   zsg701120968.hl
5'-most EST
                   BLASTX
Method
                   g1565225
NCBI GI
                   197
BLAST score
                   3.0e-15
E value
                   39
Match length
                   87
 % identity
                   (X95572) salt-tolerance protein [Arabidopsis thaliana]
NCBI Description
                   14795
 Seq. No.
                   32731 1.R1040
 Contig ID
 5'-most EST
                   LIB3106-113-Q1-K1-A2
                   BLASTX
 Method
                   q508304
 NCBI GI
                    357
 BLAST score
 E value
                   2.0e-33
                   82
 Match length
                   76
```

% identity

(L22305) corC [Medicago sativa] NCBI Description

14796 Seq. No.

32738 1.R1040 Contig ID wrg700790321.h2 5'-most EST

BLASTX Method



```
q4056433
NCBI GI
BLAST score
                  447
                  3.0e-44
E value
                  188
Match length
% identity
                  (AC005990) Similar to anter-specific proline-rich protein
NCBI Description
                  (CEX) gb_X60376 from Brassica napus. [Arabidopsis thaliana]
                  14797
Seq. No.
                  32746 1.R1040
Contig ID
                  leu701154230.h1
5'-most EST
```

 Seq. No.
 14798

 Contig ID
 32747 1.R1040

 5'-most EST
 LIB3055-004-Q1-N1-F8

 Method
 BLASTX

 NCBI GI
 g130759

 BLAST score
 465

NCBI GI g130759
BLAST score 465
E value 1.0e-46
Match length 126
% identity 68

NCBI Description PROLYL ENDOPEPTIDASE (POST-PROLINE CLEAVING ENZYME) (PE) >gi\_108383 pir\_A37942 prolyl oligopeptidase (EC 3.4.21.26) - pig >gi\_164621 (M64227) prolyl endopeptidase [Sus scrofa]

 Seq. No.
 14799

 Contig ID
 32755\_1.R1040

 5'-most EST
 LIB3055-004-Q1-N1-G5

 Method
 BLASTX

 NCBI GI
 g4049399

NCBI GI g4049399 BLAST score 214 E value 4.0e-27 Match length 106 % identity 58

NCBI Description (Y09581) FRO2 [Arabidopsis thaliana]

 Seq. No.
 14800

 Contig ID
 32758\_1.R1040

 5'-most EST
 sat701003886.h1

Seq. No. 14801

Contig ID 32771 1.R1040 5'-most EST uC-gmflminsoy007h03b1

 Seq. No.
 14802

 Contig ID
 32771\_3.R1040

 5'-most EST
 kl1701206929.h1

Seq. No. 14803 Contig ID 32774\_1.R1040

5'-most EST jC-gmf102220068a09a1
Method BLASTX
NCBI GI g1055130
BLAST score 334
E value 6.0e-31
Match length 169

% identity 42



(U39998) coded for by C. elegans cDNA yk92b11.3; coded for NCBI Description by C. elegans cDNA yk92b11.5; coded for by C. elegans cDNA yk78c2.5; coded for by C. elegans cDNA cm9a8; coded for by C. elegans cDNA yk66h8.3; coded for by C. elegans cDNA yk78c2.3

14804 Seq. No.

32775 1.R1040 Contig ID

5'-most EST jC-gmle01810048h01a1

Method BLASTX g3757521 NCBI GI 188 BLAST score 6.0e-14 E value Match length 204

% identity

(AC005167) unknown protein [Arabidopsis thaliana] NCBI Description

14805 Seq. No.

32778 1.R1040 Contig ID wrg700791852.hl 5'-most EST

BLASTX Method g4427003 NCBI GI 1051 BLAST score E value 1.0e-114 Match length 283 73 % identity

(AF127664) NBD-like protein [Arabidopsis thaliana] NCBI Description

14806 Seq. No.

32789 1.R1040 Contig ID vwf700677874.h1 5'-most EST

14807 Seq. No.

Contig ID 32795 1.R1040 zhf700960263.h1 5'-most EST

Method BLASTX q4490297 NCBI GI 398 BLAST score E value 4.0e-38 Match length 255 37 % identity

(AL035678) putative protein [Arabidopsis thaliana] NCBI Description

Seq. No. 14808

32796 1.R1040 Contig ID

uC-gmrominsoy110a10b1 5'-most EST

Seq. No. 14809

32801 1.R1040 Contig ID

uC-qmflminsoy043g05b1 5'-most EST

BLASTX Method g4335745 NCBI GI BLAST score 475 1.0e-61 E value Match length 283 45 % identity

NCBI Description (AC006284) putative hydrolase (contains an

• .



esterase/lipase/thioesterase active site serine domain (prosite: PS50187) [Arabidopsis thaliana]

Seq. No. 14810

Contig ID 32801\_2.R1040 5'-most EST uaw700666674.h1

Method BLASTX
NCBI GI g4335745
BLAST score 167
E value 1.0e-11
Match length 71
% identity 44

NCBI Description (AC006284) putative hydrolase (contains an

esterase/lipase/thioesterase active site serine domain

(prosite: PS50187) [Arabidopsis thaliana]

Seq. No. 14811

Contig ID 32802 1.R1040

5'-most EST LIB3055-004-Q1-N1-A8

Method BLASTX
NCBI GI g2764941
BLAST score 370
E value 4.0e-35
Match length 98
% identity 62

NCBI Description (X98255) transcriptionally stimulated by gibberellins;

expressed in meristematic region, and style [Arabidopsis

thalianal

Seq. No. 14812

Contig ID 32805\_1.R1040 5'-most EST gsv70\overline{1}050070.h1

Method BLASTX
NCBI GI g3786006
BLAST score 451
E value 1.0e-44
Match length 152
% identity 61

NCBI Description (AC005499) hypothetical protein [Arabidopsis thaliana]

Seq. No. 14813

Contig ID 32805 2.R1040 5'-most EST fC-gmst700660978f1

Method BLASTX
NCBI GI g3786006
BLAST score 408
E value 6.0e-40
Match length 120
% identity 65

NCBI Description (AC005499) hypothetical protein [Arabidopsis thaliana]

Seq. No. 14814

Contig ID 32810\_1.R1040

5'-most EST LIB3055-003-Q1-N1-G4

Method BLASTX NCBI GI g4572671 BLAST score 523



E value 6.0e-53 Match length 277 % identity 40

NCBI Description (AC006954) putative cyclic nucleotide regulated ion channel

[Arabidopsis thaliana]

Seq. No. 14815

Contig ID 32817\_1.R1040 5'-most EST rca700999292.h1

Method BLASTN
NCBI GI g984307
BLAST score 59
E value 2.0e-24
Match length 91
% identity 89

NCBI Description Glycine max ribosomal protein S16 (rps16) gene, partial

cds, beta-carboxyltransferase (accD), photosystem I component (psaI), ORF 202 protein (ORF 203), ORF 151 protein (ORF 151), ORF 103 protein (ORF 103), ORF 229

precurso

Seq. No. 14816

Contig ID 32817\_2.R1040 5'-most EST wrg700792076.h1

Seq. No. 14817

Contig ID 32818\_1.R1040 5'-most EST vzy700756728.h1

Method BLASTX
NCBI GI g2505872
BLAST score 287
E value 1.0e-25
Match length 94
% identity 64

NCBI Description (Y12227) hypothetical protein [Arabidopsis thaliana]

Seq. No. 14818

Contig ID 32819\_1.R1040

5'-most EST LIB3109-022-Q1-K1-B10

Method BLASTX
NCBI GI g4539306
BLAST score 227
E value 1.0e-18
Match length 162
% identity 39

NCBI Description (AL049480) pumilio-like protein [Arabidopsis thaliana]

Seq. No. 14819

Contig ID 32823\_1.R1040 5'-most EST fC-gmle700739717a1

Seq. No. 14820

Contig ID 32829\_1.R1040 5'-most EST xpa700797256.h1

Method BLASTX
NCBI GI g4417304
BLAST score 931



1.0e-101 E value Match length 287 57 % identity

(AC006446) putative beta-1,4-mannosyl-glycoprotein NCBI Description

beta-1,4-N-acetylglucosaminyltransferase [Arabidopsis

thaliana]

14821 Seq. No.

32829 2.R1040 Contig ID

LIB3138-054-Q1-N1-E1 5'-most EST

BLASTX Method g4417304 NCBI GI 316 BLAST score E value 7.0e-29 150 Match length 45 % identity

(AC006446) putative beta-1,4-mannosyl-glycoprotein NCBI Description

beta-1,4-N-acetylglucosaminyltransferase [Arabidopsis

thaliana]

Seq. No. 14822

32833 1.R1040 Contig ID

LIB3094-056-Q1-K1-B10 5'-most EST

BLASTN Method NCBI GI g3600062 100 BLAST score 8.0e-49 E value Match length 428 81 % identity

Arabidopsis thaliana BAC T25C13 NCBI Description

Seq. No. 14823

32833 2.R1040 Contig ID

5'-most EST uC-gmrominsoy115e03b1

Method BLASTN NCBI GI g3600062 BLAST score 117 E value 7.0e-59 Match length 585 80 % identity

NCBI Description Arabidopsis thaliana BAC T25C13

Seq. No.

14824 32835 1.R1040

Contiq ID 5'-most EST fua701037260.h1

BLASTX Method g4539400 NCBI GI BLAST score 207 E value 3.0e-16 Match length 121 % identity

(AL035526) putative protein [Arabidopsis thaliana] NCBI Description

Seq. No. 14825

32847 1.R1040 Contig ID 5'-most EST gsv701044628.h1

BLASTX Method

NCBI GI

E value

BLAST score

g3668087

1.0e-57



```
NCBI GI
                  q3759184
BLAST score
                  1082
E value
                  1.0e-118
Match length
                  284
                  73
% identity
NCBI Description (AB018441) phi-1 [Nicotiana tabacum]
                  14826
Seq. No.
                  32847_3.R1040
Contig ID
5'-most EST
                  uC-gmropic059g09b1
Method
                  BLASTX
NCBI GI
                  q3759184
BLAST score
                  204
E value
                  3.0e-16
                  47
Match length
                  79
% identity
NCBI Description (AB018441) phi-1 [Nicotiana tabacum]
Seq. No.
                  14827
                  32848 1.R1040
Contig ID
5'-most EST
                  hrw701059308.hl
                  BLASTX
Method
NCBI GI
                  g1246403
BLAST score
                  426
                  1.0e-41
E value
                  112
Match length
                  72
% identity
                  (X94698) TINY [Arabidopsis thaliana] >qi 3406035 (AC005405)
NCBI Description
                  TINY [Arabidopsis thaliana]
                  14828
Seq. No.
                  32848 2.R1040
Contig ID
5'-most EST
                  uC-gmropic108f07b1
Method
                  BLASTX
NCBI GI
                  g1246403
BLAST score
                  318
                  3.0e-29
E value
Match length
                  123
% identity
                  65
                  (X94698) TINY [Arabidopsis thaliana] >qi 3406035 (AC005405)
NCBI Description
                  TINY [Arabidopsis thaliana]
                  14829
Seq. No.
                  32850 1.R1040
Contig ID
5'-most EST
                  jC-gmle01810091b05a1
                  14830
Seq. No.
Contig ID
                  32850 2.R1040
5'-most EST
                  LIB3055-003-Q1-N1-B9
Seq. No.
                  14831
                  32851 1.R1040
Contig ID
5'-most EST
                  LIB3106-043-Q1-K1-B10
Method
                  BLASTX
```



Match length % identity 35

(AC004667) hypothetical protein [Arabidopsis thaliana] NCBI Description

Seq. No. 14832

32854 1.R1040 Contig ID

5'-most EST LIB3055-003-Q1-N1-C12

14833 Seq. No.

32860 1.R1040 Contig ID 5'-most EST  $dpv70\overline{1}103629.h1$ 

Seq. No. 14834

32864 1.R1040 Contig ID 5'-most EST q5606188

Seq. No. 14835

Contig ID 32864 3.R1040

5'-most EST LIB3138-010-Q1-N1-F7

14836 Seq. No.

32867 1.R1040 Contig ID

5'-most EST LIB3106-071-P1-K1-E2

Method BLASTX g2760839 NCBI GI 333 BLAST score 7.0e-31 E value 92 Match length % identity 67

NCBI Description

(AC003105) putative receptor kinase [Arabidopsis thaliana]

Seq. No. 14837

Contig ID 32872 1.R1040

uC-gmflminsoy027e02b1 5'-most EST

Method BLASTX g3860256 NCBI GI BLAST score 305 8.0e-28 E value Match length 85 68 % identity

(AC005824) putative tRNA isopentenylpyrophosphate NCBI Description

transferase [Arabidopsis thaliana]

14838 Seq. No.

32876 1.R1040 Contig ID

5'-most EST LIB3055-002-Q1-B1-H9

Method BLASTX NCBI GI g4567267 BLAST score 485 1.0e-48 E value 102 Match length 85 % identity

(AC006841) putative zinc finger protein [Arabidopsis NCBI Description

thaliana]

14839 Seq. No.

Contig ID 32884 1.R1040



5'-most EST LIB3055-002-Q1-B1-G8

Method BLASTX
NCBI GI g1176658
BLAST score 201
E value 1.0e-15
Match length 70
% identity 60

NCBI Description HYPOTHETICAL 200.6 KD PROTEIN B0228.2 IN CHROMOSOME II

>gi\_726363 (U23168) No definition line found

[Caenorhabditis elegans]

Seq. No. 14840

Contig ID 32891\_1.R1040 5'-most EST uC-gmropic034g12b1

Seq. No. 14841

Contig ID 32897\_1.R1040 5'-most EST asn701133301.h1

Seq. No. 14842

Contig ID 32902\_1.R1040 5'-most EST seb700651803.h1

Method BLASTX
NCBI GI g4490748
BLAST score 418
E value 1.0e-40
Match length 94
% identity 79

NCBI Description (AL035708) putative protein [Arabidopsis thaliana]

Seq. No.

Contig ID 32902\_2.R1040

5'-most EST LIB3092-054-Q1-K1-G4

14843

Method BLASTX
NCBI GI g4490748
BLAST score 261
E value 1.0e-22
Match length 62
% identity 77

NCBI Description (AL035708) putative protein [Arabidopsis thaliana]

Seq. No. 14844

Contig ID 32905 1.R1040

5'-most EST LIB3055-002-Q1-B1-E9

Seq. No. 14845

Contig ID 32909 1.R1040

5'-most EST LIB $30\overline{5}5-002-Q1-B1-D3$ 

Seq. No. 14846

Contig ID 32913\_1.R1040

5'-most EST jC-gmle01810065g04d1

Method BLASTX
NCBI GI g183250
BLAST score 186
E value 1.0e-13
Match length 67





% identity NCBI Description (M64979) glial factor-1 [Homo sapiens] Seq. No. 14847 32918 1.R1040 Contig ID 5'-most EST uC-gmflminsoy001a09b1 Method BLASTX NCBI GI q3298544 BLAST score 274 E value 1.0e-23 Match length 89 % identity 60 NCBI Description (AC004681) unknown protein [Arabidopsis thaliana] Seq. No. 32918 2.R1040 Contig ID 5'-most EST jex700907356.hl Seq. No. 14849 Contig ID 32919 1.R1040 5'-most EST LIB3055-002-Q1-B1-C5 Seq. No. 14850 32921 1.R1040 Contig ID 5'-most EST LIB3055-002-Q1-B1-C7 Seq. No. 14851 32927 1.R1040 Contig ID 5'-most EST wvk700681406.h2 Seq. No. 14852 32927 3.R1040 Contig ID 5'-most EST wvk700686582.h1 Seq. No. 14853 32930 1.R1040 Contig ID 5'-most EST rlr700897236.h1 Method BLASTX NCBI GI q3033386 BLAST score 251 1.0e-21 E value Match length 97 % identity 44 NCBI Description (AC004238) RING3-like protein [Arabidopsis thaliana] Seq. No. 14854 Contig ID 32931 1.R1040

5'-most EST LIB3055-002-Q1-B1-A1

Seq. No. 14855

32936 1.R1040 Contig ID

5'-most EST jC-gmle01810053e06a1

Method BLASTX NCBI GI g1653516 BLAST score 160 E value 9.0e-11 Match length 49



% identity NCBI Description (D90914) hypothetical protein [Synechocystis sp.] 14856 Seq. No. 32938 1.R1040 Contig ID 5'-most EST LIB3055-002-Q1-B1-A8 Method BLASTX NCBI GI q4455362 BLAST score 147 2.0e-09 E value Match length 77 45 % identity NCBI Description (AL035524) putative protein [Arabidopsis thaliana] 14857 Seq. No. Contig ID 32939 1.R1040 5'-most EST LIB3055-002-Q1-B1-B10 Seq. No. 14858 Contig ID 32940 1.R1040 5'-most EST LIB3055-002-Q1-B1-B11 Method BLASTX NCBI GI g585662 BLAST score 608 E value 4.0e-63 Match length 194 % identity 61 NCBI Description PEROXIDASE PRECURSOR >gi 303851 dbj BAA03911 (D16442) peroxidase [Oryza sativa] Seq. No. 14859 32941 1.R1040 Contig ID 5'-most EST dpv701101376.h1 Method BLASTX NCBI GI q1491710 BLAST score 270 E value 1.0e-23 Match length 110 % identity 49 NCBI Description (X96506) alpha subunit; forms heterodimer with NC2 alpha/Dr1 [Homo sapiens] Seq. No. 14860 32941 2.R1040 Contig ID 5'-most EST uC-gmropic0001g11b1 Method BLASTX NCBI GI g1491710 BLAST score 165 E value 2.0e-11 Match length 53 % identity 58

(X96506) alpha subunit; forms heterodimer with NC2 NCBI Description

alpha/Drl [Homo sapiens]

14861 Seq. No.

Contig ID 32951 1.R1040

5'-most EST jC-gmle01810087e06a1



Seq. No. 14862

Contig ID 32960 1.R1040

LIB3107-041-Q1-K1-D6 5'-most EST

Method BLASTX NCBI GI g1171577 BLAST score 663 1.0e-69 E value 170 Match length % identity 71

NCBI Description (X95343) hypersensitivity-related gene [Nicotiana tabacum]

Seq. No. 14863

32963 1.R1040 Contig ID 5'-most EST eep700865650.h1

Seq. No.

14864 Contig ID 32970 1.R1040

5'-most EST LIB3055-001-Q1-B1-E10

Seq. No. 14865

Contig ID 32983 1.R1040 5'-most EST  $ncj70\overline{0}982727.h1$ 

Seq. No. 14866

Contig ID 32985\_1.R1040  $leu70\overline{1}144574.h1$ 5'-most EST

Seq. No. 14867

Contig ID 32985 3.R1040 5'-most EST leu701156254.h1

Seq. No. 14868

32986 1.R1040 Contig ID

5'-most EST uC-gmflminsoy047d05b1

Method BLASTX NCBI GI q3559816 BLAST score 1450 E value 0.0e + 00477 Match length % identity

(Y15782) transketolase 2 [Capsicum annuum] NCBI Description

Seq. No. 14869

32986\_2.R1040 Contig ID

5'-most EST LIB3106-063-Q1-K1-F6

Method BLASTX NCBI GI g3559816 BLAST score 524 E value 2.0e-53 115 Match length 88 % identity

NCBI Description (Y15782) transketolase 2 [Capsicum annuum]

Seq. No. 14870

Contig ID 32989 1.R1040 5'-most EST  $kmv70\overline{0}740958.h1$ 



Method BLASTX
NCBI GI g465535
BLAST score 184
E value 8.0e-14
Match length 87
% identity 44

NCBI Description HYPOTHETICAL 32.7 KD PROTEIN IN NTH2-COQ1 INTERGENIC REGION >gi\_626491\_pir\_\_S44561 hypothetical protein YBR002c - yeast

(Saccharomyces cerevisiae) >gi\_403317\_emb\_CAA81271\_

(Z26494) unknown [Saccharomyces cerevisiae] >gi\_536188\_emb\_CAA84938\_ (Z35871) ORF YBR002c

[Saccharomyces cerevisiae] >gi 4126457 dbj BAA36577

(AB013497) cis-prenyltransferase [Saccharomyces cerevisiae]

>gi 1582565 prf 2118405F ORF YBR0107 [Saccharomyces

cerevisiae]

Seq. No. 14871

Contig ID 32995 1.R1040

5'-most EST LIB3055-001-Q1-B1-D1

Method BLASTX
NCBI GI g3738302
BLAST score 526
E value 2.0e-53
Match length 142
% identity 73

NCBI Description (AC005309) tubby-like protein [Arabidopsis thaliana]

>gi\_4249398 (AC006072) putative tubby protein [Arabidopsis

thaliana]

Seq. No. 14872

Contig ID 33012 1.R1040

5'-most EST LIB3055-012-Q1-N1-A4

Seq. No. 14873

Contig ID 33027\_1.R1040 5'-most EST kl1701208762.h1

Method BLASTX
NCBI GI g2829893
BLAST score 1085
E value 1.0e-143
Match length 443
% identity 61

NCBI Description (AC002311) phosphoglucomutase [Arabidopsis thaliana]

Seq. No. 14874

Contig ID 33047\_1.R1040 5'-most EST gsv701055086.h1

Method BLASTX
NCBI GI g3877358
BLAST score 189
E value 3.0e-14
Match length 91
% identity 27

NCBI Description (Z66520) similar to RBB3 like protein; cDNA EST EMBL: C08891

comes from this gene; cDNA EST EMBL: C09371 comes from this

gene; cDNA EST yk468f10.5 comes from this gene

[Caenorhabditis elegans]

BLAST score

Match length

E value

498

270

1.0e-82



```
Seq. No.
                   14875
                   33054 1.R1040
Contig ID
5'-most EST
                   LIB3055-001-01-B1-A3
Method
                   BLASTX
NCBI GI
                   q3252868
BLAST score
                   261
E value
                   3.0e-22
Match length
                   119
% identity
                   46
NCBI Description
                  (AF033536) putative zinc transporter [Arabidopsis thaliana]
Seq. No.
                   14876
                   33057 1.R1040
Contig ID
                   zzp700834748.hl
5'-most EST
Method
                  BLASTX
NCBI GI
                   g1279640
BLAST score
                   317
E value
                   4.0e-29
Match length
                   76
% identity
                   72
NCBI Description
                  (X92204) NAM [Petunia x hybrida]
Seq. No.
                   14877
Contig ID
                   33069 1.R1040
5'-most EST
                  uC-gmflminsoy091a02b1
Method
                  BLASTX
NCBI GI
                  q4337025
BLAST score
                   436
                   6.0e-43
E value
Match length
                  140
                   63
% identity
NCBI Description
                  (AF123253) AIM1 protein [Arabidopsis thaliana]
                   14878
Seq. No.
                   33075 1.R1040
Contig ID
5'-most EST
                  hrw701058121.h1
Method
                  BLASTX
NCBI GI
                  q4263515
BLAST score
                   660
E value
                  8.0e-69
Match length
                  311
% identity
                  47
NCBI Description
                  (AC004044) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  14879
                  33075 2.R1040
Contig ID
5'-most EST
                  LIB3092-015-Q1-K1-D12
Seq. No.
                  14880
Contig ID
                  33077 1.R1040
5'-most EST
                  LIB3055-003-Q1-N1-H10
Method
                  BLASTX
NCBI GI
                  g1706336
```

```
% identity
NCBI Description
                  UROPORPHYRINOGEN DECARBOXYLASE >gi_1001337_dbj_BAA10824_
                   (D64006) uroporphyrinogen decarboxylase [Synechocystis sp.]
                   14881
Seq. No.
Contig ID
                   33077 2.R1040
5'-most EST
                   q5342625
Method
                   BLASTX
NCBI GI
                   q1706336
BLAST score
                   254
                   7.0e-22
E value
Match length
                   101
% identity
                   44
NCBI Description
                  UROPORPHYRINOGEN DECARBOXYLASE >gi_1001337_dbj_BAA10824_
                   (D64006) uroporphyrinogen decarboxylase [Synechocystis sp.]
                   14882
Seq. No.
Contig ID
                   33078 1.R1040
5'-most EST
                   LIB3055-003-Q1-N1-H12
Method
                   BLASTX
NCBI GI
                   q4204095
BLAST score
                   404
E value
                   2.0e-39
Match length
                   141
% identity
                   58
                  (AF030260) CYP94A1 [Vicia sativa]
NCBI Description
Seq. No.
                   14883
                   33088 1.R1040
Contig ID
                  LIB3055-008-Q1-N1-C1
5'-most EST
Method
                  BLASTX
NCBI GI
                   g2706515
BLAST score
                   536
E value
                  1.0e-54
Match length
                  157
% identity
                   68
                  (Y12689) isoflavone reductase-like protein [Citrus x
NCBI Description
                   paradisi]
                   14884
Seq. No.
                   33098 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810090d07a1
Method
                   BLASTX
NCBI GI
                  g4558564
BLAST score
                   468
E value
                  1.0e-46
                  157
Match length
% identity
                   61
                  (AC007138) predicted protein of unknown function
NCBI Description
```

Seq. No. 14885

Contig ID 33100 1.R1040

5'-most EST jC-gmf102220081d07d1

[Arabidopsis thaliana]

Seq. No. 14886

Contig ID 33117\_1.R1040

2501



5'-most EST fua701036956.h1

Method BLASTX
NCBI GI g2826882
BLAST score 502
E value 2.0e-50
Match length 106
% identity 92

NCBI Description (AJ223634) transcription factor IIA small subunit

[Arabidopsis thaliana]

Seq. No. 14887

Contig ID 33127\_1.R1040 5'-most EST dpv701097195.h1

Seq. No. 14888

Contig ID 33129\_1.R1040 5'-most EST fde700873814.h1

Seq. No. 14889

Contig ID 33145\_1.R1040 5'-most EST sat701003746.h1

Method BLASTX
NCBI GI g3873408
BLAST score 360
E value 1.0e-33
Match length 155
% identity 49

NCBI Description (L76926) putative zinc finger protein [Arabidopsis

thaliana]

Seq. No. 14890

Contig ID 33150 1.R1040

5'-most EST uC-gmrominsoy058e12b1

Method BLASTN
NCBI GI g2062705
BLAST score 37
E value 5.0e-11
Match length 37
% identity 38

NCBI Description Human butyrophilin (BTF5) mRNA, complete cds

Seq. No. 14891

Contig ID 33151\_1.R1040 5'-most EST gsv701050013.h1

Method BLASTX
NCBI GI g3122858
BLAST score 591
E value 7.0e-68
Match length 211
% identity 67

NCBI Description D-3-PHOSPHOGLYCERATE DEHYDROGENASE PRECURSOR

>gi 2189964 dbj BAA20405 (AB003280) Phosphoglycerate

dehydrogenase [Arabidopsis thaliana]

>gi\_2804258\_dbj\_BAA24440\_ (AB010407) phosphoglycerate

dehydrogenase [Arabidopsis thaliana]

Seq. No. 14892

33151 2 P

Contig ID 33151 2.R1040 5'-most EST seb700653251.h1

Method BLASTX
NCBI GI g2911042
BLAST score 173
E value 2.0e-12
Match length 52
% identity 63

NCBI Description (AL021961) Phosphoglycerate dehydrogenase - like protein

[Arabidopsis thaliana]

Seq. No. 14893

Contig ID 33155\_1.R1040 5'-most EST dpv701097343.h1

Method BLASTX
NCBI GI g2642154
BLAST score 313
E value 1.0e-28
Match length 161
% identity 50

NCBI Description (AC003000) unknown protein [Arabidopsis thaliana]

>gi\_3790595 (AF079186) RING-H2 finger protein RHC2a

[Arabidopsis thaliana]

Seq. No. 14894

Contig ID 33157 1.R1040

5'-most EST LIB30 $\overline{5}6$ -014-Q1-N1-E10

Seq. No. 14895

Contig ID 33159\_1.R1040 5'-most EST asn701142781.h1

Method BLASTX
NCBI GI g3176684
BLAST score 334
E value 6.0e-31
Match length 149
% identity 46

NCBI Description (AC003671) Contains similarity to equilibratiave nucleoside

transporter 1 gb\_U81375 from Homo sapiens. ESTs gb\_N65317, gb T20785, gb AA586285 and qb AA712578 come from this gene.

[Arabidopsis thaliana]

Seq. No. 14896

Contig ID 33161 1.R1040

5'-most EST LIB3056-014-Q1-N1-E5

Method BLASTX
NCBI GI g2651308
BLAST score 178
E value 6.0e-13
Match length 61
% identity 61

NCBI Description (AC002336) putative myosin heavy chain [Arabidopsis

thaliana]

Seq. No. 14897

Contig ID 33169\_1.R1040

5'-most EST jC-gmst02400030c12a1



```
BLASTX
Method
NCBI GI
                  g2275204
BLAST score
                  210
                  2.0e-16
E value
                  66
Match length
                  67
% identity
                  (AC002337) DNA binding protein isolog [Arabidopsis
NCBI Description
                  thaliana]
                  14898
Seq. No.
                  33174 1.R1040
Contig ID
5'-most EST
                  vwf700676806.h1
Seq. No.
                  14899
                  33175 1.R1040
Contig ID
                  pmv700890841.h1
5'-most EST
                  BLASTX
Method
                  g2244994
NCBI GI
                  1690
BLAST score
                  0.0e+00
E value
                  465
Match length
                  77
% identity
                  (Z97341) similarity to isp4 protein - fission yeast
NCBI Description
                   [Arabidopsis thaliana]
                  14900
Seq. No.
                  33183 1.R1040
Contig ID
                  LIB3056-014-Q1-N1-C9
5'-most EST
                   14901
Seq. No.
                   33186 1.R1040
Contig ID
5'-most EST
                  LIB3139-044-P1-N1-H10
Seq. No.
                   14902
                   33192 1.R1040
Contig ID
5'-most EST
                   LIB3056-014-Q1-N1-A2
Method
                  BLASTX
NCBI GI
                   g2739431
BLAST score
                   242
                   1.0e-20
E value
                   94
Match length
                   51
% identity
                  (U70368) hematopoietic-specific IL-2 deubiquitinating
NCBI Description
                   enzyme [Mus musculus]
                   14903
Seq. No.
                   33196 1.R1040
Contig ID
5'-most EST
                   uC-qmronoir009g01b1
                   BLASTX
Method
                   q3924598
NCBI GI
                   232
BLAST score
```

3.0e-19 E value 113 Match length 42 % identity

NCBI Description (AF069442) putative oxidoreductase [Arabidopsis thaliana]

Seq. No. 14904



Contig ID 33200 1.R1040 5'-most EST ncj700988181.h1 BLASTX

 NCBI GI
 g3201626

 BLAST score
 566

 E value
 2.0e-58

 Match length
 140

 % identity
 76

NCBI Description (AC004669) putative protein kinase MAP3K [Arabidopsis

thaliana]

Seq. No. 14905

Contig ID 33206\_1.R1040

5'-most EST LIB3056-013-Q1-N1-G11

Seq. No. 14906

Contig ID 33209\_1.R1040

5'-most EST LIB3056-013-Q1-N1-G3

Seq. No. 14907

Contig ID 33211\_1.R1040 5'-most EST crh700851270.h1

Seq. No. 14908

Contig ID 33217\_1.R1040

5'-most EST g5753534

Method BLASTX

NCBI GI g2688820

BLAST score 339

E value 1.0e-31

Match length 159

% identity 45

NCBI Description (U93271) enoyl-CoA hydratase [Prunus armeniaca]

Seq. No. 14909

Contig ID 33218 1.R1040 5'-most EST sat701011932.h1

Seq. No. 14910

Contig ID 33218\_2.R1040 5'-most EST smc700747434.h1

Seq. No. 14911

Contig ID 33223\_1.R1040 5'-most EST rca701000361.h1

Method BLASTN
NCBI GI g303729
BLAST score 153
E value 2.0e-80
Match length 468
% identity 83

NCBI Description Pea mRNA for GTP-binding protein, complete cds

Seq. No. 14912

Contig ID 33226\_1.R1040

5'-most EST LIB3139-036-P1-N1-E11

Method BLASTX

```
g4455342
NCBI GI
BLAST score
                  385
                  5.0e-37
E value
                  153
Match length
                  57
% identity
                  (AL035522) O-methyltransferase-like protein [Arabidopsis
NCBI Description
                  thaliana]
                  14913
Seq. No.
                  33227 1.R1040
Contig ID
                  g4396936
5'-most EST
                  14914
Seq. No.
Contig ID
                  33227 2.R1040
                  LIB3056-013-Q1-N1-E8
5'-most EST
                  14915
Seq. No.
                  33234 1.R1040
Contig ID
                  fua701037120.h1
5'-most EST
                  14916
Seq. No.
                  33239 1.R1040
Contig ID
5'-most EST
                  LIB3056-013-Q1-N1-D10
Seq. No.
                  14917
                  33241 1.R1040
Contig ID
                  trc700564588.h1
5'-most EST
                  14918
Seq. No.
                   33243 1.R1040
Contig ID
5'-most EST
                  dpv701102776.h1
                   14919
Seq. No.
Contig ID
                   33244 1.R1040
5'-most EST
                   LIB3056-013-Q1-N1-D5
Method
                   BLASTX
NCBI GI
                   g3702323
                   279
BLAST score
E value
                   2.0e-51
Match length
                   130
                   87
% identity
NCBI Description (AC005397) unknown protein [Arabidopsis thaliana]
```

Seq. No. 14920

Contig ID 33245\_1.R1040

5'-most EST LIB3056-013-Q1-N1-D6

Method BLASTX
NCBI GI g2262173
BLAST score 486
E value 6.0e-49
Match length 116
% identity 76

NCBI Description (AC002329) NADPH thioredoxin reductase [Arabidopsis

thaliana]

Seq. No. 14921

Contig ID 33245\_2.R1040



```
jC-gmro02910019h04a1
5 -most EST
                   14922
Seq. No.
                   33247 1.R1040
Contig ID
                   eep700865442.h1
5'-most EST
                   BLASTX
Method
                   q2129698
NCBI GI
BLAST score
                   598
                   9.0e-62
E value
                   144
Match length
                   78
% identity
                   protein kinase ATN1 (EC 2.7.1.-) - Arabidopsis thaliana
NCBI Description
                   >gi 1054633 emb_CAA63387_ (X92728) protein kinase
                   [Arabidopsis thaliana]
                   14923
Seq. No.
                   33247 2.R1040
Contig ID
5'-most EST
                   LIB3056-013-Q1-N1-D8
                   14924
Seq. No.
                   33250 1.R1040
Contig ID
                   q4397333
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3242708
                   704
BLAST score
                   2.0e-74
E value
                   171
Match length
                   77
% identity
                   (AC003040) putative serine/threonine protein kinase
NCBI Description
                   [Arabidopsis thaliana]
                   14925
Seq. No.
                   33251 1.R1040
Contig ID
                   leu701149879.hl
5'-most EST
Method
                   BLASTX
                   g4544432
NCBI GI
                   304
BLAST score
                   1.0e-27
E value
Match length
                   65
% identity
                   85
                   (AC006955) putative mannose-1-phosphate guanyltransferase
NCBI Description
                   [Arabidopsis thaliana]
                   14926
Seq. No.
                   33251 2.R1040
Contig ID
                   kl1701203670.h2
5'-most EST
                   BLASTX
Method
                   q4544432
NCBI GI
                   786
BLAST score
                   7.0e-84
E value
                   242
Match length
                   72
 % identity
NCBI Description (AC006955) putative mannose-1-phosphate guanyltransferase
                   [Arabidopsis thaliana]
```

Seq. No. 14927

Contig ID 33253\_1.R1040



```
uC-gmrominsoy027a03b1
5'-most EST
Method
                  BLASTX
                  a2146797
NCBI GI
                  287
BLAST score
                  2.0e-25
E value
                  140
Match length
% identity
                  protein disulfide-isomerase (EC 5.3.4.1) - Castor bean
NCBI Description
                  >gi_1134968 (U41385) protein disulphide isomerase PDI
                  [Ricinus communis] >gi 1587210 prf__2206331A protein
                  disulfide isomerase [Ricinus communis]
Seq. No.
                  14928
```

33262\_1.R1040 Contig ID fC-qmse7000755416f1 5'-most EST BLASTX Method

q4539320 NCBI GI BLAST score 1009 1.0e-110 E value 249 Match length 71 % identity

(AL035679) putative endo-1, 4-beta-glucanase [Arabidopsis NCBI Description

thaliana]

Seq. No. 14929

33264 1.R1040 Contig ID

LIB3056-013-Q1-N1-C2 5'-most EST

14930 Seq. No.

33264 2.R1040 Contig ID

LIB3106-026-Q1-K1-F11 5'-most EST

14931 Seq. No.

33272 1.R1040 Contig ID

5'-most EST LIB3056-012-Q1-N1-H6

Seq. No. 14932

33273 1.R1040 Contig ID wrg700789257.h2 5'-most EST

BLASTX Method g2894534 NCBI GI 734 BLAST score 7.0e-78 E value 162 Match length 88 % identity

NCBI Description (AJ224327) aquaporin [Oryza sativa]

14933 Seq. No.

33274 1.R1040 Contig ID pxt700944513.h1 5'-most EST

BLASTX Method g2979494 NCBI GI 170 BLAST score 1.0e-13 E value 126 Match length 40 % identity

NCBI Description (AB012138) germin-like protein [Lycopersicon esculentum]



```
14934
Seq. No.
                  33278 1.R1040
Contig ID
                  dpv701102213.h1
5'-most EST
                  BLASTX
Method
                  g2832648
NCBI GI
                  345
BLAST score
                  2.0e-32
E value
                  74
Match length
                  89
% identity
                   (AL021710) membrane-bound small GTP-binding - like protein
NCBI Description
                   [Arabidopsis thaliana]
                  14935
Seq. No.
Contig ID
                   33278 2.R1040
                   uC-gmflminsoy025a12b1
5'-most EST
                   BLASTX
Method
                   g303740
NCBI GI
                   671
BLAST score
                   1.0e-70
E value
                   146
Match length
                   90
% identity
                  (D12543) GTP-binding protein [Pisum sativum]
NCBI Description
                   14936
Seq. No.
                   33290 1.R1040
Contig ID
                   trc700565955.hl
5'-most EST
                   BLASTX
Method
                   g1199772
NCBI GI
                   283
BLAST score
                   8.0e-25
E value
                   136
Match length
                   48
% identity
                   (D83226) extensin like protein [Populus nigra]
NCBI Description
                   >gi_1199774_dbj_BAA11855_ (D83227) extensin like protein
                   [Populus nigra]
                   14937
Seq. No.
                   33290 2.R1040
Contig ID
                   iC-qmro02910068b08a1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q1199772
                   280
BLAST score
                   9.0e-25
E value
Match length
                   136
 % identity
                   (D83226) extensin like protein [Populus nigra]
 NCBI Description
                   >gi_1199774_dbj_BAA11855_ (D83227) extensin like protein
                    [Populus nigra]
                    14938
 Seq. No.
                    33290 3.R1040
 Contig ID
                    sat701011442.h1
 5'-most EST
```

2509

BLASTX

326

g4103618

3.0e-30

Method

NCBI GI

E value

BLAST score

Match length 48 % identity

(AF026382) HyPRP [Fragaria x ananassa] NCBI Description

14939 Seq. No.

33290 4.R1040 Contig ID

5'-most EST uC-gmropic100a11b1

BLASTX Method g629597 NCBI GI BLAST score 163 3.0e-11 E value 34 Match length 85 % identity

proline-rich protein - rape >gi\_545029\_bbs\_142669 (S68113) NCBI Description

proline-rich SAC51 [Brassica napus=oilseed rape, pods,

Peptide, 147 aa] [Brassica napus]

14940 Seq. No.

33290 5.R1040 Contig ID sat701006242.h2 5'-most EST

14941 Seq. No.

33290 6.R1040 Contig ID 5'-most EST fua701039503.hl

14942 Seq. No.

33290\_7.R1040 Contig ID uC-gmropic075h09b1 5'-most EST

Method BLASTX q4454097 NCBI GI 205 BLAST score 5.0e-16 E value 126 Match length 38

% identity

(X85206) hybrid proline-rich protein [Catharanthus roseus] NCBI Description

14943 Seq. No.

33299 1.R1040 Contig ID

LIB3107-041-Q1-K1-E4 5'-most EST

Seq. No. 14944

33303 1.R1040 Contig ID

jC-gmro02910006a12a1 5'-most EST

Seq. No. 14945

33305 1.R1040 Contig ID  $cle70\overline{0}967740.h1$ 5'-most EST

Method BLASTX q4049346 NCBI GI 217 BLAST score 2.0e-17 E value 98 Match length 46 % identity

(AL034567) putative protein [Arabidopsis thaliana] NCBI Description

Seq. No.

14946

Contig ID

33309 1.R1040



```
jex700906690.hl
5'-most EST
                  BLASTX
Method
                  q2190547
NCBI GI
                   691
BLAST score
                  8.0e-73
E value
                   229
Match length
                   56
% identity
                   (AC001229) ESTs
NCBI Description
                  gb_T43256,gb_46316,gb_N64930,gb_AA395255,gb_AA404382 come
                   from this gene. [Arabidopsis thaliana]
                   14947
Seq. No.
                   33313 1.R1040
Contig ID
                   uC-gmronoir0001d02b1
5'-most EST
                   14948
Seq. No.
                   33314 1.R1040
Contig ID
                   LIB3093-057-Q1-K1-C6
5'-most EST
                   14949
Seq. No.
                   33315 1.R1040
Contig ID
                   LIB3109-057-Q1-K1-A9
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3955021
                   343
BLAST score
                   2.0e-32
E value
                   88
Match length
                   75
% identity
                  (AJ010811) HB2 homeodomain protein [Populus tremula x
NCBI Description
                   Populus tremuloides]
                   14950
Seq. No.
                   33315 2.R1040
Contig ID
5'-most EST
                   sat701005938.hl
                   BLASTX
Method
NCBI GI
                   q3955021
BLAST score
                   463
                   2.0e-46
E value
Match length
                   113
% identity
                   77
                   (AJ010811) HB2 homeodomain protein [Populus tremula x
NCBI Description
                   Populus tremuloides]
                   14951
Seq. No.
```

33317 1.R1040 Contig ID  $zhf70\overline{0}956458.h1$ 5'-most EST

Method BLASTX q3738297 NCBI GI BLAST score 440 3.0e-43E value 173 Match length 22 % identity

NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]

14952 Seq. No.

33317 2.R1040 Contig ID

LIB3170-081-Q1-J1-A2 5'-most EST



14953 Seq. No.

33320 1.R1040 Contig ID

LIB3087-002-Q1-K1-H12 5'-most EST

14954 Seq. No.

33327 1.R1040 Contig ID  $smc70\overline{0}747773.h1$ 5'-most EST

Seq. No. 14955

33327 2.R1040 Contig ID

LIB3056-012-Q1-N1-D7 5'-most EST

BLASTX Method g4417304 NCBI GI BLAST score 177 E value 9.0e-13 Match length 67 % identity 54

(AC006446) putative beta-1,4-mannosyl-glycoprotein NCBI Description

beta-1,4-N-acetylglucosaminyltransferase [Arabidopsis

thaliana]

14956 Seq. No.

33334\_1.R1040 Contig ID uC-gmropic006g10b1 5'-most EST

BLASTX Method g3540207 NCBI GI BLAST score 442 8.0e-44 E value 129 Match length 71 % identity

(AC004260) Putative protein kinase [Arabidopsis thaliana] NCBI Description

14957 Seq. No.

33353 1.R1040 Contig ID rlr700898766.hl 5'-most EST

BLASTX Method g3395436 NCBI GI 638 BLAST score 2.0e-66 E value 202 Match length 62 % identity

NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]

14958 Seq. No.

33353 2.R1040 Contig ID hyd700728358.h1 5'-most EST BLASTX

Method q3395436 NCBI GI BLAST score 276 E value 2.0e-24 110 Match length % identity 49

NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]

14959 Seq. No.

33359 1.R1040 Contig ID



5'-most EST g5753559
Method BLASTX
NCBI GI g4104933
BLAST score 530
E value 5.0e-54
Match length 177
% identity 60

NCBI Description (AF042346) putative phenylalanyl-tRNA synthetase

beta-subunit; PheHB [Homo sapiens]

Seq. No. 14960

Contig ID 33361 1.R1040 5'-most EST bnu700967690.h1

Method BLASTX
NCBI GI g3885329
BLAST score 417
E value 7.0e-41
Match length 110
% identity 73

NCBI Description (AC005623) alien-like protein [Arabidopsis thaliana]

Seq. No. 14961

Contig ID 33361\_2.R1040

5'-most EST LIB3107-004-Q1-K1-A1

Method BLASTX
NCBI GI g3885329
BLAST score 364
E value 9.0e-35
Match length 100
% identity 70

NCBI Description (AC005623) alien-like protein [Arabidopsis thaliana]

Seq. No. 14962

Contig ID 33362\_1.R1040

5'-most EST uC-gmflminsoy030b11b1

Method BLASTX
NCBI GI g1871176
BLAST score 212
E value 7.0e-17
Match length 101
% identity 45

NCBI Description (U90439) unknown protein [Arabidopsis thaliana]

Seq. No. 14963

Contig ID 33367\_1.R1040 5'-most EST kl1701208503.h1

Method BLASTX
NCBI GI g3169172
BLAST score 419
E value 5.0e-41
Match length 136
% identity 56

NCBI Description (AC004401) putative serine carboxypeptidase I [Arabidopsis

thaliana] >gi\_3445214 (AC004786) putative serine

carboxypeptidase I [Arabidopsis thaliana]

Seq. No. 14964



```
33372 1.R1040
Contig ID
                  zzp700834608.hl
5'-most EST
                  BLASTX
Method
                   g2244899
NCBI GI
                   1402
BLAST score
                  1.0e-156
E value
                   440
```

60 % identity NCBI Description (Z97338) similar to UFD1 protein [Arabidopsis thaliana]

14965 Seq. No.

Match length

33378 1.R1040 Contig ID

5'-most EST LIB3056-011-Q1-N1-G9

Method BLASTN q3309259 NCBI GI 44 BLAST score E value 3.0e-15 Match length 135 % identity

NCBI Description Arabidopsis thaliana BAC F4H6, chromosome IV, complete

sequence [Arabidopsis thaliana]

14966 Seq. No.

33378 2.R1040 Contig ID zzp700831046.hl 5'-most EST

14967 Seq. No.

Contig ID 33381 1.R1040 5'-most EST qsv701048544.h1

BLASTX Method q3063699 NCBI GI 475 BLAST score 2.0e-47 E value Match length 213

% identity

NCBI Description (AL022537) putative protein [Arabidopsis thaliana]

14968 Seq. No.

33381 2.R1040 Contig ID

uC-qmflminsoy001a06b1 5'-most EST

14969 Seq. No.

33383 1.R1040 Contig ID

LIB3138-027-Q1-N1-B6 5'-most EST

14970 Seq. No.

33392 1.R1040 Contig ID asn701132213.h2 5'-most EST

BLASTX Method g3157943 NCBI GI 223 BLAST score 4.0e-18 E value 88 Match length 55 % identity

NCBI Description (AC002131) Contains similarity to BAP31 protein gb\_X81816

from Mus musculus. [Arabidopsis thaliana]

```
Seq. No.
                  33395 1.R1040
Contig ID
                  hyd700725331.hl
5'-most EST
                  BLASTX
Method
NCBI GI
                  q3449282
BLAST score
                  1096
                  1.0e-120
E value
                  253
Match length
% identity
                   (AB006139) phosphoribosylformimino-5-aminoimidazole
NCBI Description
                  carboxamide ribotide isomerase [Arabidopsis thaliana]
                  >gi 3449284_dbj BAA32457_ (AB008929)
                  N'-5'-phosphoribosyl-formimino-5-aminoimidazole-
                   4-carboxamide ribonucleotide isomerase [Arabidopsis
                   thaliana] >gi_4510353_gb_AAD21442.1_ (AC006921)
                  phosphoribosylformimino-5-aminoimidazole carboxamide
                   ribotide isomerase [Arabidopsis thaliana]
                   14972
Seq. No.
                   33401 1.R1040
Contig ID
                   smc700746052.h1
5'-most EST
                   BLASTX
Method
                   q2465008
NCBI GI
                   259
BLAST score
                   2.0e-22
E value
                   111
Match length
% identity
                  (AJ001445) ripening-induced protein [Fragaria vesca]
NCBI Description
                   14973
Seq. No.
                   33403 1.R1040
Contig ID
                   LIB30\overline{5}6-011-Q1-N1-D11
5'-most EST
                   BLASTX
Method
                   g3327275
NCBI GI
                   506
BLAST score
                   3.0e-75
E value
                   229
Match length
                   61
% identity
                  (AB016002) PKn3 [Ipomoea nil]
NCBI Description
                   14974
Seq. No.
                   33403 2.R1040
Contig ID
                   LIB3109-009-Q1-K1-E3
5'-most EST
                   BLASTX
Method
                   g2935573
NCBI GI
                   208
BLAST score
                   3.0e-19
E value
                   108
Match length
```

53 % identity NCBI Description

(AF050180) KNOX class homeodomain protein [Oryza sativa]

14975 Seq. No.

33407 1.R1040 Contig ID

jC-gmro02910026a01a1 5'-most EST

14976 Seq. No.

33410 1.R1040 Contig ID



```
LIB3056-011-Q1-N1-D8
5'-most EST
                  14977
Seq. No.
                  33417 1.R1040
Contig ID
                  LIB3106-015-Q1-K1-C5
5'-most EST
                  BLASTX
Method
                  g1707018
NCBI GI
                  523
BLAST score
                  3.0e-53
E value
                  150
Match length
% identity
                  75
NCBI Description (U78721) CutA isolog [Arabidopsis thaliana]
                  14978
Seq. No.
                  33417 2.R1040
Contig ID
                   taw700655937.h1
5'-most EST
                  BLASTX
Method
                   q1707018
NCBI GI
                   421
BLAST score
                   3.0e-42
E value
                   134
Match length
% identity
                   76
NCBI Description (U78721) CutA isolog [Arabidopsis thaliana]
                   14979
Seq. No.
                   33421 1.R1040
Contig ID
                   pmv700890502.h1
5'-most EST
                   BLASTX
Method
                   g2654868
NCBI GI
                   597
BLAST score
                   5.0e-62
E value
                   148
Match length
                   72
% identity
                  (AF015301) RbohAp108 [Arabidopsis thaliana]
NCBI Description
                   14980
Seq. No.
                   33435 1.R1040
Contig ID
                   LIB3139-012-P1-N1-B11
5'-most EST
                   BLASTX
Method
                   q2723496
NCBI GI
                   197
BLAST score
                   4.0e-24
E value
                   211
Match length
                   32
% identity
NCBI Description (AB009972) beta-1,4-xylosidase [Aspergillus oryzae]
                   14981
Seq. No.
                   33436 1.R1040
Contig ID
                   LIB3170-078-Q1-K1-A10
 5'-most EST
 Seq. No.
                   14982
                   33439 1.R1040
 Contig ID
                   LIB3167-004-P1-K1-H4
 5'-most EST
                   BLASTX
 Method
```

g2266985

519 8.0e-53

NCBI GI BLAST score

E value



Match length 134 % identity 75 NCBI Description (Y13943) METRS [Arabidopsis thaliana]

Seq. No. 14983

Contig ID 33447\_1.R1040 5'-most EST sat701015463.h1

Method BLASTN
NCBI GI g3511284
BLAST score 98
E value 1.0e-47
Match length 182
% identity 88

NCBI Description Populus alba x Populus tremula cellulose synthase (cell)

mRNA, complete cds

Seq. No. 14984

Contig ID 33448\_1.R1040

5'-most EST uC-gmrominsoy217g12b1

Method BLASTX
NCBI GI g3169883
BLAST score 1761
E value 0.0e+00
Match length 512
% identity 68

NCBI Description (AF033194) dehydroquinate dehydratase/shikimate:NADP

oxidoreductase [Lycopersicon esculentum] >gi\_3169888 (AF034411) dehydroquinate dehydratase/shikimate:NADP

oxidoreductase [Lycopersicon esculentum]

Seq. No. 14985

Contig ID 33455\_1.R1040

5'-most EST LIB3167-010-P1-K1-A5

Seq. No. 14986

Contig ID 33467\_1.R1040

5'-most EST LIB3056-010-Q1-N1-E7

Method BLASTX
NCBI GI g3548810
BLAST score 272
E value 1.0e-23
Match length 238
% identity 34

NCBI Description (AC005313) putative chloroplast nucleoid DNA binding

protein [Arabidopsis thaliana]

Seq. No. 14987

Contig ID 33469\_1.R1040

5'-most EST uC-gmrominsoy048a07b1

Method BLASTX
NCBI GI 94262241
BLAST score 331
E value 7.0e-31
Match length 99
% identity 75

NCBI Description (AC006200) unknown protein [Arabidopsis thaliana]

```
14988
```

Seq. No. Contig ID

33482 1.R1040 rca701001410.h1

5'-most EST BLASTX Method NCBI GI q3046694 BLAST score 1843 E value 0.0e + 00Match length 451 % identity

NCBI Description (AL022224) vacuolar sorting receptor-like protein

[Arabidopsis thaliana]

14989 Seq. No.

Contig ID 33483 1.R1040

5'-most EST LIB3109-028-Q1-K1-C4

14990 Seq. No.

33484 1.R1040 Contig ID smc700744913.hl 5'-most EST

14991 Seq. No.

Contig ID 33486 1.R1040 5'-most EST zsg701127493.h1

Seq. No. 14992

Contig ID 33489 1.R1040

5'-most EST LIB3107-041-Q1-K1-A8

Method BLASTX NCBI GI g2245004 BLAST score 1155 E value 1.0e-127 401 Match length

% identity 57

NCBI Description (Z97341) similarity to membrane transport protein

[Arabidopsis thaliana]

Seq. No. 14993

33493 1.R1040 Contig ID 5'-most EST zhf700955347.h1

BLASTX Method NCBI GI q2979555 BLAST score 211 E value 1.0e-16 Match length 107 % identity

NCBI Description (AC003680) unknown protein [Arabidopsis thaliana]

14994 Seq. No.

33494 1.R1040 Contig ID

5'-most EST uC-gmflminsoy045d01b1

Method BLASTX NCBI GI q2547036 BLAST score 222 E value 4.0e-18 Match length 95 % identity 52

NCBI Description (Y13920) ribosomal protein S2 [Triticum aestivum]



Seq. No. 14995

Contig ID 33502\_1.R1040 5'-most EST sat701004354.h1

Seq. No. 14996

Contig ID 33503\_1.R1040

5'-most EST LIB3056-010-Q1-N1-B9

Seq. No. 14997

Contig ID 33503 2.R1040

5'-most EST fC-gmle700558413f2

Seq. No. 14998

Contig ID 33503\_3.R1040

5'-most EST uC-gmrominsoy039d11b1

Seq. No. 14999

Contig ID 33504\_1.R1040 5'-most EST gsv701044945.h1

Method BLASTX
NCBI GI g461753
BLAST score 221
E value 5.0e-18
Match length 100
% identity 52

NCBI Description ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA HOMOLOG

PRECURSOR >gi\_419773\_pir\_\_S31164 ATP-dependent ClpB

proteinase regulatory chain homolog precursor, chloroplast - garden pea >gi\_169128 (L09547) nuclear encoded precursor

to chloroplast protein [Pisum sativum]

Seq. No. 15000

Contig ID 33506\_1.R1040

5'-most EST LIB3056-006-Q1-N1-D9

Seq. No. 15001

Contig ID 33507\_1.R1040

5'-most EST LIB3056-010-Q1-N1-C12

Seq. No. 15002

Contig ID 33511\_1.R1040

5'-most EST LIB3056-010-Q1-N1-C6

Method BLASTX
NCBI GI g4191793
BLAST score 323
E value 9.0e-30
Match length 193
% identity 43

NCBI Description (AC005917) putative zinc finger protein [Arabidopsis

thaliana]

Seq. No. 15003

Contig ID 33518 1.R1040

5'-most EST LIB3056-007-Q1-N1-E3

Method BLASTX NCBI GI g2244757



```
BLAST score
                  2.0e-20
E value
Match length
                  119
                  46
% identity
NCBI Description (Z97335) hypothetical protein [Arabidopsis thaliana]
                  15004
Seq. No.
                  33520 1.R1040
Contig ID
                  jC-gmst02400072e08a1
5'-most EST
                  BLASTX
Method
                  g1354849
NCBI GI
                  554
BLAST score
                  1.0e-56
E value
                  167
Match length
% identity
                   62
                  (U57350) epoxide hydrolase [Nicotiana tabacum]
NCBI Description
                  15005
Seq. No.
                  33520 2.R1040
Contig ID
                  leu701148110.h1
5'-most EST
                  BLASTX
Method
                   g1354849
NCBI GI
                   526
BLAST score
                   1.0e-53
E value
                   164
Match length
% identity
                   61
                  (U57350) epoxide hydrolase [Nicotiana tabacum]
NCBI Description
                   15006
Seq. No.
                   33525 1.R1040
Contig ID
                   LIB3107-059-Q1-K1-G2
5'-most EST
                   BLASTX
Method
                   g4538911
NCBI GI
                   520
BLAST score
                   2.0e-52
E value
                   304
Match length
                   39
% identity
                  (AL049482) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   15007
Seq. No.
Contig ID
                   33531 1.R1040
                   LIB3056-009-Q1-N1-F7
5'-most EST
                   15008
Seq. No.
                   33534 1.R1040
Contig ID
5'-most EST
                   vzy700753545.h1
                   15009
Seq. No.
Contig ID
                   33539 1.R1040
5'-most EST
                   LIB3056-009-Q1-N1-G4
```

Seq. No.

15010

Contig ID 5'-most EST

33546\_1.R1040 epx701104774.h1

Seq. No.

15011

Contig ID

33548\_1.R1040

```
5'-most EST LIB3056-009-Q1-N1-E10
```

Method BLASTX
NCBI GI g3924596
BLAST score 526
E value 8.0e-54
Match length 128

Match length 128 % identity 76

NCBI Description (AF069442) putative phospho-ser/thr phosphatase

[Arabidopsis thaliana]

Seq. No. 15012

Contig ID 33563\_1.R1040 5'-most EST gsv701049429.h1

Method BLASTX
NCBI GI g116527
BLAST score 207
E value 3.0e-16
Match length 61
% identity 59

NCBI Description PROBABLE CLPP-LIKE PROTEASE (ENDOPEPTIDASE CLP) (ORF 196)

>gi\_1143166 (U32397) ClpP protease [Nicotiana tabacum]
>gi\_2924270\_emb\_CAA77422\_ (Z00044) ATP-dependent protease

proteolytic subuni [Nicotiana tabacum]

Seq. No. 15013

Contig ID 33564\_1.R1040

5'-most EST LIB3056-009-Q1-N1-F5

Seq. No. 15014

Contig ID 33568\_1.R1040

5'-most EST LIB3056-009-Q1-N1-C7

Seq. No. 15015

Contig ID 33577 1.R1040

5'-most EST g4290666

Seq. No. 15016

Contig ID 33579\_1.R1040

5'-most EST LIB3056-009-Q1-N1-D9

Method BLASTX
NCBI GI g3482973
BLAST score 804
E value 7.0e-86
Match length 275
% identity 66

NCBI Description (AL031369) putative protein [Arabidopsis thaliana]

Seq. No. 15017

Contig ID 33584 1.R1040

5'-most EST jC-gmst02400073g04a1

Method BLASTX
NCBI GI g3023713
BLAST score 819
E value 1.0e-87
Match length 174
% identity 90

NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)





(2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (OSE1) >gi\_780372 (U09450) enolase [Oryza sativa]

Seq. No. 15018

Contig ID 33587\_1.R1040 5'-most EST sat701012133.h1

Method BLASTX
NCBI GI g571484
BLAST score 1332
E value 1.0e-147
Match length 326
% identity 78

NCBI Description (U16727) peroxidase precursor [Medicago truncatula]

Seq. No. 15019

Contig ID 33587 2.R1040

5'-most EST jC-gmro02910025f08a1

Method BLASTN
NCBI GI g1502377
BLAST score 58
E value 1.0e-23
Match length 178
% identity 83

NCBI Description Medicago truncatula peroxidase precursor (ripl) gene,

complete cds

Seq. No. 15020

Contig ID 33587\_3.R1040 5'-most EST hrw701061555.h1

Method BLASTX
NCBI GI g571484
BLAST score 283
E value 2.0e-37
Match length 104
% identity 76

NCBI Description (U16727) peroxidase precursor [Medicago truncatula]

Seq. No. 15021

Contig ID 33588\_1.R1040 5'-most EST zsg701117528.h2

Seq. No. 15022

Contig ID 33592 1.R1040

5'-most EST uC-gmrominsoy027f10b1

Seq. No. 15023

Contig ID 33596\_1.R1040 5'-most EST gsv701054216.h1

Seq. No. 15024

Contig ID 33597\_1.R1040 5'-most EST ncj700976321.h1

Seq. No. 15025

Contig ID 33605\_1.R1040

5'-most EST uC-gmrominsoy0001c11b1

Method BLASTX



NCBI GI g3451071 BLAST score 166 E value 2.0e-11 Match length 64 % identity 50

NCBI Description (AL031326) beta adaptin - like protein [Arabidopsis

thaliana]

Seq. No. 15026

Contig ID 33612\_1.R1040 5'-most EST euj700698024.h1

Method BLASTX
NCBI GI g3757521
BLAST score 472
E value 5.0e-47
Match length 262
% identity 42

NCBI Description (AC005167) unknown protein [Arabidopsis thaliana]

Seq. No. 15027

Contig ID 33614\_1.R1040 5'-most EST zhf700955235.h1

Method BLASTX
NCBI GI g3420047
BLAST score 230
E value 4.0e-19
Match length 104
% identity 51

NCBI Description (AC004680) putative protein kinase [Arabidopsis thaliana]

Seq. No. 15028

Contig ID 33614\_2.R1040 5'-most EST smc700746493.h1

Method BLASTX
NCBI GI g3420047
BLAST score 175
E value 6.0e-13
Match length 68
% identity 53

NCBI Description (AC004680) putative protein kinase [Arabidopsis thaliana]

Seq. No. 15029

Contig ID 33616 1.R1040

5'-most EST LIB3073-012-Q1-K1-B2

Seq. No. 15030

Contig ID 33618\_1.R1040 5'-most EST sat701008522.h1

Seq. No. 15031

Contig ID 33623\_1.R1040

5'-most EST LIB3056-008-Q1-N1-G10

Seq. No. 15032

Contig ID 33630 1.R1040

5'-most EST jC-gmro02910013a04a1



```
Seq. No.
                  33630 2.R1040
Contig ID
                  LIB3138-083-P1-N1-F9
5'-most EST
Seq. No.
                  15034
                  33632 1.R1040
Contig ID
                  crh700851865.hl
5'-most EST
                  BLASTX
Method
```

g4204304 NCBI GI BLAST score 886 1.0e-112 E value 235 Match length 77 % identity

(AC003027) lcl\_prt\_seq No definition line found NCBI Description [Arabidopsis thaliana]

15035 Seq. No.

33634 1.R1040 Contig ID

uC-qmflminsoy002c11b1 5'-most EST

15036 Seq. No. 33649 1.R1040 Contig ID g5606071 5'-most EST BLASTX Method g4469019 NCBI GI

BLAST score 1540 1.0e-172 E value 391 Match length 79 % identity

(AL035602) putative protein [Arabidopsis thaliana] NCBI Description

15037 Seq. No.

33649 3.R1040 Contig ID vwf700678118.hl 5'-most EST

Method BLASTX g4469019 NCBI GI BLAST score 184 5.0e-14 E value 58 Match length 62 % identity

(AL035602) putative protein [Arabidopsis thaliana] NCBI Description

15038 Seq. No.

33650 1.R1040 Contig ID 5'-most EST gsv701052825.hl

BLASTX Method q4454307 NCBI GI 553 BLAST score E value 6.0e-57 113 Match length % identity

(AJ132763) cyclophilin [Pseudotsuga menziesii] NCBI Description

15039 Seq. No.

33654 1.R1040 Contig ID V4R-01-Q1-B1-B12 5'-most EST



```
15040
Seq. No.
                   33656 1.R1040
Contig ID
                  wvk700683379.hl
5'-most EST
                  15041
Seq. No.
                   33656 2.R1040
Contig ID
                  fde700874046.hl
5'-most EST
                   15042
Seq. No.
                   33659 1.R1040
Contig ID
                  ncj700985806.hl
5'-most EST
                   BLASTX
Method
                   g3122367
NCBI GI
                   144
BLAST score
                   8.0e-09
E value
                   150
Match length
                   28
% identity
NCBI Description LIGATIN >gi_1377880 (U58337) ligatin [Mus musculus]
                   15043
Seq. No.
                   33659 2.R1040
Contig ID
                   smc700747892.h1
5'-most EST
                   15044
Seq. No.
                   33661 1.R1040
Contig ID
                   LIB3139-117-P1-N1-G7
5'-most EST
                   15045
Seq. No.
                   33668 1.R1040
Contig ID
                   seb70\overline{0}649793.h1
5'-most EST
                   BLASTX
Method
                   g3451474
NCBI GI
                   652
BLAST score
                   4.0e-68
E value
Match length
                   216
                   56
% identity
                   (AL031349) conserved hypothetical protein
NCBI Description
                   [Schizosaccharomyces pombe]
                   15046
Seq. No.
                   33670 1.R1040
Contig ID
                   LIB3093-046-Q1-K1-G1
5'-most EST
                   BLASTX
Method
                   q4512699
NCBI GI
BLAST score
                   422
                   2.0e-41
E value
                   102
Match length
                   73
% identity
                   (AC006569) putative NADH-ubiquinone oxireductase
NCBI Description
                    [Arabidopsis thaliana]
```

15047 Seq. No.

Contig ID

33675 1.R1040

LIB3056-008-Q1-N1-B7 5'-most EST

Seq. No.

15048

Contig ID

33676\_1.R1040

2525



```
5'-most EST
                     LIB3139-104-P1-N1-E4
                     15049
Seq. No.
                     33678 1.R1040
Contig ID
5'-most EST
                     LIB3056-008-Q1-N1-C1
                     BLASTN
Method
NCBI GI
                     q2264314
                     57
BLAST score
                     4.0e-23
E value
                     198
Match length
% identity
                     Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                     MOK4, complete sequence [Arabidopsis thaliana]
                     15050
Seq. No.
                     33679 1.R1040
Contig ID
5'-most EST
                     fC-qmst700890233f2
Method
                     BLASTX
                     q417562
NCBI GI
                     394
BLAST score
                     2.0e-37
E value
                     260
Match length
% identity
                     PROTEIN-TYROSINE PHOSPHATASE YVH1 (PTPASE YVH1)
NCBI Description
                     >gi_320806_pir__S31304 protein-tyrosine-phosphatase (EC
3.1.3.48) YVH1 - yeast (Saccharomyces cerevisiae)
>gi_172168 (L04673) phosphatase [Saccharomyces cerevisiae]
                     >gi_557832 emb_CAA86186_ (Z38061) yvh1, len: 364, CAI: 0.17, PVH1_YEAST Q02256 PROTEIN-TYROSINE PHOSPHATASE YVH1
                      [Saccharomyces cerevisiae]
Seq. No.
                     15051
Contig ID
                     33679 2.R1040
                     xpa70\overline{0}793513.h1
5'-most EST
Method
                     BLASTX
                      g2832664
NCBI GI
BLAST score
                      163
                      6.0e-11
E value
Match length
                      99
                      37
% identity
                      (ALO21710) pollen-specific protein - like [Arabidopsis
NCBI Description
                      thaliana]
                      15052
Seq. No.
                      33679 3.R1040
Contig ID
                     bth700849288.h1
5'-most EST
                      15053
Seq. No.
                      33684 1.R1040
Contig ID
                      trc700561278.h1
5'-most EST
                      BLASTX
Method
                      g2582381
NCBI GI
BLAST score
                      165
                      2.0e-11
E value
                      97
Match length
                      49
% identity
```

NCBI Description (AF021220) cation-chloride co-transporter [Nicotiana



. No. 15054

Seq. No. 15054 Contig ID 33695 1.R1040

5'-most EST LIB3139-121-P1-N1-F2

Method BLASTX
NCBI GI g3386619
BLAST score 367
E value 7.0e-35
Match length 148
% identity 51

NCBI Description (AC004665) hypothetical protein [Arabidopsis thaliana]

Seq. No. 15055

Contig ID 33700\_1.R1040 5'-most EST uC-gmropic070a12b1

Method BLASTX
NCBI GI g3912923
BLAST score 142
E value 1.0e-08
Match length 76
% identity 51

NCBI Description (AF001308) hypothetical protein [Arabidopsis thaliana]

Seq. No. 15056

Contig ID 33700\_2.R1040 5'-most EST V4R-01-Q1-B1-A7

Seq. No. 15057

Contig ID 33706\_1.R1040 5'-most EST 6HA-01-Q1-B1-G7

Method BLASTX
NCBI GI g4176527
BLAST score 153
E value 1.0e-09
Match length 264
% identity 21

NCBI Description (AL035263) hypothetical protein [Schizosaccharomyces pombe]

Seq. No. 15058

Contig ID 33708 1.R1040

5'-most EST jC-gmro02800041b08a1

Seq. No. 15059

Contig ID 33712 1.R1040

5'-most EST uC-gmrominsoy187g10b1

Method BLASTX
NCBI GI g4572674
BLAST score 370
E value 4.0e-35
Match length 185
% identity 49

NCBI Description (AC006954) unknown protein [Arabidopsis thaliana]

Seq. No. 15060

Contig ID 33712\_2.R1040

5'-most EST LIB3139-119-P1-N1-A9



```
BLASTX
Method
                  q4572674
NCBI GI
BLAST score
                  245
                  1.0e-20
E value
                  126
Match length
                  49
% identity
NCBI Description (AC006954) unknown protein [Arabidopsis thaliana]
                  15061
Seq. No.
                  33718_1.R1040
Contig ID
                  LIB3056-007-Q1-N1-E6
5'-most EST
                  BLASTX
Method
                   g3953458
NCBI GI
BLAST score
                   838
                   1.0e-89
E value
                   365
Match length
                   72
% identity
                  (AC002328) F20N2.3 [Arabidopsis thaliana]
NCBI Description
                   15062
Seq. No.
                   33721_1.R1040
Contig ID
                   LIB3056-007-Q1-N1-F1
5'-most EST
                   15063
Seq. No.
                   33723 1.R1040
Contig ID
                   kmv700741323.hl
5'-most EST
                   15064
Seq. No.
                   33726 1.R1040
Contig ID
                   LIB3056-007-Q1-N1-C5
5'-most EST
                   BLASTX
Method
                   g3786012
NCBI GI
                   182
BLAST score
E value
                   2.0e-13
Match length
                   48
                   69
% identity
                  (AC005499) putative acid phosphatase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   15065
                   33729 1.R1040
Contig ID
5'-most EST
                   jC-qmro02910074a01a1
                   BLASTX
Method
NCBI GI
                   g3297815
BLAST score
                   180
E value
                   4.0e-13
Match length
                   50
% identity
                   (AL031032) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   15066
                   33730 1.R1040
Contig ID
                   LIB3056-007-Q1-N1-D1
5'-most EST
```

15067 Seq. No. Contig ID

33731\_1.R1040 uC-gmronoir011b07b1 5'-most EST

BLASTX Method

2528



NCBI GI g3850064
BLAST score 431
E value 3.0e-42
Match length 219
% identity 42

NCBI Description (Z97208) putative Na/H exchanger [Schizosaccharomyces

pombe]

Seq. No. 15068

Contig ID 33736\_1.R1040

5'-most EST LIB3056-007-Q1-N1-A5

Seq. No. 15069

Contig ID 33738 1.R1040 5'-most EST sat701007982.h1

Method BLASTX
NCBI GI g1755166
BLAST score 727
E value 7.0e-77
Match length 202
% identity 70

NCBI Description (U75194) germin-like protein [Arabidopsis thaliana]

Seq. No. 15070

Contig ID 33747\_1.R1040

5'-most EST LIB3056-006-Q1-N1-H1

Seq. No. 15071

Contig ID 33748\_1.R1040 5'-most EST g4282573

Seq. No. 15072

Contig ID 33750\_1.R1040

5'-most EST LIB3056-006-Q1-N1-H2

Method BLASTX
NCBI GI g2435512
BLAST score 294
E value 2.0e-33
Match length 122
% identity 63

NCBI Description (AF024504) No definition line found [Arabidopsis thaliana]

Seq. No. 15073

Contig ID 33758\_1.R1040

5'-most EST LIB3106-062-Q1-K1-C6

Method BLASTX
NCBI GI 94206195
BLAST score 560
E value 2.0e-57
Match length 178
% identity 64

NCBI Description (AF071527) hypothetical protein [Arabidopsis thaliana] >gi 4262169 gb AAD14469\_ (AC005275) hypothetical protein

[Arabidopsis thaliana]

Seq. No. 15074

Contig ID 33758\_2.R1040

```
5'-most EST
                  jC-gmle01810093g03a1
                  15075
Seq. No.
                  33769 1.R1040
Contig ID
                  pmv700891653.h1
5'-most EST
                  15076
Seq. No.
Contig ID
                  33770 1.R1040
                  jC-gmst02400057f08a1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g2979559
BLAST score
                  310
E value
                  1.0e-27
Match length
                   66
                   88
% identity
                  (AC003680) putative DNA binding protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   15077
                   33774 1.R1040
Contig ID
                   jC-gmro02910026d02d1
5'-most EST
                  BLASTX
Method
                   g3510251
NCBI GI
BLAST score
                   638
                   1.0e-66
E value
Match length
                   176
                   69
% identity
                  (AC005310) unknown protein [Arabidopsis thaliana]
NCBI Description
                   15078
Seq. No.
                   33788 1.R1040
Contig ID
                   trc700563909.h1
5'-most EST
                   15079
Seq. No.
                   33788 2.R1040
Contig ID
                   pxt700944605.h1
5'-most EST
Method
                   BLASTX
                   q2245131
NCBI GI
BLAST score
                   143
E value
                   1.0e-08
Match length
                   106
                   40
% identity
```

(Z97344) hypothetical protein [Arabidopsis thaliana] NCBI Description

Seq. No.

15080

Contig ID

33789 1.R1040

5'-most EST

LIB3170-003-Q1-K1-A12

NCBI GI

Method

BLASTX q2342683

BLAST score

159

E value

1.0e-10

15081

Match length

65

% identity

68

NCBI Description

(AC000106) Contains similarity to Bos beta-mannosidase

(gb\_U46067). [Arabidopsis thaliana]

Seq. No.

2530



```
33791 1.R1040
Contig ID
5'-most EST
                  LIB3087-003-Q1-K1-F4
                  BLASTX
Method
                   q4519671
NCBI GI
BLAST score
                   343
                   5.0e-32
E value
Match length
                   109
% identity
NCBI Description (AB017693) transfactor [Nicotiana tabacum]
                   15082
Seq. No.
                   33791_2.R1040
Contig ID
5'-most EST
                   sat701014709.hl
                   BLASTX
Method
                   q4519671
NCBI GI
                   304
BLAST score
                   1.0e-27
E value
                   99
Match length
                   63
% identity
                  (AB017693) transfactor [Nicotiana tabacum]
NCBI Description
                   15083
Seq. No.
                   33792 1.R1040
Contig ID
5'-most EST
                   hrw701061013.h1
                   15084
Seq. No.
Contig ID
                   33793 1.R1040
                   LIB3056-006-Q1-N1-B8
5'-most EST
                   15085
Seq. No.
                   33798 1.R1040
Contig ID
                   eep700867581.hl
5'-most EST
                   BLASTX
Method
                   g2129953
NCBI GI
BLAST score
                   462
                   3.0e-46
E value
Match length
                   105
                   74
% identity
                   laccase (EC 1.10.3.2) - common tobacco >gi_1685087 (U43542)
NCBI Description
                   diphenol oxidase [Nicotiana tabacum]
                   15086
Seq. No.
                   33802 1.R1040
Contig ID
                   sat701009927.h2
 5'-most EST
 Seq. No.
                   15087
                   33808 1.R1040
 Contig ID
                   jC-gmro02800043g09a1
 5'-most EST
                   15088
 Seq. No.
                   33810 1.R1040
 Contig ID
                   trc700562488.hl
 5'-most EST
                   BLASTX
Method
                   g3885338
 NCBI GI
```

2531

152

97

9.0e-10

BLAST score

E value Match length



% identity 32
NCBI Description (AC005623) unknown protein [Arabidopsis thaliana]

Seq. No. 15089

Contig ID 33812\_1.R1040 5'-most EST sat701011888.h1

Seq. No. 15090

Contig ID 33815\_1.R1040 5'-most EST zhf700965049.h1

Method BLASTX
NCBI GI g4220476
BLAST score 1019
E value 1.0e-126
Match length 311
% identity 71

NCBI Description (AC006069) ribophorin I-like protein [Arabidopsis thaliana]

Seq. No. 15091

Contig ID 33820 1.R1040

5'-most EST LIB3056-006-Q1-N1-B11

Seq. No. 15092

Contig ID 33822\_1.R1040

5'-most EST LIB3107-067-Q1-K1-E12

Method BLASTX
NCBI GI g120777
BLAST score 200
E value 2.0e-15
Match length 88
% identity 45

NCBI Description SUCCINATE-SEMIALDEHYDE DEHYDROGENASE (NADP+) (SSDH)

>gi\_147901 (M88334) succinic semialdehyde dehydrogenase

[Escherichia coli] >gi\_1789015 (AE000351)

succinate-semialdehyde dehydrogenase, NADP-dependent

activity [Escherichia coli]

Seq. No. 15093

Contig ID 33824\_1.R1040 5'-most EST g5606127

Seq. No. 15094

Contig ID 33824 2.R1040

5'-most EST LIB3139-022-P1-N1-G9

Seq. No. 15095

Contig ID 33828\_1.R1040

5'-most EST jC-gmro02910022d03a1

Seq. No. 15096

Contig ID 33828 2.R1040

5'-most EST uC-gmrominsoy198f08b1

Seq. No. 15097

Contig ID 33828\_3.R1040 5'-most EST epx701106096.h1

5'-most EST

Method

NCBI GI BLAST score

E value

```
15098
Seq. No.
                  33835 1.R1040
Contig ID
                  jC-gmle01810041g04a1
5'-most EST
Seq. No.
                  15099
                  33835 2.R1040
Contig ID
                  asn701131538.h1
5'-most EST
                  BLASTX
Method
                   g2462825
NCBI GI
BLAST score
                   160
                   1.0e-10
E value
                   41
Match length
                   68
% identity
                  (AF000657) contains Procite 'RNP1' putative RNA-binding
NCBI Description
                   region [Arabidopsis thaliana]
                   15100
Seq. No.
                   33848 1.R1040
Contig ID
                   bth700844245.h1
5'-most EST
                   BLASTX
Method
                   g3377843
NCBI GI
BLAST score
                   946
                   1.0e-102
E value
                   301
Match length
                   67
% identity
                   (AF076274) contains similarity to rat p47 protein
NCBI Description
                   (GB:AB002086) [Arabidopsis thaliana]
                   15101
Seq. No.
                   33849 1.R1040
Contig ID
                   jC-gmst02400067c07a1
5'-most EST
                   BLASTX
Method
                   g3036816
NCBI GI
                   252
BLAST score
                   4.0e-21
E value
                   241
Match length
                   36
% identity
                   (AL022373) myosin-like protein [Arabidopsis thaliana]
NCBI Description
                   15102
Seq. No.
                   33852 1.R1040
Contig ID
                   LIB3056-005-Q1-N1-F3
5'-most EST
                   BLASTX
Method
                   q2827623
NCBI GI
BLAST score
                   343
                   3.0e - 32
E value
                   89
Match length
                   74
 % identity
NCBI Description (AL021636) putative protein [Arabidopsis thaliana]
 Seq. No.
                   15103
                   33856 1.R1040
 Contig ID
```

2533

LIB3056-005-Q1-N1-F8

BLASTX

211 2.0e-16

g3157941



Match length 99
% identity 46
NCBI Description (AC002131) Contains similarity to hypothetical protein gb U95973 from A. thaliana. [Arabidopsis thaliana]

Seq. No. 15104

Contig ID 33864 1.R1040

5'-most EST LIB3056-005-Q1-N1-D2

Method BLASTX
NCBI GI g2245087
BLAST score 264
E value 4.0e-23
Match length 129
% identity 47

NCBI Description (Z97343) hypothetical protein [Arabidopsis thaliana]

Seq. No. 15105

Contig ID 33866\_1.R1040 5'-most EST eep700866045.h1

Method BLASTX
NCBI GI g1709745
BLAST score 655
E value 2.0e-80
Match length 288
% identity 52

NCBI Description SERINE/THREONINE PROTEIN PHOSPHATASE 5 (PP5) (PROTEIN

PHOSPHATASE T) (PPT) >gi\_663080\_emb\_CAA54454\_ (X77237)

protein phosphatase T (PPT) [Rattus norvegicus]

Seq. No. 15106

Contig ID 33866\_2.R1040

5'-most EST LIB3139-092-P1-N1-B6

Method BLASTX
NCBI GI g4512673
BLAST score 220
E value 7.0e-18
Match length 68
% identity 71

NCBI Description (AC006931) putative phosphoprotein phosphatase [Arabidopsis

thaliana]

Seq. No. 15107

Contig ID 33869\_1.R1040 5'-most EST smc700749524.h1

Seq. No. 15108

Contig ID 33873\_1.R1040

5'-most EST LIB3056-003-Q1-N1-G11

Method BLASTX
NCBI GI g4336426
BLAST score 164
E value 3.0e-11
Match length 55
% identity 56

NCBI Description (AF090835) Ca2+-dependent protein kinase [Mesembryanthemum

crystallinum]



15109 Seq. No. 33873 2.R1040 Contig ID bth700848422.hl 5'-most EST Method BLASTX g3283996 NCBI GI 175 BLAST score 1.0e-12 E value 67 Match length 51 % identity (AF072908) calcium-dependent protein kinase [Nicotiana NCBI Description tabacum] 15110 Seq. No. 33874\_1.R1040 Contig ID jC-gmf102220063a11a1 5'-most EST Method BLASTX q4191396 NCBI GI 487 BLAST score 2.0e-55 E value 362 Match length 39 % identity (AF096304) putative sterol reductase SR-1 [Homo sapiens] NCBI Description >gi\_4191403 (AF096303) putative sterol reductase SR-1 [Homo sapiens] 15111 Seq. No. 33878 1.R1040 Contig ID sat701014304.h1 5'-most EST 15112 Seq. No. 33878 2.R1040 Contig ID sat701005564.h1 5'-most EST 15113 Seq. No. 33879 1.R1040 Contig ID LIB3093-022-Q1-K1-E12 5'-most EST BLASTX Method q129808 NCBI GI BLAST score 1242 1.0e-137 E value 319 Match length 77 % identity

CATIONIC PEROXIDASE 2 PRECURSOR >gi\_99873\_pir\_\_B38265 NCBI Description peroxidase (EC 1.11.1.7) precursor, cationic (clone PNC2) peanut >gi\_166475 (M37637) cationic peroxidase [Arachis

hypogaea]

15114 Seq. No.

33881 1.R1040 Contig ID

jC-gmst02400071d08a1 5'-most EST

Method BLASTX NCBI GI q4220477 BLAST score 247 1.0e-20 E value Match length 102 43 % identity

NCBI Description (AC006069) unknown protein [Arabidopsis thaliana]

NCBI GI

E value

BLAST score

Match length



```
15115
Seq. No.
                  33883 1.R1040
Contig ID
                  zhf700951986.hl
5'-most EST
Method
                  BLASTX
NCBI GI
                  q3149952
BLAST score
                  1754
                  0.0e + 00
E value
Match length
                  514
                  68
% identity
NCBI Description (AB010259) DRH1 [Arabidopsis thaliana]
Seq. No.
                  15116
                  33893 1.R1040
Contig ID
5'-most EST
                  LIB3092-034-Q1-K1-C1
Method
                  BLASTX
                  q4510376
NCBI GI
BLAST score
                  498
                  9.0e-50
E value
Match length
                  379
                  36
% identity
                 (AC007017) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  15117
Contig ID
                  33893_2.R1040
5'-most EST
                  uC-gmflminsoy045b12b1
Method
                  BLASTX
                  a4510376
NCBI GI
BLAST score
                  287
E value
                  9.0e-26
Match length
                  87
                  59
% identity
NCBI Description (AC007017) unknown protein [Arabidopsis thaliana]
                  15118
Seq. No.
                  33893 3.R1040
Contig ID
5'-most EST
                  uC-gmropic059g01b1
                  BLASTX
Method
NCBI GI
                  g4510376
BLAST score
                  145
E value
                  5.0e-09
                  41
Match length
% identity
NCBI Description
                 (AC007017) unknown protein [Arabidopsis thaliana]
Seq. No.
                  15119
                  33898 1.R1040
Contig ID
5'-most EST
                  LIB3056-004-Q1-N1-H11
                  15120
Seq. No.
Contig ID
                  33899 1.R1040
5'-most EST
                  sat701003784.h1
Method
                  BLASTX
```

2536

q4455270

5.0e-15

198

55



% identity 64
NCBI Description (AL035527) putative protein [Arabidopsis thaliana]

Seq. No. 15121

Contig ID 33899 2.R1040

5'-most EST jC-gmfl02220125f05a1

Seg. No. 15122

Contig ID 33900\_1.R1040 5'-most EST fC-gmro700748571a2

Seq. No. 15123

Contig ID 33902 1.R1040

5'-most EST LIB3 $\overline{10}$ 6-009-Q1-K1-C1

Method BLASTX
NCBI GI g2795809
BLAST score 1173
E value 1.0e-129
Match length 257
% identity 82

NCBI Description (AC003674) putative expansin [Arabidopsis thaliana]

Seq. No. 15124

Contig ID 33902\_2.R1040 5'-most EST sat701003023.h1

Method BLASTX
NCBI GI g3461837
BLAST score 703
E value 2.0e-74
Match length 150
% identity 81

NCBI Description (AC005315) putative expansin [Arabidopsis thaliana]

>gi 3927842 (AC005727) expansin AtEx6 [Arabidopsis

thaliana]

Seq. No. 15125

Contig ID 33902\_3.R1040 5'-most EST pcp700992585.h1

Method BLASTX
NCBI GI g2795809
BLAST score 150
E value 9.0e-10
Match length 70
% identity 70

NCBI Description (AC003674) putative expansin [Arabidopsis thaliana]

Seq. No. 15126

Contig ID 33911\_1.R1040 5'-most EST trc700561366.h1

Method BLASTX
NCBI GI g1432056
BLAST score 584
E value 5.0e-60
Match length 332
% identity 47

NCBI Description (U56834) WRKY3 [Petroselinum crispum]



```
15127
Seq. No.
                  33911 2.R1040
Contig ID
                  LIB3093-016-Q1-K1-H6
5'-most EST
                  BLASTX
Method
                  g1432056
NCBI GI
                  221
BLAST score
                  1.0e-17
E value
Match length
                  52
                  75
% identity
NCBI Description (U56834) WRKY3 [Petroselinum crispum]
                  15128
Seq. No.
                  33911_3.R1040
Contig ID
                  jC-gmst02400049c05a1
5'-most EST
                  BLASTX
Method
                  q1432056
NCBI GI
                  188
BLAST score
                  6.0e-14
E value
                  127
Match length
                  39
% identity
NCBI Description (U56834) WRKY3 [Petroselinum crispum]
                  15129
Seq. No.
Contig ID
                   33911 4.R1040
                  pmv700889957.h1
5'-most EST
                   15130
Seq. No.
                   33915 1.R1040
Contig ID
5'-most EST
                  LIB3139-013-P1-N1-B5
Method
                  BLASTX
                   g2492863
NCBI GI
                   1170
BLAST score
                   1.0e-128
E value
Match length
                   425
                   54
% identity
                   ORNITHINE AMINOTRANSFERASE (ORNITHINE--OXO-ACID
NCBI Description
                   AMINOTRANSFERASE) >gi_4416517_gb_AAB18259_ (U74303)
                   ornithine transaminase [Emericella nidulans]
                   15131
Seq. No.
                   33918 1.R1040
Contig ID
                   kl1701209378.h1
5'-most EST
                   15132
Seq. No.
                   33918 2.R1040
Contig ID
                   uC-gmrominsoy057b02b1
5'-most EST
Seq. No.
                   15133
                   33918 3.R1040
```

Contig ID

5'-most EST

leu701156453.h1

Seq. No.

15134

Contig ID

33919 1.R1040

5'-most EST Method

LIB3056-004-Q1-N1-G1 BLASTX

NCBI GI

g2262116

BLAST score

401

```
E value 6.0e-53
Match length 324
% identity 40
```

NCBI Description (AC002343) cellulose synthase isolog [Arabidopsis thaliana]

Seq. No. 15135

Contig ID 33927\_1.R1040
5'-most EST g4437151
Method BLASTX
NCBI GI g3695059
BLAST score 436
E value 3.0e-43
Match length 122

% identity 72
NCBI Description (AF064787) rac GTPase activating protein 1 [Lotus

japonicus]

Seq. No. 15136

Contig ID 33932 1.R1040

5'-most EST LIB3056-004-Q1-N1-E11

Seq. No. 15137

Contig ID 33932 2.R1040 5'-most EST vzy700755326.h1

Seq. No. 3 15138

Contig ID 33935\_1.R1040

5'-most EST LIB31 $\overline{0}6$ -096-Q1-K1-C7

Method BLASTX
NCBI GI g3080433
BLAST score 582
E value 5.0e-65
Match length 226
% identity 59

NCBI Description (AL022605) putative gamma-glutamyltransferase [Arabidopsis

thaliana]

Seq. No. 15139

Contig ID 33941\_1.R1040

5'-most EST jC-gmro02910026g01d1

Method BLASTX
NCBI GI g2642154
BLAST score 336
E value 5.0e-31
Match length 121
% identity 53

NCBI Description (AC003000) unknown protein [Arabidopsis thaliana]

>gi 3790595 (AF079186) RING-H2 finger protein RHC2a

[Arabidopsis thaliana]

Seq. No. 15140

Contig ID 33942\_1.R1040

5'-most EST LIB3056-004-Q1-N1-F10

Method BLASTX
NCBI GI g4510371
BLAST score 248
E value 5.0e-21



```
Match length
                   58
% identity
                   (AC007017) putative harpin-induced protein [Arabidopsis
NCBI Description
                  thaliana]
                   15141
Seq. No.
                   33946_1.R1040
Contig ID
                   epx701110486.hl
5'-most EST
                  BLASTX
Method
                   g4056490
NCBI GI
BLAST score
                   266
                   4.0e-23
E value
                   94
Match length
                   57
% identity
                  (AC005896) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   15142
Seq. No.
                   33950 1.R1040
Contig ID
                   dpv701103437.hl
5'-most EST
                   15143
Seq. No.
                   33971 1.R1040
Contig ID
                   LIB3093-018-Q1-K2-D4
5'-most EST
                   BLASTX
Method
                   g4512670
NCBI GI
BLAST score
                   170
                   7.0e-12
E value
Match length
                   130
                   32
% identity
                  (AC006931) putative cytochrome P450 [Arabidopsis thaliana]
NCBI Description
                   15144
Seq. No.
                   33972 1.R1040
Contig ID
                   LIB3056-004-Q1-N1-C1
5'-most EST
                   BLASTX
Method
                   g4580519
NCBI GI
                   1004
BLAST score
                   1.0e-109
E value
                   358
Match length
                   59
 % identity
                   (AF036303) scarecrow-like 6 [Arabidopsis thaliana]
NCBI Description
                   15145
 Seq. No.
                   33974 1.R1040
 Contig ID
 5'-most EST
                   gsv701048675.hl
                   15146
 Seq. No.
                   33978 1.R1040
 Contig ID
 5'-most EST
                   eep700869926.hl
                   BLASTX
 Method
```

NCBI GI q4309732 214 BLAST score 7.0e-17 E value 65 Match length % identity

NCBI Description (AC006439) hypothetical protein [Arabidopsis thaliana]



Seq. No. 1514

Contig ID 33979\_1.R1040 5'-most EST jsh701068392.h1

Seq. No. 15148

Contig ID 33980\_1.R1040 5'-most EST g4260051

Seq. No. 15149

Contig ID 33981\_1.R1040

5'-most EST LIB3056-003-Q1-N1-H6

Seq. No. 15150

Contig ID 33989\_1.R1040

5'-most EST LIB3107-003-Q1-K1-G3

Method BLASTX
NCBI GI g2828296
BLAST score 2503
E value 0.0e+00
Match length 549
% identity 62

NCBI Description (AL021687) RNase L inhibitor [Arabidopsis thaliana]

Seq. No. 15151

Contig ID 33990\_1.R1040

5'-most EST LIB3072-027-Q1-E1-H6

Seq. No. 15152

Contig ID 33990 2.R1040

5'-most EST LIB3072-027-Q1-E1-H4

Seq. No. 15153

Contig ID 33994\_1.R1040

5'-most EST LIB3056-003-Q1-N1-F12

Seq. No. 15154

Contig ID 33997 1.R1040

5'-most EST LIB3056-003-Q1-N1-F5

Seq. No. 15155

Contig ID 34002\_1.R1040

5'-most EST LIB3167-078-P1-K2-H4

Seq. No. 15156

Contig ID 34020\_1.R1040 5'-most EST leu701145205.h1

Seq. No. 15157

Contig ID 34027\_1.R1040

5'-most EST uC-gmrominsoy123b05b1

Method BLASTX
NCBI GI g1665817
BLAST score 382
E value 3.0e-36
Match length 199
% identity 41

NCBI Description (D87466) Similar to S.cerevisiae hypothetical protein L3111



## (S59316) [Homo sapiens]

```
15158
Seq. No.
                  34033 1.R1040
Contig ID
                  trc700562274.h1
5'-most EST
                  15159
Seq. No.
                   34033 2.R1040
Contig ID
                  LIB3139-026-P1-N1-G4
5'-most EST
                   15160
Seq. No.
                   34042_1.R1040
Contig ID
5'-most EST
                   uC-gmropic058b12b1
Method
                   BLASTX
                   q2842424
NCBI GI
                   498
BLAST score
                   1.0e-52
E value
                   158
Match length
                   66
% identity
                  (AJ223948) RNA helicase [Homo sapiens]
NCBI Description
                   15161
Seq. No.
                   34043_1.R1040
Contig ID
                   hyd700729495.hl
5'-most EST
Method
                   BLASTX
                   a1402918
NCBI GI
                   878
BLAST score
                   1.0e-94
E value
Match length
                   215
                   80
% identity
                   (X98320) peroxidase [Arabidopsis thaliana]
NCBI Description
                   >qi 1429215 emb CAA67310_ (X98774) peroxidase ATP6a
                   [Arabidopsis thaliana]
                   15162
Seq. No.
                   34043 2.R1040
Contig ID
                   uC-gmronoir053a08b1
5'-most EST
                   BLASTX
Method
                   q1402918
NCBI GI
                   289
BLAST score
                   8.0e-31
E value
                   86
Match length
                   84
% identity
                   (X98320) peroxidase [Arabidopsis thaliana]
NCBI Description
                   >gi_1429215_emb_CAA67310_ (X98774) peroxidase ATP6a
                   [Arabidopsis thaliana]
                   15163
Seq. No.
                   34050 1.R1040
Contig ID
                   epx701109062.h1
5'-most EST
                   BLASTX
Method
                   g418754
NCBI GI
                   566
BLAST score
                   4.0e-58
E value
Match length
                   249
```

NCBI Description catechol oxidase (EC 1.10.3.1) precursor - fava bean

49

% identity

```
Seq. No.
                  15164
                  34051 1.R1040
Contig ID
                  uC-gmrominsoy139h02b1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q3868857
BLAST score
                   441
                  2.0e-43
E value
                   124
Match length
                   73
% identity
NCBI Description (AB013886) RAV1 [Arabidopsis thaliana]
Seq. No.
                   15165
                   34054 1.R1040
Contig ID
5'-most EST
                  LIB3056-003-Q1-N1-B12
                   15166
Seq. No.
                   34057 1.R1040
Contig ID
5'-most EST
                   sat701003814.hl
                   15167
Seq. No.
                   34058 1.R1040
Contig ID
5'-most EST
                   LIB3056-003-Q1-N1-B5
                   15168
Seq. No.
                   34062 1.R1040
Contig ID
5'-most EST
                   q5058508
                   BLASTX
Method
NCBI GI
                   g3482979
BLAST score
                   205
E value
                   1.0e-15
Match length
                   92
% identity
                   41
                   (AL031369) putative protein [Arabidopsis thaliana]
NCBI Description
                   >gi_4567258_gb_AAD23672.1_AC007070_21 (AC007070)
                   hypothetical protein [Arabidopsis thaliana]
                   15169
Seq. No.
                   34062 2.R1040
Contig ID
                   leu701148831.h1
5'-most EST
                   15170
Seq. No.
                   34062 3.R1040
Contig ID
5'-most EST
                   zsg701118642.h1
Seq. No.
                   15171
                   34064 1.R1040
Contig ID
                   LIB31\overline{0}7-080-Q1-K1-G10
5'-most EST
                   BLASTX
Method
```

Method BLASTX
NCBI GI g2160182
BLAST score 177
E value 2.0e-12
Match length 148
% identity 34

NCBI Description (AC000132) ESTs gb\_ATTS1236,gb\_T43334,gb\_N97019,gb\_AA395203 come from this gene. [Arabidopsis thaliana]



Seq. No.

34064 2.R1040 Contig ID q5606637 5'-most EST

15173 Seq. No.

34064 4.R1040 Contig ID 5'-most EST xpa700797687.h1

15174 Seq. No.

34075 1.R1040 Contig ID 5'-most EST zhf700960194.h1

BLASTX Method g3367521 NCBI GI BLAST score 356 2.0e-33 E value 225 Match length 10 % identity

(AC004392) Similar to gb U08285 membrane-associated NCBI Description

salt-inducible protein from Nicotiana tabacum. ESTs gb T44131 and gb\_T04378 come from this gene. [Arabidopsis

thaliana]

15175 Seq. No.

Contig ID 34081 1.R1040 fua701040809.hl 5'-most EST

BLASTX Method q584862 NCBI GI 417 BLAST score 9.0e-41 E value 141 Match length 59 % identity

CYTOCHROME P450 71A3 (CYPLXXIA3) (P-450EG3) NCBI Description

>gi\_480397\_pir\_\_S36807 cytochrome P450 71A3 - eggplant
(fragment) >gi\_408142\_emb\_CAA50313\_ (X70982) P450

hydroxylase [Solanum melongena]

15176 Seq. No.

34087 1.R1040 Contig ID sat701013090.h1 5'-most EST

BLASTN Method g2244741 NCBI GI 34 BLAST score 2.0e-09 E value Match length 46 93 % identity

Antirrhinum majus mRNA for bZIP DNA-binding protein, 1095 NCBI Description

рþ

15177 Seq. No.

34087 2.R1040 Contig ID uaw700667012.hl 5'-most EST

BLASTN Method g4457220 NCBI GI 34 BLAST score 2.0e-09 E value 50 Match length 92 % identity



NCBI Description Capsicum chinense putative bZIP DNA-binding protein mRNA, complete cds

15178 Seq. No. 34102 1.R1040 Contig ID g3258668 5'-most EST BLASTN Method NCBI GI g984755 BLAST score 111 3.0e-55 E value 111 Match length

100 % identity

NCBI Description O.sativa mRNA for chilling-inducible protein

15179 Seq. No.

34102 2.R1040 Contig ID

LIB3056-002-Q1-B1-D8 5'-most EST

BLASTX Method g4204300 NCBI GI 198 BLAST score 2.0e-15 E value 64 Match length 61

% identity

(AC003027) Unknown protein [Arabidopsis thaliana] NCBI Description

15180 Seq. No.

34109 1.R1040 Contig ID trc700568330.h1 5'-most EST

15181 Seq. No.

34110 1.R1040 Contig ID

5'-most EST uC-gmronoir064b12b1

Seq. No. 15182

34111 1.R1040 Contig ID

LIB3056-002-Q1-B1-D12 5'-most EST

15183 Seq. No.

34116 1.R1040 Contig ID

LIB3094-017-Q1-K1-C7 5'-most EST

15184 Seq. No.

34117\_1.R1040 Contig ID ncj700979323.hl 5'-most EST BLASTX Method

g3176726 NCBI GI BLAST score 801 9.0e-86 E value 206 Match length 72 % identity

(AC002392) putative serine proteinase [Arabidopsis NCBI Description

thaliana]

15185 Seq. No.

34125 1.R1040 Contig ID

5'-most EST LIB3056-002-Q1-B1-D1



```
Seq. No.
                  34127 1.R1040
Contig ID
                  epx701110255.hl
5'-most EST
                  BLASTX
Method
                  g2462828
NCBI GI
                  548
BLAST score
                  1.0e-71
E value
Match length
                   232
                   57
% identity
NCBI Description (AF000657) hypothetical protein [Arabidopsis thaliana]
                   15187
Seq. No.
                   34127 2.R1040
Contig ID
                   pmv700891261.hl
5'-most EST
                   BLASTX
Method
                   q2462828
NCBI GI
                   201
BLAST score
                   9.0e-16
E value
Match length
                   60
                   60
% identity
NCBI Description (AF000657) hypothetical protein [Arabidopsis thaliana]
                   15188
Seq. No.
Contig ID
                   34128 1.R1040
5'-most EST
                   LIB3056-002-Q1-B1-B7
Method
                   BLASTX
                   q3047125
NCBI GI
                   155
BLAST score
                   4.0e-10
E value
                   72
Match length
                   51
% identity
                  (AF058919) No definition line found [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   15189
                   34128 2.R1040
Contig ID
5'-most EST
                   LIB3170-006-Q1-J1-F4
                   15190
Seq. No.
                   34132 1.R1040
Contig ID
                   xpa700792563.hl
5'-most EST
                   BLASTX
Method
                   g3135611
NCBI GI
                   147
BLAST score
                   4.0e-09
E value
Match length
                   93
                   45
% identity
                   (AF062485) cellulose synthase [Arabidopsis thaliana]
NCBI Description
                   15191
Seq. No.
                   34155 1.R1040
Contig ID
                   uC-gmropic045e10b1
5'-most EST
                   BLASTX
Method
                   g1717755
NCBI GI
                   310
BLAST score
                   3.0e-28
E value
```

98

60

Match length

% identity



NCBI Description TROPINONE REDUCTASE HOMOLOG (P29X) >gi\_539028\_pir\_\_C48674 tropinone reductase homolog - jimsonweed >gi\_424158 (L20475) 29kDa protein; high homology to aa sequence of tropinone reductases [Datura stramonium]

Seq. No. 15192

Contig ID 34164\_1.R1040

5'-most EST LIB3139-062-P1-N1-B4

Method BLASTX
NCBI GI g4559333
BLAST score 156
E value 2.0e-15
Match length 92
% identity 32

NCBI Description (AC007087) unknown protein [Arabidopsis thaliana]

Seq. No. 15193

Contig ID 34175\_1.R1040 5'-most EST pcp700993918.h1

Seq. No. 15194

Contig ID 34179\_1.R1040 5'-most EST uC-gmropic096h08b1

Seq. No. 15195

Contig ID 34179\_3.R1040 5'-most EST zsg701129478.h1

Seq. No. 15196

Contig ID 34180\_1.R1040 5'-most EST wvk700683579.h1

Seq. No. 15197

Contig ID 34180 2.R1040

5'-most EST LIB3093-015-Q1-K1-A2

Method BLASTN
NCBI GI g3128136
BLAST score 35
E value 5.0e-10
Match length 147
% identity 88

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K1F13, complete sequence [Arabidopsis thaliana]

Seq. No. 15198

Contig ID 34181\_1.R1040 5'-most EST uC-gmropic037b12b1

Method BLASTX
NCBI GI 94415914
BLAST score 223
E value 3.0e-18
Match length 79
% identity 56

NCBI Description (AC006282) unknown protein [Arabidopsis thaliana]

Seq. No.

15199

Contig ID 34188\_1.R1040

```
5'-most EST
                  LIB3056-001-Q1-B1-C8
                  15200
Seq. No.
                  34204 1.R1040
Contig ID
                  smc700746134.hl
5'-most EST
                  BLASTX
Method
NCBI GI
                  g4490311
BLAST score
                  142
                   1.0e-08
E value
                  70
Match length
                   46
% identity
                  (AL035678) putative protein [Arabidopsis thaliana]
NCBI Description
                   15201
Seq. No.
                   34215 1.R1040
Contig ID
                   fC-gmle700743470d3
5'-most EST
                   15202
Seq. No.
                   34225 1.R1040
Contig ID
                   LIB3056-011-Q1-N1-F8
5'-most EST
                   15203
Seq. No.
                   34225 2.R1040
Contig ID
5'-most EST
                   LIB3170-038-Q1-J1-B7
Method
                   BLASTX
                   q4567197
NCBI GI
                   197
BLAST score
                   3.0e-15
E value
Match length
                   56
                   75
% identity
NCBI Description (AC007168) unknown protein [Arabidopsis thaliana]
                   15204
Seq. No.
                   34232 1.R1040
Contig ID
5'-most EST
                   fua701043069.h1
Method
                   BLASTX
                   g3805962
NCBI GI
                   816
BLAST score
                   2.0e-87
E value
                   185
Match length
% identity
                   81
                  (Y13772) laccase [Populus balsamifera subsp. trichocarpa]
NCBI Description
                   15205
Seq. No.
                   34232 2.R1040
Contig ID
                   smc700750140.h1
5'-most EST
                   {\tt BLASTX}
Method
                   g3805962
NCBI GI
                   172
BLAST score
                   1.0e-12
E value
                   52
Match length
                   65
% identity
                  (Y13772) laccase [Populus balsamifera subsp. trichocarpa]
NCBI Description
```

15206

34235 1.R1040

LIB3139-086-P1-N1-C12

Seq. No.

Contig ID

5'-most EST



Seq. No. 15207

Contig ID 34240\_1.R1040 5'-most EST gsv701044421.h1

Seq. No. 15208

Contig ID 34242\_1.R1040

5'-most EST LIB3107-002-Q1-K1-F6

Seq. No. 15209

Contig ID 34244\_1.R1040

5'-most EST LIB3056-002-Q1-B1-E3

Method BLASTX
NCBI GI g166878
BLAST score 199
E value 4.0e-15
Match length 106
% identity 43

NCBI Description (M95796) St12p protein [Arabidopsis thaliana]

Seq. No. 15210

Contig ID 34251\_1.R1040 5'-most EST fua701043216.h1

Seq. No. 15211

Contig ID 34251\_2.R1040 5'-most EST gsv701049501.h1

Seq. No. 15212

Contig ID 34258\_1.R1040

5'-most EST LIB3056-007-Q1-N1-B12

Method BLASTN
NCBI GI g1276902
BLAST score 181
E value 4.0e-97
Match length 445
% identity 85

NCBI Description Citrus limon phenylalanine ammonia-lyase (pal6) mRNA,

complete cds

Seq. No. 15213

Contig ID 34264\_1.R1040

5'-most EST uC-gmrominsoy086a06b1

Method BLASTN
NCBI GI g2995454
BLAST score 147
E value 8.0e-77
Match length 351
% identity 85

NCBI Description L.luteus mRNA for tRNA-glutamine synthetase

Seq. No. 15214

Contig ID 34265\_1.R1040

5'-most EST jC-gmle01810091c09a1

Method BLASTN
NCBI GI g414665
BLAST score 560



E value 0.0e+00
Match length 709
% identity 99

NCBI Description G.max gene for coproporphyrinogen oxidase

Seq. No. 15215

Contig ID 34271\_1.R1040 5'-most EST zsg701127294.h1

Method BLASTX
NCBI GI g2623295
BLAST score 340
E value 2.0e-31
Match length 269
% identity 32

% identity 32
NCBI Description (AC002409) hypothetical protein [Arabidopsis thaliana]

Seq. No. 15216

Contig ID 34271\_2.R1040 5'-most EST uxk700670993.h1

Seq. No. 15217

Contig ID 34280\_1.R1040

5'-most EST LIB3109-052-Q1-K1-H4

Seq. No. 15218

Contig ID 34281\_1.R1040 5'-most EST pxt700943540.h1

Seq. No. 15219

Contig ID 34289\_1.R1040

5'-most EST uC-gmflminsoy070f08b1

Method BLASTN
NCBI GI g2632108
BLAST score 291
E value 1.0e-162
Match length 479
% identity 90

NCBI Description Pisum sativum mRNA for phospholipid glutathione peroxidase

Seq. No. 15220

Contig ID 34289\_3.R1040 5'-most EST rca700997878.h1

Method BLASTN
NCBI GI g2632108
BLAST score 108
E value 1.0e-53
Match length 168
% identity 91

NCBI Description Pisum sativum mRNA for phospholipid glutathione peroxidase

Seq. No. 15221

Contig ID 34329\_1.R1040 5'-most EST g4405704

Seq. No. 15222

Contig ID 34329\_2.R1040

5'-most EST LIB3065-025-Q1-N1-G6



```
15223
Seq. No.
                   34333 1.R1040
Contig ID
                   kl170\overline{1}206110.h1
5'-most EST
                   BLASTX
Method
                   g3335333
NCBI GI
BLAST score
                   326
                   4.0e-30
E value
Match length
                   109
                   61
% identity
                   (ACO04512) Similar to chloroplast membrane-associated 30KD
NCBI Description
                   protein precursor (IM30) gb_M73744 from Pisum sativum.
                   ESTs gb_N37557, gb_W43887 and gb_AA042479 come from this
                   gene. [Arabidopsis thaliana]
                   15224
Seq. No.
                   34334 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy058f10b1
Method
                   BLASTX
NCBI GI
                   g3757521
BLAST score
                   1156
                   1.0e-127
E value
                   286
Match length
% identity
                   75
                  (AC005167) unknown protein [Arabidopsis thaliana]
NCBI Description
                   15225
Seq. No.
                   34359 1.R1040
Contig ID
5'-most EST
                   ssr700560378.hl
                   BLASTX
Method
                   g2960216
NCBI GI
BLAST score
                   408
E value
                   1.0e-39
Match length
                   99
                   81
% identity
                   (AJ223384) 26S proteasome regulatory ATPase subunit 10b
NCBI Description
                   (S10b) [Manduca sexta]
Seq. No.
                   15226
                   34359 2.R1040
Contig ID
5'-most EST
                   jC-gmro02910033a12d1
                   15227
Seq. No.
                   34369 1.R1040
Contig ID
                   a1170\overline{0}863128.h1
5'-most EST
Method
                   BLASTN
                   g167227
NCBI GI
BLAST score
                   159
                   3.0e-84
E value
                   311
Match length
% identity
```

Seq. No. 15228

Contig ID 34384\_1.R1040 5'-most EST ncj700984528.h1

NCBI Description Canavalia ensiformis urease (ure) mRNA, complete cds



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Seq. No. 1522
```

Contig ID 34392\_1.R1040 5'-most EST ncj700982077.h1

Seq. No. 15230

Contig ID 34403\_1.R1040

5'-most EST LIB3065-023-Q1-N1-H3

Seq. No. 15231

Contig ID 34453\_1.R1040 5'-most EST pmv700894679.h1

Method BLASTX
NCBI GI g4508083
BLAST score 270
E value 1.0e-23
Match length 152
% identity 8

NCBI Description (AC005882) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 15232

Contig ID 34477\_1.R1040

5'-most EST LIB3093-039-Q1-K1-C12

Method BLASTX
NCBI GI g2245020
BLAST score 266
E value 3.0e-23
Match length 89
% identity 66

NCBI Description (Z97341) growth regulator homolog [Arabidopsis thaliana]

Seq. No. 15233

Contig ID 34512\_1.R1040 5'-most EST zpv700757801.h1

Method BLASTN
NCBI GI g1431744
BLAST score 62
E value 2.0e-26
Match length 178
% identity 90

NCBI Description Glycine max sucrose binding protein (sbp) mRNA, complete

cds

Seq. No. 15234

Contig ID 34522\_1.R1040 5'-most EST wvk700683426.h1

Method BLASTX
NCBI GI g1711406
BLAST score 335
E value 2.0e-31
Match length 140
% identity 54

NCBI Description POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L2 (SNF2-ALPHA)

>gi\_542839\_pir\_\_S39580 HBRM protein - human

>gi\_414117\_emb\_CAA51407\_ (X72889) HBRM [Homo sapiens]

Seq. No. 15235

Contig ID 34576\_1.R1040



5'-most EST q5606883 15236 Seq. No. 34583 1.R1040 Contig ID 5'-most EST q5058138 BLASTX Method NCBI GI q4033468 178 BLAST score 8.0e-13 E value Match length 41 % identity 85 NCBI Description ARGININE/SERINE-RICH SPLICING FACTOR RSP40 >gi\_2582641\_emb\_CAA67800\_ (X99437) splicing factor
[Arabidopsis thaliana] >gi\_2980800\_emb\_CAA18176\_ (AL022197) splicing factor At-SRp40 [Arabidopsis thaliana] 15237 Seq. No. Contig ID 34583 2.R1040 5'-most EST jC-gmf102220052g11a1 BLASTX Method g4033469 NCBI GI 636 BLAST score E value 3.0e-66 Match length 230 % identity ARGININE/SERINE-RICH SPLICING FACTOR RSP41 NCBI Description >gi 1707370 emb CAA67799 (X99436) splicing factor [Arabidopsis thaliana] 15238 Seq. No. 34583 4.R1040 Contig ID 5'-most EST crh700853023.h1 BLASTX Method q4033469 NCBI GI BLAST score 166 9.0e-12 E value 40 Match length 70 % identity ARGININE/SERINE-RICH SPLICING FACTOR RSP41 NCBI Description >gi 1707370 emb CAA67799 (X99436) splicing factor [Arabidopsis thaliana] 15239 Seq. No. 34589 1.R1040 Contig ID 5'-most EST LIB3065-018-Q1-N1-G2 15240 Seq. No. 34595 1.R1040 Contig ID 5'-most EST LIB3065-018-Q1-N1-H4

Seq. No. 15241

Contig ID 34597 1.R1040

5'-most EST jC-gmro02910029e05a1

Method BLASTX
NCBI GI g2911071
BLAST score 226
E value 2.0e-18



Match length 153 % identity 37

NCBI Description (AL021960) hypothetical protein [Arabidopsis thaliana]

Seq. No. 15242

Contig ID 34604\_1.R1040

5'-most EST LIB3065-016-Q1-N1-H2

Seq. No. 15243

Contig ID 34607\_2.R1040

5'-most EST LIB3065-018-Q1-N1-C8

Seq. No. 15244

Contig ID 34618\_1.R1040

5'-most EST uC-gmflminsoy036f04b1

Seq. No. 15245

Contig ID 34626\_1.R1040

5'-most EST LIB3139-053-P1-N1-C7

Method BLASTX
NCBI GI g3355474
BLAST score 658
E value 7.0e-69
Match length 135
% identity 90

NCBI Description (AC004218) unknown protein [Arabidopsis thaliana]

Seq. No. 15246

34627 1.R1040 Contig ID g5678005 5'-most EST BLASTX Method g3668087 NCBI GI 383 BLAST score 2.0e-39 E value 148 Match length 14 % identity

NCBI Description (AC004667) hypothetical protein [Arabidopsis thaliana]

Seq. No. 15247

Contig ID 34631\_1.R1040

5'-most EST LIB3065-018-Q1-N1-B1

Method BLASTX
NCBI GI g1732406
BLAST score 270
E value 5.0e-24
Match length 82

% identity 68
NCBI Description (U81157) S25-XP1 DNA binding protein [Nicotiana tabacum]

Seq. No. 15248

Contig ID 34634\_1.R1040

5'-most EST LIB3065-017-Q1-N1-G12

Method BLASTX
NCBI GI g2462745
BLAST score 389
E value 7.0e-38
Match length 86

2554



```
% identity
NCBI Description (AC002292) Hypothetical protein [Arabidopsis thaliana]
                  15249
Seq. No.
                  34644 2.R1040
Contig ID
5'-most EST
                  leu701151933.hl
                  15250
Seq. No.
                  34644 3.R1040
Contig ID
                  vzy700751940.hl
5'-most EST
                  15251
Seq. No.
Contig ID
                  34677 1.R1040
                  qsv701054440.hl
5'-most EST
                  BLASTX
Method
                  g322754
NCBI GI
                  851
BLAST score
E value
                  2.0e-91
Match length
                  213
                   71
% identity
                  DNA-binding protein GT-la - common tobacco >gi_170271
NCBI Description
                   (M93436) DNA-binding protein [Nicotiana tabacum]
Seq. No.
                   15252
                   34704 1.R1040
Contig ID
                  bth700844181.h1
5'-most EST
                   BLASTX
Method
                   q2827544
NCBI GI
BLAST score
                   645
                   5.0e-67
E value
                   215
Match length
                   61
% identity
                   (AL021635) HSP associated protein like [Arabidopsis
NCBI Description
                   thaliana]
                   15253
Seq. No.
                   34721 1.R1040
Contig ID
                   LIB3065-015-Q1-N1-E6
5'-most EST
                   15254
Seq. No.
                   34723 1.R1040
Contig ID
                   LIB3106-031-Q1-K1-E11
5'-most EST
                   15255
Seq. No.
                   34731 1.R1040
Contig ID
                   LIB3065-015-Q1-N1-D6
5'-most EST
                   15256
Seq. No.
                   34737 1.R1040
Contig ID
5'-most EST
                   sat701004901.hl
                   BLASTX
Method
```

NCBI GI g3242722
BLAST score 344
E value 2.0e-32
Match length 110
% identity 55

NCBI Description (AC003040) putative acetone-cyanohydrin lyase [Arabidopsis



## thaliana]

```
15257
Seq. No.
                  34743 1.R1040
Contig ID
                  jC-gmro02910054b10d1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q4454471
                  335
BLAST score
                  2.0e-31
E value
Match length
% identity
                  (AC006234) putative G protein coupled receptor [Arabidopsis
NCBI Description
                  thaliana]
                  15258
Seq. No.
                  34759 1.R1040
Contig ID
                  LIB3170-045-Q1-J1-A7
5'-most EST
Seq. No.
                  15259
                  34761 1.R1040
Contig ID
                  jC-gmle01810032a03d1
5'-most EST
                  15260
Seq. No.
Contig ID
                  34762_1.R1040
                  LIB3170-045-Q1-J1-C7
5'-most EST
Method
                  BLASTN
                  q510545
NCBI GI
BLAST score
                   138
E value
                   3.0e-71
                   234
Match length
                   90
% identity
NCBI Description P.sativum mRNA for starch branching enzyme I
Seq. No.
                   15261
                   34772 1.R1040
Contig ID
                   fde700876305.hl
5'-most EST
Method
                   BLASTX
                   g2129892
NCBI GI
BLAST score
                   230
                   8.0e-19
E value
                   149
Match length
                   42
% identity
                   probable finger protein Pszfl - garden pea
NCBI Description
                   >gi_861091_emb_CAA60828_ (X87374) putative zinc finger
                   protein [Pisum sativum]
Seq. No.
                   15262
                   34774 1.R1040
Contig ID
                   jC-gmro02910050b08d1
5'-most EST
                   BLASTX
Method
                   g2739168
NCBI GI
                   270
BLAST score
                   1.0e-23
E value
                   97
Match length
                   53
% identity
                   (AF032386) aldose-1-epimerase-like protein [Nicotiana
NCBI Description
```

tabacum]



Seq. No. 15263

Contig ID 34777\_1.R1040 5'-most EST leu701148231.h1

Seq. No. 15264

Contig ID 34777\_2.R1040 5'-most EST fua701039926.h1

Seq. No. 15265

Contig ID 34777\_3.R1040 5'-most EST vwf700673938.h1

Seq. No. 15266

Contig ID 34788\_1.R1040

5'-most EST LIB3106-091-Q1-K1-G9

Method BLASTX
NCBI GI g2739381
BLAST score 575
E value 5.0e-59
Match length 248
% identity 53

NCBI Description (AC002505) putative patatin [Arabidopsis thaliana]

Seq. No. 15267

Contig ID 34795\_1.R1040 5'-most EST fde700870885.h1

Seq. No. 15268

Contig ID 34802\_1.R1040 5'-most EST zsg701124658.h1

Method BLASTX
NCBI GI 94567279
BLAST score 238
E value 3.0e-20
Match length 59
% identity 75

NCBI Description (AC006841) putative serine/threonine protein kinase

[Arabidopsis thaliana]

Seq. No. 15269

Contig ID 34803\_1.R1040

5'-most EST LIB3065-014-Q1-N1-C12

Method BLASTX
NCBI GI g2281115
BLAST score 437
E value 2.0e-43
Match length 95
% identity 88

NCBI Description (AC002330) putative cullin-like 1 protein [Arabidopsis

thaliana]

15270

Seq. No.

Contig ID 34808\_1.R1040 5'-most EST pxt700946012.h1

Seq. No. 15271



```
34811 1.R1040
Contig ID
                  jC-gmst02400013b12a1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q2582381
                  722
BLAST score
                  2.0e-76
E value
                  265
Match length
                  85
% identity
                   (AF021220) cation-chloride co-transporter [Nicotiana
NCBI Description
                  tabacum]
                   15272
Seq. No.
                   34811 2.R1040
Contig ID
                   ssr700558465.hl
5'-most EST
Method
                   BLASTX
                   q2582381
NCBI GI
                   420
BLAST score
                   1.0e-42
E value
                   91
Match length
                   92
% identity
                   (AF021220) cation-chloride co-transporter [Nicotiana
NCBI Description
                   tabacum]
                   15273
Seq. No.
                   34835_1.R1040
Contig ID
                   LIB3065-013-Q1-N1-F10
5'-most EST
                   15274
Seq. No.
                   34851 1.R1040
Contig ID
                   epx701104723.h1
5'-most EST
                   BLASTX
Method
                   g4191791
NCBI GI
                   1112
BLAST score
                   1.0e-122
E value
Match length
                   332
                   63
% identity
                   (AC005917) putative sf21 {Helianthus annuus} protein
NCBI Description
                   [Arabidopsis thaliana]
                   15275
Seq. No.
                   34859 1.R1040
Contig ID
                   LIB3065-012-Q1-N1-H5
5'-most EST
                   BLASTX
Method
                   q4325282
NCBI GI
BLAST score
                   340
                   1.0e-31
E value
```

154 Match length 42 % identity

(AF123310) NAC domain protein NAM [Arabidopsis thaliana] NCBI Description >gi\_4325286\_gb\_AAD17314\_ (AF123311) NAC domain protein NAM

[Arabidopsis thaliana]

Seq. No.

34861 1.R1040 Contig ID uC-gmropic034f08b1 5'-most EST

15276

BLASTX Method g543565 NCBI GI



BLAST score 282 E value 7.0e-25 Match length 71 % identity 66

NCBI Description hypothetical 10.0K protein - Zinnia elegans

>gi\_493721\_dbj\_BAA06462\_ (D30802) TED4 [Zinnia elegans]
>gi\_641903 (U19266) putative nonspecific lipid transfer;

auxin induced gene [Zinnia elegans]

Seq. No. 15277

Contig ID 34861\_2.R1040

5'-most EST LIB3170-048-Q1-J1-B2

Method BLASTX
NCBI GI g543565
BLAST score 286
E value 3.0e-25
Match length 73
% identity 66

NCBI Description hypothetical 10.0K protein - Zinnia elegans

>gi\_493721\_dbj\_BAA06462\_ (D30802) TED4 [Zinnia elegans]
>gi\_641903 (U19266) putative nonspecific lipid transfer;

auxin induced gene [Zinnia elegans]

Seq. No. 15278

Contig ID 34865\_1.R1040

5'-most EST LIB3065-013-Q1-N1-A12

Method BLASTX
NCBI GI g3646373
BLAST score 549
E value 2.0e-56
Match length 117
% identity 85

NCBI Description (AJ011078) RGP1 protein [Oryza sativa]

Seq. No. 15279

Contig ID 34873\_1.R1040 5'-most EST wrg700790729.h1

Method BLASTX
NCBI GI g2618691
BLAST score 1074
E value 1.0e-117
Match length 411
% identity 54

NCBI Description (AC002510) putative chloroplast envelope Ca2+-ATPase

[Arabidopsis thaliana]

Seq. No. 15280

Contig ID 34877\_1.R1040

5'-most EST LIB3065-012-Q1-N1-G12

Seq. No. 15281

Contig ID 34878 1.R1040

5'-most EST LIB3167-049-P1-K1-E4

Seq. No. 15282

Contig ID 34882\_1.R1040

5'-most EST jC-gmst02400005e10a1



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15283
Seq. No.
                   34886 1.R1040
Contig ID
                  jC-gmro02910032b02a1
5'-most EST
                  15284
Seq. No.
                   34886 2.R1040
Contiq ID
                   leu70\overline{1}149103.h1
5'-most EST
                  BLASTX
Method
                   g1653516
NCBI GI
                   238
BLAST score
                   1.0e-19
E value
                   79
Match length
                   57
% identity
                  (D90914) hypothetical protein [Synechocystis sp.]
NCBI Description
                   15285
Seq. No.
                   34894 1.R1040
Contig ID
                   wvk70\overline{0}686640.h1
5'-most EST
                   BLASTX
Method
                   g2392025
NCBI GI
                   767
BLAST score
                   1.0e-81
E value
                   196
Match length
                   76
% identity
                   (D88420) stromal ascorbate peroxidase [Cucurbita sp.]
NCBI Description
                   15286
Seq. No.
                   34894 2.R1040
Contig ID
5'-most EST
                   epx701104872.h1
                   15287
Seq. No.
                   34906 1.R1040
Contig ID
                   k11701203991.h2
5'-most EST
                   BLASTX
Method
                   q3219823
NCBI GI
BLAST score
                   408
                   1.0e-39
E value
                   168
Match length
% identity
                   49
                   PUTATIVE 3-ISOPROPYLMALATE DEHYDRATASE LARGE SUBUNIT
NCBI Description
                    (ISOPROPYLMALATE ISOMERASE) (ALPHA-IPM ISOMERASE) (IPMI)
                   >gi 2127740 pir__C64362 aconitate hydratase (EC 4.2.1.3) -
                   Methanococcus jannaschii >gi_1591201 (U67499)
                   3-isopropylmalate dehydratase (leuC) [Methanococcus
                   jannaschii]
                   15288
Seq. No.
                    34907 1.R1040
Contig ID
                    jC-gmf102220088g07a1
 5'-most EST
                    BLASTX
Method
                    g2117355
NCBI GI
                    731
 BLAST score
                    1.0e-128
E value
                    385
Match length
                    64
 % identity
NCBI Description mitochondrial processing peptidase (EC 3.4.99.41) alpha-II
```



chain precursor - potato >gi\_587562\_emb\_CAA56520\_ (X80236) mitochondrial processing peptidase [Solanum tuberosum]

Seq. No. 15289

Contig ID 34907\_2.R1040 5'-most EST g4306001

Seq. No. 15290

Contig ID 34909\_1.R1040

5'-most EST LIB3170-045-Q1-J1-H5

Method BLASTX
NCBI GI g2827658
BLAST score 325
E value 5.0e-30
Match length 133
% identity 49

NCBI Description (AL021637) putative protein [Arabidopsis thaliana]

Seq. No. 15291

Contig ID 34910 1.R1040

5'-most EST jC-gmf102220125c08a1

Seq. No. 15292

Contig ID 34916\_1.R1040 5'-most EST kl1701207355.h1

Method BLASTX
NCBI GI g2809259
BLAST score 466
E value 1.0e-46
Match length 115
% identity 72

NCBI Description (AC002560) F21B7.28 [Arabidopsis thaliana]

Seq. No. 15293

Contig ID 34918\_1.R1040 5'-most EST awf700839078.h1

Method BLASTX
NCBI GI g4538913
BLAST score 589
E value 1.0e-60
Match length 204
% identity 64

NCBI Description (AL049482) putative protein [Arabidopsis thaliana]

Seq. No. 15294

Contig ID 34923\_1.R1040

5'-most EST LIB3065-012-Q1-N1-A11

Seq. No. 15295

Contig ID 34929\_1.R1040

5'-most EST LIB3170-046-Q1-J1-A5

Seq. No. 15296

Contig ID 34934\_1.R1040

5'-most EST jC-gmro02910012g07a1

Seq. No. 15297



```
34938 1.R1040
Contig ID
                  jC-qmf102220127h08d1
5'-most EST
                  BLASTN
Method
                  g1694899
NCBI GI
                  254
BLAST score
E value
                  1.0e-140
                  558
Match length
                  87
% identity
NCBI Description P.sativum mRNA for Copl protein
Seq. No.
                  15298
                  34941 1.R1040
Contig ID
                  k11701207125.h1
5'-most EST
                  BLASTX
Method
                  q3879775
NCBI GI
                  161
BLAST score
                  1.0e-10
E value
Match length
                  128
% identity
                  (Z68752) Similarity to Serpentwood strictosidine synthase
NCBI Description
                  precursor (SW:STSY_RAUSE); cDNA EST yk364d8.3 comes from
                  this gene; cDNA EST yk364d8.5 comes from this gene
                   [Caenorhabditis elegans]
                   15299
Seq. No.
                   34943 1.R1040
Contig ID
5'-most EST
                  LIB3170-046-Q1-J1-E3
Seq. No.
                   15300
                   34945 1.R1040
Contig ID
                   LIB3170-047-Q1-J1-D3
5'-most EST
                   15301
Seq. No.
                   34949 1.R1040
Contig ID
                   LIB3170-047-Q1-J1-E3
5'-most EST
                  BLASTX
Method
                   q2501499
NCBI GI
                   237
BLAST score
                   7.0e-20
E value
                   119
Match length
                   40
% identity
                   INDOLE-3-ACETATE BETA-GLUCOSYLTRANSFERASE (IAA-GLU
NCBI Description
                   SYNTHETASE) ((URIDINE
                   5'-DIPHOSPHATE-GLUCOSE: INDOL-3-YLACETYL)-BETA-D-GLUCOSYL
                   TRANSFERASE) >gi_626043_pir__A54739 indole-3-acetate
                   beta-glucosyltransferase (EC 2.4.1.121) - maize >gi_548195
                   (L34847) IAA-glu synthetase [Zea mays]
                   15302
```

Seq. No. 34955 1.R1040 Contig ID fC-gmle700872894f3 5'-most EST BLASTX Method NCBI GI g2335097 BLAST score 615 9.0e-64 E value 141 Match length % identity 84



NCBI Description (AC002339) putative receptor-like protein kinase [Arabidopsis thaliana]

Seq. No. 15303

Contig ID 34956\_1.R1040

5'-most EST LIB3065-011-Q1-N1-F11

Seq. No. 15304

Contig ID 34959 1.R1040

5'-most EST uC-gmrominsoy056f11b1

Seq. No. 15305

Contig ID 34961 1.R1040

5'-most EST LIB3106-059-Q1-K1-F2

Seq. No. 15306

Contig ID 34968 1.R1040

5'-most EST LIB3170-045-Q1-J1-C4

Seq. No. 15307

Contig ID 34969 1.R1040

5'-most EST LIB3065-011-Q1-N1-D12

Seq. No. 15308

Contig ID 34973\_1.R1040 5'-most EST dpv701103339.h1

Method BLASTX
NCBI GI g3269291
BLAST score 542
E value 6.0e-70
Match length 210
% identity 64

NCBI Description (AL030978) putative receptor protein kinase [Arabidopsis

thaliana]

Seq. No. 15309

Contig ID 34989\_1.R1040

5'-most EST LIB3170-045-Q1-J1-H4

Seq. No. 15310

Contig ID 34990\_1.R1040 5'-most EST ncj700985662.h1

Method BLASTX
NCBI GI g2911040
BLAST score 550
E value 3.0e-56
Match length 190
% identity 61

NCBI Description (AL021961) receptor protein kinase - like protein

[Arabidopsis thaliana]

Seg. No. 15311

Contig ID 34995\_1.R1040 5'-most EST trc700565513.h1

Method BLASTX NCBI GI g2464855 BLAST score 530



E value 1.0e-53 Match length 247 % identity 49

NCBI Description (Z99707) myb-related protein [Arabidopsis thaliana]

Seq. No. 15312

Contig ID 34995\_2.R1040

5'-most EST LIB3139-081-P1-N1-C4

Seq. No. 15313

Contig ID 34995\_3.R1040

5'-most EST uC-gmflminsoy082e03b1

Method BLASTX
NCBI GI g2642435
BLAST score 252
E value 7.0e-22
Match length 54
% identity 83

NCBI Description (AC002391) MYB-related protein [Arabidopsis thaliana]

Seq. No. 15314

Contig ID 35005\_1.R1040

5'-most EST LIB3170-046-Q1-J1-C4

Method BLASTX
NCBI GI g585452
BLAST score 281
E value 8.0e-25
Match length 89
% identity 62

NCBI Description MALATE OXIDOREDUCTASE (NAD), MITOCHONDRIAL 59 KD ISOFORM

PRECURSOR (MALIC ENZYME) (ME) (NAD-DEPENDENT MALIC ENZYME) (NAD-ME) >gi\_1076666 pir\_A53318 malate dehydrogenase (decarboxylating) (EC 1.1.1.39) 59K chain precursor, mitochondrial - potato >gi\_438131\_emb\_CAA80547\_ (Z23002)

precursor of the 59kDa subunit of the mitochondrial NAD+-dependent malic enzyme [Solanum tuberosum]

Seq. No. 15315

Contig ID 35011 1.R1040

5'-most EST LIB3170-046-Q1-J1-A4

Seq. No. 15316

Contig ID 35015\_1.R1040

5'-most EST LIB3065-010-Q1-N1-F6

Seq. No. 15317

Contig ID 35020\_1.R1040 5'-most EST uC-gmropic016e04b1

Method BLASTX
NCBI GI 94220514
BLAST score 501
E value 1.0e-50
Match length 158
% identity 65

NCBI Description (AL035356) putative protein [Arabidopsis thaliana]

Seq. No. 15318



Contig ID 35022\_1.R1040 5'-most EST sat701014507.h1

Method BLASTX
NCBI GI g3540181
BLAST score 202
E value 1.0e-15
Match length 83
% identity 53

NCBI Description (AC004122) Unknown protein [Arabidopsis thaliana]

Seq. No. 15319

Contig ID 35026\_1.R1040

5'-most EST uC-gmrominsoy305f09b1

Seq. No. 15320

Contig ID 35026\_2.R1040 5'-most EST bth700846229.h1

Seq. No. 15321

Contig ID 35031 1.R1040

5'-most EST LIB3065-010-Q1-N1-H11

Method BLASTX
NCBI GI g4512667
BLAST score 558
E value 2.0e-57
Match length 135
% identity 74

NCBI Description (AC006931) putative MAP kinase [Arabidopsis thaliana]

Seq. No. 15322

35038 1.R1040 Contig ID g5753548 5'-most EST BLASTX Method NCBI GI q2431769 BLAST score 180 1.0e-14 E value 72 Match length 61 % identity

NCBI Description (U62752) acidic ribosomal protein Pla [Zea mays]

Seq. No. 15323

Contig ID 35039\_1.R1040 5'-most EST fua701042720.h1

Seq. No. 15324

Contig ID 35040\_1.R1040

5'-most EST LIB3092-045-Q1-K1-F9

Seq. No. 15325

Contig ID 35046\_1.R1040

5'-most EST LIB3170-047-Q1-J1-H2

Method BLASTX
NCBI GI g2289001
BLAST score 556
E value 3.0e-57
Match length 140
% identity 77



NCBI Description (AC002335) small nuclear ribonucleoprotein isolog [Arabidopsis thaliana]

Seq. No. 15326

Contig ID 35048 1.R1040

5'-most EST LIB3065-010-Q1-N1-F4

Method BLASTX
NCBI GI g4538897
BLAST score 675
E value 7.0e-71
Match length 193
% identity 64

NCBI Description (AL049482) AX110P-like protein [Arabidopsis thaliana]

Seq. No. 15327

Contig ID 35060 1.R1040

5'-most EST LIB3065-010-Q1-N1-D12

Method BLASTX
NCBI GI g4454480
BLAST score 917
E value 3.0e-99
Match length 228
% identity 71

NCBI Description (AC006234) putative (1-4)-beta-mannan endohydrolase

[Arabidopsis thaliana]

Seq. No. 15328

Contig ID 35064\_1.R1040

5'-most EST LIB3170-045-Q1-J1-E3

Method BLASTX
NCBI GI 9818849
BLAST score 376
E value 4.0e-75
Match length 195
% identity 72

NCBI Description (U25430) nucleotide pyrophosphatase precursor [Oryza

sativa]

Seq. No. 15329

Contig ID 35070\_1.R1040 5'-most EST leu701148665.h1

Method BLASTX
NCBI GI g2194125
BLAST score 583
E value 4.0e-60
Match length 137
% identity 76

NCBI Description (AC002062) ESTs gb\_R30459,gb\_N38441 come from this gene.

[Arabidopsis thaliana]

Seq. No. 15330

Contig ID 35070\_2.R1040
5'-most EST g4292203
Method BLASTX
NCBI GI g2194125
BLAST score 254
E value 6.0e-22



Match length 56
% identity 75
NCBI Description (AC002062) ESTs gb\_R30459,gb\_N38441 come from this gene.

[Arabidopsis thaliana]

Seq. No. 15331

Contig ID 35072\_1.R1040 5'-most EST zhf700957772.h1

Method BLASTX
NCBI GI g100370
BLAST score 241
E value 2.0e-20
Match length 75
% identity 61

NCBI Description pathogenesis-related protein 1 - common tobacco

>gi\_20056\_emb\_CAA36790\_ (X52555) PR-1 protein (AA 1-184)

[Nicotiana tabacum]

Seq. No. 15332

Contig ID 35073\_1.R1040

5'-most EST LIB3065-010-Q1-N1-B11

Seq. No. 15333

Contig ID 35077\_1.R1040 5'-most EST pcp700993912.h1

Seq. No. 15334

Contig ID 35077\_2.R1040 5'-most EST asn701142860.h1

Seq. No. 15335

Contig ID 35078\_1.R1040

5'-most EST LIB3106-010-Q1-K1-B9

Method BLASTN
NCBI GI g1209062
BLAST score 46
E value 1.0e-16
Match length 226
% identity 50

NCBI Description Phaseolus vulgaris proline-rich protein precursor mRNA,

complete cds

Seq. No. 15336

Contig ID 35088\_1.R1040 5'-most EST zhf700963276.h1

Method BLASTX
NCBI GI g886130
BLAST score 543
E value 1.0e-55
Match length 146
% identity 68

NCBI Description (U28148) putative pectinesterase [Medicago sativa]

Seq. No. 15337

Contig ID 35090\_1.R1040

5'-most EST LIB3065-009-Q1-N1-H7

Method BLASTN



```
q4455189
NCBI GI
BLAST score
                   36
                   1.0e-10
E value
                   109
Match length
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23
NCBI Description
                   (ESSAII project)
                   15338
Seq. No.
                   35091 1.R1040
Contig ID
5'-most EST
                   LIB3170-047-Q1-J1-C3
                   BLASTX
Method
NCBI GI
                   q2829876
BLAST score
                   157
                   2.0e-10
E value
Match length
                   98
                   45
% identity
                  (AC002396) Unknown protein [Arabidopsis thaliana]
NCBI Description
                   15339
Seq. No.
                   35091 2.R1040
Contig ID
                   eep700868430.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4539454
                   154
BLAST score
                   6.0e-10
E value
Match length
                   37
                   81
% identity
                   (ALO49500) contains EST gb:AA728416 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   15340
                   35100 1.R1040
Contig ID
                   jC-gmro02800043b03a1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3881381
                   567
BLAST score
                   5.0e-58
E value
                   307
Match length
% identity
                   45
                   (Z68270) Similarity to Yeast Man(0)-alpha-mannosidase
NCBI Description
                   (SW:MNS1 YEAST); cDNA EST EMBL:D71247 comes from this gene;
                   cDNA EST EMBL: D73896 comes from this gene [Caenorhabditis
                   elegans]
                   15341
 Seq. No.
                   35113 1.R1040
Contig ID
                   leu701145831.h1
 5'-most EST
Method
                   BLASTX
                   q3928543
NCBI GI
                   1184
BLAST score
                   1.0e-130
E value
                   415
Match length
 % identity
                   (AB016819) UDP-glucose glucosyltransferase [Arabidopsis
 NCBI Description
```

Seq. No.

thaliana]

15342



Contig ID 35114\_1.R1040

5'-most EST LIB3065-009-Q1-N1-D6

Method BLASTX
NCBI GI g100226
BLAST score 225
E value 2.0e-18
Match length 116
% identity 42

NCBI Description hypothetical protein - tomato >gi\_19275\_emb\_CAA78112\_ (Z12127) protein of unknown function [Lycopersicon

esculentum] >gi 445619 prf 1909366A Leu zipper protein

[Lycopersicon esculentum]

Seq. No. 15343

Contig ID 35120 1.R1040

5'-most EST LIB3109-017-Q1-K1-H11

Method BLASTX
NCBI GI g3688177
BLAST score 299
E value 4.0e-27
Match length 98
% identity 57

NCBI Description (AL031804) putative protein [Arabidopsis thaliana]

Seq. No. 15344

Contig ID 35121 1.R1040

5'-most EST LIB3065-009-Q1-N1-E5

Seq. No. 15345

Contig ID 35121\_2.R1040 5'-most EST uxk700672274.h1

Seq. No. 15346

Contig ID 35124\_1.R1040
5'-most EST g4396915
Method BLASTX
NCBI GI g4006827
BLAST score 1034
E value 1.0e-113

Match length 261 % identity 76

NCBI Description (AC005970) subtilisin-like protease [Arabidopsis thaliana]

Seq. No. 15347

Contig ID 35128 1.R1040

5'-most EST LIB3170-045-Q1-J1-G2

Seq. No. 15348

Contig ID 35128\_2.R1040 5'-most EST pxt700944372.h1

Seq. No. 15349

Contig ID 35135 1.R1040

5'-most EST LIB3065-009-Q1-N1-C9

Method BLASTX NCBI GI g2435519 BLAST score 202



E value 1.0e-15 Match length 75 % identity

NCBI Description (AF024504) similar to mouse MEM3 (GB:U47024 and S. cerevisiae vacuolar sorting protein 35 (SW; P34110)

[Arabidopsis thaliana]

15350 Seq. No.

35135 2.R1040 Contig ID 5'-most EST wvk700684127.h1

Method BLASTX g2435519 NCBI GI BLAST score 528 E value 6.0e-54 156 Match length 68 % identity

(AF024504) similar to mouse MEM3 (GB:U47024 and S. NCBI Description cerevisiae vacuolar sorting protein 35 (SW; P34110)

[Arabidopsis thaliana]

Seq. No. 15351

Contig ID 35151 1.R1040

5'-most EST LIB3065-009-Q1-N1-B2

Method BLASTX NCBI GI q4204303 BLAST score 324 E value 1.0e-29 Match length 65 % identity 91

(AC003027) lcl prt seq No definition line found NCBI Description

[Arabidopsis thaliana]

Seq. No. 15352

35152 1.R1040 Contig ID

5'-most EST LIB3065-009-Q1-N1-B3

Method BLASTX NCBI GI g3043656 BLAST score 583 E value 4.0e-60 190 Match length % identity 56

NCBI Description (AB011138) KIAA0566 protein [Homo sapiens]

Seq. No. 15353

Contig ID 35155 1.R1040

5'-most EST LIB3170-043-Q1-J1-H12

Seq. No. 15354

35157 1.R1040 Contig ID

5'-most EST LIB3065-009-Q1-N1-B9

Seq. No. 15355

Contig ID 35157 2.R1040 5'-most EST zzp700832239.h1

BLASTX Method NCBI GI q3402672 BLAST score 592



```
2.0e-61
E value
Match length
                  156
% identity
                  (AC004697) putative white protein [Arabidopsis thaliana]
NCBI Description
                  15356
Seq. No.
                  35175 1.R1040
Contig ID
5'-most EST
                  jC-gmle01810041c10d1
                  15357
Seq. No.
                  35177 1.R1040
Contig ID
5'-most EST
                  bth700845872.h1
Method
                  BLASTX
                   q1352186
NCBI GI
                   446
BLAST score
                   4.0e-44
E value
                   153
Match length
% identity
                   51
                  ALLENE OXIDE SYNTHASE PRECURSOR (HYDROPEROXIDE DEHYDRASE)
NCBI Description
                   (CYTOCHROME P450 74) >gi_404866 (U00428) allene oxide
                   synthase [Linum usitatissimum]
                   15358
Seq. No.
                   35179 1.R1040
Contig ID
                   q4288001
5'-most EST
                   BLASTX
Method
                   q4210332
NCBI GI
BLAST score
                   1309
                   1.0e-145
E value
                   360
Match length
                   74
% identity
                   (AJ223803) 2-oxoglutarate dehydrogenase E2 subunit
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   15359
                   35184 1.R1040
Contig ID
                   LIB3065-008-Q1-N1-G12
5'-most EST
                   BLASTX
Method
                   q3068717
NCBI GI
                   425
BLAST score
                   6.0e-42
E value
                   134
Match length
                   60
% identity
                   (AF049236) unknown [Arabidopsis thaliana]
NCBI Description
                   15360
Seq. No.
                   35211 1.R1040
Contig ID
                   LIB3065-008-Q1-N1-C1
 5'-most EST
                   BLASTX
Method
                   g2696611
NCBI GI
 BLAST score
                   255
                   6.0e-22
 E value
```

127 Match length 43 % identity

(D78303) RNA splicing-related protein [Rattus norvegicus] NCBI Description

15361 Seq. No.



Contig ID 35214\_1.R1040 5'-most EST LIB3107-030-Q1-K1-G5

Seq. No. 15362

Contig ID 35214\_3.R1040

5'-most EST jC-gmle01810051g04a1

Seq. No. 15363

Contig ID 35218\_1.R1040

5'-most EST jC-gmst02400052e10a1

Seq. No. 15364

Contig ID 35223\_1.R1040

5'-most EST LIB3065-007-Q1-N1-H8

Method BLASTX
NCBI GI g3128170
BLAST score 320
E value 1.0e-29
Match length 114
% identity 58

NCBI Description (AC004521) hypothetical protein [Arabidopsis thaliana]

Seq. No. 15365

Contig ID 35226\_1.R1040

5'-most EST LIB3065-008-Q1-N1-A10

Method BLASTX
NCBI GI g3695408
BLAST score 288
E value 2.0e-25
Match length 90
% identity 66

NCBI Description (AF096373) contains similarity to Solanum lycopersicum

(tomato) wound-induced protein (GB:X59882) [Arabidopsis thaliana] >gi\_4538956 emb\_CAB39780.1\_ (AL049488) probable

wound-induced protein [Arabidopsis thaliana]

Seq. No. 15366

Contig ID 35226 2.R1040

5'-most EST LIB3107-079-Q1-K1-E12

Method BLASTX
NCBI GI g3695408
BLAST score 242
E value 3.0e-20
Match length 90
% identity 57

NCBI Description (AF096373) contains similarity to Solanum lycopersicum

(tomato) wound-induced protein (GB:X59882) [Arabidopsis thaliana] >gi\_4538956\_emb\_CAB39780.1\_ (AL049488) probable

wound-induced protein [Arabidopsis thaliana]

Seq. No. 15367

Contig ID 35226 3.R1040

5'-most EST LIB3092-029-Q1-K1-H11

Method BLASTX
NCBI GI g3695408
BLAST score 259
E value 4.0e-22



Match length % identity 61 NCBI Description (AF096373) contains similarity to Solanum lycopersicum (tomato) wound-induced protein (GB:X59882) [Arabidopsis thaliana] >gi\_4538956\_emb\_CAB39780.1\_ (AL049488) probable wound-induced protein [Arabidopsis thaliana] 15368 Seq. No. 35226 4.R1040 Contig ID 5'-most EST LIB3107-037-Q1-K1-A3 Method BLASTX NCBI GI q3695408 BLAST score 181 E value 2.0e-13 Match length 84 50 % identity (AF096373) contains similarity to Solanum lycopersicum NCBI Description (tomato) wound-induced protein (GB:X59882) [Arabidopsis thaliana] >gi\_4538956\_emb\_CAB39780.1\_ (AL049488) probable wound-induced protein [Arabidopsis thaliana] Seq. No. 15369 Contig ID 35228 1.R1040 5'-most EST LIB3065-008-Q1-N1-A3 BLASTX Method a4105800 NCBI GI BLAST score 521 E value 5.0e-53 Match length 128 73 % identity NCBI Description (AF049931) PGP301 [Petunia x hybrida] Seq. No. 15370 35228 2.R1040 Contig ID jC-gmf102220079e02d1 5'-most EST Method BLASTX g4204257 NCBI GI BLAST score 249 3.0e-21 E value Match length 64 72 % identity (AC005223) 5493 [Arabidopsis thaliana] NCBI Description Seq. No. 15371

35235 1.R1040 Contig ID 5'-most EST zhf700959629.h1

Method BLASTX NCBI GI g3953462 BLAST score 208 E value 4.0e-16 Match length 127 34 % identity

NCBI Description (AC002328) F20N2.7 [Arabidopsis thaliana]

Seq. No. 15372

Contig ID 35239 1.R1040

5'-most EST LIB3170-045-Q1-J1-B1



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15373
Seq. No.
                   35243 1.R1040
Contig ID
                   LIB3065-007-Q1-N1-H1
5'-most EST
                   BLASTX
Method
                   q3953470
NCBI GI
BLAST score
                   403
                   2.0e-39
E value
                   134
Match length
% identity
                   73
NCBI Description (AC002328) F20N2.15 [Arabidopsis thaliana]
Seq. No.
                   15374
                   35244 1.R1040
Contig ID
5'-most EST
                   LIB3170-045-Q1-J1-E1
                   BLASTX
Method
                   g3759184
NCBI GI
BLAST score
                   644
                   3.0e-67
E value
                   233
Match length
% identity
                   56
NCBI Description (AB018441) phi-1 [Nicotiana tabacum]
Seq. No.
                   15375
                   35249 1.R1040
Contig ID
5'-most EST
                   jex70\overline{0}908859.h1
                   15376
Seq. No.
Contig ID
                   35250 1.R1040
5'-most EST
                   LIB3065-007-Q1-N1-H6
Seq. No.
                   15377
Contig ID
                   35252 1.R1040
5'-most EST
                   LIB3065-007-Q1-N1-F10
                   15378
Seq. No.
                   35255 1.R1040
Contig ID
5'-most EST
                   LIB3065-007-Q1-N1-F2
Method
                   BLASTN
                   g1781039
NCBI GI
BLAST score
                   112
                   7.0e-56
E value
Match length
                   275
% identity
                   85
                  M.sativa mRNA for delta-1-pyrroline-5-carboxylate synthase,
NCBI Description
                   P5CS-2
Seq. No.
                   15379
                   35257 1.R1040
Contig ID
                   LIB3065-007-Q1-N1-F4
5'-most EST
```

15380 Seq. No.

Contig ID 35258 1.R1040

5'-most EST LIB3107-006-Q1-K1-C3

Seq. No. 15381

35268 1.R1040 Contig ID



```
5'-most EST pmv700894621.h1
Seg. No. 15382
```

Seq. No. 15382 Contig ID 35269\_1.R1040

5'-most EST LIB3106-109-Q1-K1-A5

Seq. No. 15383

Contig ID 35271\_1.R1040

5'-most EST LIB3170-047-Q1-J1-C5

Method BLASTX
NCBI GI g1176671
BLAST score 296
E value 1.0e-26
Match length 103
% identity 50

NCBI Description PUTATIVE GLUCOSYLTRANSFERASE C08B11.8

>gi\_3874174\_emb\_CAA86666\_ (Z46676) C08B11.8 [Caenorhabditis

elegans]

Seq. No. 15384

Contig ID 35276 1.R1040

5'-most EST LIB3170-042-Q1-J1-E12

Seq. No. 15385

Contig ID 35285 1.R1040

5'-most EST LIB3106-013-Q1-K1-H4

Seq. No. 15386

Contig ID 35286\_1.R1040 5'-most EST pmv700891246.h1

Method BLASTX
NCBI GI g2194143
BLAST score 291
E value 5.0e-26
Match length 114
% identity 54

NCBI Description (AC002062) No definition line found [Arabidopsis thaliana]

Seq. No. 15387

Contig ID 35294\_1.R1040 5'-most EST rlr700898415.h1

Method BLASTX
NCBI GI g2463298
BLAST score 146
E value 1.0e-08
Match length 71
% identity 44

NCBI Description (Z94892) putative [Nostoc commune]

Seq. No. 15388

Contig ID 35294\_2.R1040 5'-most EST zsg701122521.h1

Seq. No. 15389

Contig ID 35294\_3.R1040 5'-most EST fC-gmst700889547f4



```
Seq. No. 15390
Contig ID 35294 4.R1040
```

5'-most EST ssr700555228.h1

Seq. No. 15391

Contig ID 35309\_1.R1040

5'-most EST LIB3170-043-Q1-J1-A11

Method BLASTX
NCBI GI g2864609
BLAST score 171
E value 6.0e-12
Match length 56
% identity 61

NCBI Description (AL021811) putative protein [Arabidopsis thaliana]

>gi\_4049337\_emb\_CAA22562\_ (AL034567) putative protein

[Arabidopsis thaliana]

Seq. No. 15392

Contig ID 35310\_1.R1040 5'-most EST uC-gmropic102b07b1

Method BLASTX
NCBI GI g4415931
BLAST score 439
E value 2.0e-43
Match length 120
% identity 65

NCBI Description (AC006418) unknown protein [Arabidopsis thaliana]

>qi 4559393 gb AAD23053.1 AC006526 18 (AC006526) unknown

protein [Arabidopsis thaliana]

Seq. No. 15393

Contig ID 35319\_1.R1040

5'-most EST LIB3170-044-Q1-J1-D4

Seq. No. 15394

Contig ID 35324\_1.R1040 5'-most EST ncj700976047.h1

Method BLASTX
NCBI GI g3928090
BLAST score 146
E value 5.0e-09
Match length 73
% identity 42

NCBI Description (AC005770) putative MTN3 protein [Arabidopsis thaliana]

Seq. No. 15395

Contig ID 35328 1.R1040

5'-most EST LIB3106-005-Q1-K1-B5

Method BLASTX
NCBI GI g1946369
BLAST score 197
E value 4.0e-15
Match length 106
% identity 44

NCBI Description (U93215) unknown protein [Arabidopsis thaliana]



```
Contig ID
                   35333 1.R1040
5'-most EST
                   LIB3065-006-Q1-N1-F7
Method
                   BLASTN
NCBI GI
                   g3128138
BLAST score
                   34
E value
                   3.0e-09
Match length
                   184
% identity
                   83
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MFO20, complete sequence [Arabidopsis thaliana]
Seq. No.
                   15397
Contig ID
                   35342 1.R1040
5'-most EST
                   uC-gmflminsoy035h06b1
Method
                   BLASTX
NCBI GI
                   q4490702
BLAST score
                   485
E value
                   1.0e-48
Match length
                   214
% identity
                   57
NCBI Description
                  (AL035680) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   15398
Contiq ID
                   35343 1.R1040
5'-most EST
                   LIB3065-006-Q1-N1-D10
Seq. No.
                   15399
Contig ID
                   35350 1.R1040
5'-most EST
                   awf70\overline{0}839492.h1
Method
                   BLASTX
NCBI GI
                   g1929056
BLAST score
                   892
E value
                   2.0e-96
Match length
                   221
% identity
                   78
                   (Y12090) putative 3,4-dihydroxy-2-butanone kinase
NCBI Description
                   [Lycopersicon esculentum]
                   15400
Seq. No.
Contig ID
                   35363 1.R1040
5'-most EST
                   kl1701211332.h1
Method
                   BLASTX
NCBI GI
                   g1666096
BLAST score
                   408
E value
                   8.0e-40
Match length
                   95
% identity
                   81
NCBI Description
                  (Y09113) dioxygenase [Marah macrocarpus]
```

Seq. No. 15401

Contig ID 35368 1.R1040 5'-most EST asn701133389.h1

Method BLASTX NCBI GI g2257524 BLAST score 269 1.0e-23 E value Match length 105



% identity 48

NCBI Description (AB004537) HYPOTHETICAL 47.4KD PROTEIN IN SHP1-SEC17

INTERGENIC REGION [Schizosaccharomyces pombe]

Seq. No. 15402

Contig ID 35371 1.R1040

5'-most EST LIB3170-044-Q1-J1-B4

Method BLASTX
NCBI GI g1653775
BLAST score 201
E value 1.0e-15
Match length 71
% identity 54

NCBI Description (D90916) thiol:disulfide interchange protein DsbD

[Synechocystis sp.]

Seq. No. 15403

Contig ID 35372 1.R1040

5'-most EST LIB3065-005-Q1-N1-G9

Seq. No. 15404

Contig ID 35374 1.R1040

5'-most EST jC-gmro02910002b06a1

Method BLASTX
NCBI GI g2739046
BLAST score 209
E value 8.0e-16
Match length 212
% identity 29

NCBI Description (AF024652) polyphosphoinositide binding protein Ssh2p

[Glycine max]

Seq. No. 15405

Contig ID 35375 1.R1040

5'-most EST LIB3065-005-Q1-N1-H2

Method BLASTX
NCBI GI g4406775
BLAST score 231
E value 4.0e-19
Match length 95
% identity 45

NCBI Description (AC006836) unknown protein [Arabidopsis thaliana]

Seq. No. 15406

Contig ID 35382\_1.R1040

5'-most EST LIB3073-015-Q1-K1-B12

Method BLASTX
NCBI GI 94107099
BLAST score 484
E value 2.0e-48
Match length 153
% identity 63

NCBI Description (AB015141) AHP1 [Arabidopsis thaliana]

>gi 4156245 dbj BAA37112 (AB012570) ATHP3 [Arabidopsis

thaliana]



Contig ID 35382\_2.R1040 5'-most EST uC-gmropic104e06b1

Method BLASTX
NCBI GI g4107099
BLAST score 393
E value 8.0e-38
Match length 183
% identity 49

NCBI Description (AB015141) AHP1 [Arabidopsis thaliana]

>gi 4156245 dbj BAA37112 (AB012570) ATHP3 [Arabidopsis

thaliana]

Seq. No. 15408

Contig ID 35386 1.R1040

5'-most EST LIB3170-043-Q1-J1-H10

Method BLASTX
NCBI GI g208494
BLAST score 278
E value 1.0e-24
Match length 122
% identity 48

NCBI Description (J05552) synthetic horseradish peroxidase isoenzyme C

(HRP-C) subunit alpha-1 (E.C. 1.11.1.7) [Artificial gene]

Seq. No. 15409

Contig ID 35392\_1.R1040 5'-most EST uC-gmropic111d03b1

Seq. No. 15410

Contig ID 35394\_1.R1040

5'-most EST LIB3170-041-Q1-J1-B11

Seq. No. 15411

Contig ID 35396\_1.R1040

5'-most EST LIB3139-104-P1-N1-B5

Seq. No. 15412

Contig ID 35397\_1.R1040 5'-most EST hyd700725241.h1

Method BLASTX
NCBI GI g4210449
BLAST score 355
E value 1.0e-33
Match length 97
% identity 75

NCBI Description (AB016471) ARR1 protein [Arabidopsis thaliana]

Seq. No. 15413

Contig ID 35404 1.R1040

5'-most EST LIB3065-005-Q1-N1-E10

Seq. No. 15414

Contig ID 35411 1.R1040

5'-most EST uC-gmrominsoy065h01b1

Seq. No. 15415

Contig ID 35422\_1.R1040



```
5'-most EST
                  LIB3065-005-Q1-N1-C4
Seq. No.
                  15416
Contig ID
                  35425 1.R1040
5'-most EST
                  jC-gmf102220081d12a1
Method
                  BLASTX
NCBI GI
                  g2213643
BLAST score
                  711
E value
                  2.0e-75
Match length
                  160
% identity
                  83
NCBI Description (U57338) glossyl homolog [Oryza sativa]
Seq. No.
                  15417
                  35433 1.R1040
Contig ID
5'-most EST
                  fua701037336.h1
Seq. No.
                  15418
                  35433 2.R1040
Contig ID
5'-most EST
                  LIB3065-005-Q1-N1-C1
Seq. No.
                  15419
                  35435 1.R1040
Contig ID
                  LIB3170-041-Q1-J1-C10
5'-most EST
Seq. No.
                  15420
                  35438 1.R1040
Contig ID
5'-most EST
                  g5688467
Seq. No.
                  15421
Contig ID
                  35441 1.R1040
5'-most EST
                  LIB3107-002-Q1-K1-C9
Method
                  BLASTX
                  g543813
NCBI GI
BLAST score
                  603
E value
                  2.0e-62
Match length
                  154
% identity
                  75
NCBI Description FLORAL HOMEOTIC PROTEIN APETALA1 (AGL7 PROTEIN)
                  >gi_16162_emb_CAA78909 (Z16421) AP1 [Arabidopsis thaliana]
Seq. No.
                  15422
Contig ID
                  35441 2.R1040
5'-most EST
                  LIB3109-022-Q1-K1-A6
Method
                  BLASTN
NCBI GI
                  q1049023
BLAST score
                  60
E value
                  4.0e-25
Match length
                  124
% identity
                  87
NCBI Description
                  Sinapis alba transcription factor SaMADS B mRNA, complete
```

15423

Contig ID 35448\_1.R1040 5'-most EST sat701007166.h1

Method BLASTX



NCBI GI BLAST score 221 E value 8.0e-18 Match length 140 % identity 33

NCBI Description HYPOTHETICAL 69.2 KD PROTEIN IN HSP30-PMP1 INTERGENIC

REGION >gi\_83212\_pir\_\_S19434 probable transport protein YCR023c - yeast (Saccharomyces cerevisiae)

>gi\_1907167\_emb\_CAA42315\_ (X59720) YCR023c, len:611

[Saccharomyces cerevisiae]

Seq. No. 15424

35450 1.R1040 Contiq ID 5'-most EST q4302023 Method BLASTX NCBI GI q2135800 BLAST score 158 E value 5.0e-10 Match length 195

% identity 28

nerve terminal protein - human >gi\_307426 (L19760) nerve NCBI Description

terminal protein [Homo sapiens] >gi\_521174 (L09253) this

product utilizes exon 5a [Gallus gallus]

>gi\_2116628\_dbj\_BAA20151\_ (AB003991) SNAP-25A [Rattus

rattus]

Seq. No.

15425 Contig ID 35450 2.R1040 5'-most EST bth700847040.h1

Seq. No. 15426

Contig ID 35455 1.R1040

5'-most EST uC-gmropic021e04b1 Method BLASTX

NCBI GI g3264767 BLAST score 262 2.0e-22 E value Match length 143 45 % identity

NCBI Description (AF071893) AP2 domain containing protein [Prunus armeniaca]

Seq. No. 15427

Contig ID 35455 2.R1040 5'-most EST g4396244 Method BLASTX NCBI GI g3264767 BLAST score 170 E value 5.0e-12

Match length 80 % identity 44

NCBI Description (AF071893) AP2 domain containing protein [Prunus armeniaca]

Seq. No. 15428

Contig ID 35458 1.R1040 5'-most EST trc700566486.h1



```
35467 1.R1040
Contig ID
5'-most EST
                  vwf700674346.h1
                  BLASTX
Method
                  q2688830
NCBI GI
BLAST score
                  539
                  3.0e-55
E value
Match length
                  154
% identity
                  71
NCBI Description (AF000952) putative sugar transporter [Prunus armeniaca]
                  15430
Seq. No.
Contig ID
                  35476 1.R1040
5'-most EST
                  crh700852965.h1
                  BLASTX
Method
                  q4432827
NCBI GI
                  442
BLAST score
                  3.0e-43
E value
Match length
                   394
% identity
                  31
                  (AC006593) putative ADP-ribose polymerase [Arabidopsis
NCBI Description
                  thaliana]
                  15431
Seq. No.
Contig ID
                   35477 1.R1040
5'-most EST
                  LIB3170-041-Q1-J1-H9
Seq. No.
                   15432
                   35482 1.R1040
Contig ID
5'-most EST
                  LIB3065-004-Q1-N1-C2
                   15433
Seq. No.
                   35490 1.R1040
Contig ID
5'-most EST
                   epx701105806.h1
Seq. No.
                   15434
                   35513 1.R1040
Contig ID
                   LIB3087-003-Q1-K1-B10
5'-most EST
                   BLASTX
Method
                   q4558566
NCBI GI
                   1214
BLAST score
                   1.0e-134
E value
                   368
Match length
                   58
% identity
                  (AC007138) putative raffinose synthase or seed imbibition
NCBI Description
                   protein [Arabidopsis thaliana]
                   15435
Seq. No.
                   35516 1.R1040
Contig ID
                   uC-gmropic023e12b1
5'-most EST
```

BLASTX Method NCBI GI g3033398 BLAST score 1561 1.0e-174 E value

Match length 330 89 % identity

NCBI Description (AC004238) putative phosphoribosylaminoimidazolecarboxamide formyltransferase [Arabidopsis thaliana]



```
15436
Seq. No.
                  35520 1.R1040
Contig ID
                  LIB3170-042-Q1-J1-A8
5'-most EST
Seq. No.
                  15437
                  35530 1.R1040
Contig ID
                  LIB3065-003-Q1-N1-D7
5'-most EST
Seq. No.
                  15438
                  35535 1.R1040
Contig ID
5'-most EST
                  jC-qmf102220071d06d1
                  15439
Seq. No.
Contig ID
                  35548 1.R1040
5'-most EST
                  uC-gmropic014h01b1
                  BLASTX
Method
NCBI GI
                  g125052
BLAST score
                  803
E value
                  9.0e-86
                  217
Match length
% identity
                  71
                  ISOVALERYL-COA DEHYDROGENASE PRECURSOR (IVD)
NCBI Description
                  >gi 111886 pir C34252 isovaleryl-CoA dehydrogenase (EC
                   1.3.99.10) precursor - rat >gi_204982 (J05031)
                   isovaleryl-CoA dehydrogenase precursor (EC 1.3.99.10)
                   [Rattus norvegicus]
                   15440
Seq. No.
                   35566 1.R1040
Contig ID
                  uC-gmropic008g03b1
5'-most EST
Seq. No.
                   15441
                   35566 2.R1040
Contig ID
5'-most EST
                  hyd700727849.h1
                  BLASTX
Method
                   g4490721
NCBI GI
                   150
BLAST score
                   1.0e-09
E value
                   37
Match length
                   78
% identity
                   (AL035709) squalene epoxidase-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   15442
Seq. No.
                   35586 1.R1040
Contig ID
5'-most EST
                   LIB3065-002-Q1-N1-C8
Method
                   BLASTX
                   g2257716
NCBI GI
                   148
BLAST score
```

2.0e-09 E value Match length 75 % identity

(U90439) hypothetical protein [Arabidopsis thaliana] NCBI Description

Seq. No. 15443

Contig ID 35590 1.R1040



```
jC-gmst02400049g10a1
5'-most EST
                  BLASTX
Method
                  g2462744
NCBI GI
```

238 BLAST score 2.0e-19 E value 282 Match length 25 % identity

(AC002292) Hypothetical protein [Arabidopsis thaliana] NCBI Description

15444 Seq. No.

35609 1.R1040

Contig ID

jC-gmst02400071d04a1 5'-most EST

15445 Seq. No.

35616 1.R1040 Contig ID

LIB3138-128-Q1-N1-A8 5'-most EST

BLASTX Method g3882149 NCBI GI 462 BLAST score 7.0e-46 E value 207 Match length 40 % identity

NCBI Description (AB018257) KIAA0714 protein [Homo sapiens]

Seq. No.

35630 1.R1040 Contig ID zpv700758365.hl 5'-most EST

15446

BLASTX Method g3123155 NCBI GI BLAST score 182 5.0e-13 E value 157 Match length 18 % identity

HYPOTHETICAL 49.0 KD TRP-ASP REPEATS CONTAINING PROTEIN NCBI Description F55F8.5 IN CHROMOSOME I >gi 1707049 (U80447) similar to the

beta transducin family [Caenorhabditis elegans]

15447 Seq. No.

35633 1.R1040 Contig ID fC-gmro700869958f3 5'-most EST

BLASTX Method g4567201 NCBI GI BLAST score 1388 E value 1.0e-164 Match length 399 74 % identity

(AC007168) putative aspartate aminotransferase [Arabidopsis NCBI Description

thaliana]

15448 Seq. No.

35633 3.R1040 Contig ID pcp700992612.h1 5'-most EST

15449 Seq. No.

35638 1.R1040 Contig ID

LIB3065-001-Q1-N1-H10 5'-most EST



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Seq. No.
                  15450
                  35655 1.R1040
Contig ID
                  LIB3138-034-Q1-N1-E2
5'-most EST
                  BLASTX
Method
                  g2244754
NCBI GI
BLAST score
                  972
                  1.0e-105
E value
                  290
Match length
                   65
% identity
                   (Z97335) heat shock transcription factor homolog
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   15451
                   35659 1.R1040
Contig ID
                   LIB3065-001-Q1-N1-B1
5'-most EST
Method
                  BLASTN
NCBI GI
                   g21054
BLAST score
                   494
                   0.0e+00
E value
                   1013
Match length
% identity
                   90
NCBI Description P.vulgaris mRNA for tonoplast intrinsic protein
                   15452
Seq. No.
                   35668 1.R1040
Contig ID
                   awf700842385.hl
5'-most EST
                   BLASTX
Method
                   g3004564
NCBI GI
                   443
BLAST score
                   7.0e-44
E value
                   162
Match length
                   55
% identity
                   (AC003673) putative receptor Ser/Thr protein kinase
NCBI Description
                   [Arabidopsis thaliana]
                   15453
Seq. No.
                   35689 1.R1040
Contig ID
                   uC-gmronoir061e01b1
5'-most EST
                   15454
Seq. No.
                   35697 1.R1040
Contig ID
                   LIB3170-044-Q1-J1-F11
5'-most EST
Seq. No.
                   15455
                   35700 1.R1040
Contig ID
                   g5057727
5'-most EST
                   15456
Seq. No.
                   35706 1.R1040
Contig ID
                   LIB3170-042-Q1-J1-A12
5'-most EST
```

Seq. No. 15457

Contig ID 35711\_1.R1040 5'-most EST uC-gmropic097b12b1

Seq. No. 15458

Contig ID 35712\_1.R1040

2585



```
jex700905547.hl
5'-most EST
                   BLASTX
Method
                   g4185136
NCBI GI
                   641
BLAST score
                   9.0e-67
E value
Match length
                   268
% identity
                   (AC005724) putative trehalose-6-phosphate synthase
NCBI Description
                   [Arabidopsis thaliana]
                   15459
Seq. No.
                   35733 1.R1040
Contig ID
                   LIB30\overline{6}5-013-Q1-N1-F12
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4049353
                   448
BLAST score
E value
                   2.0e-44
                   156
Match length
% identity
NCBI Description (AL034567) putative protein [Arabidopsis thaliana]
Seq. No.
                   15460
                   35765 1.R1040
Contig ID
                   hrw701061517.hl
5'-most EST
                   15461
Seq. No.
                   35769 1.R1040
Contig ID
                   LIB30\overline{6}5-020-Q1-N1-D11
5'-most EST
                   15462
Seq. No.
                   35784 1.R1040
Contig ID
5'-most EST
                   LIB3065-021-Q1-N1-A11
                   15463
Seq. No.
                   35799 1.R1040
Contig ID
                   kl1701209426.h1
5'-most EST
Seq. No.
                   15464
                   35821 1.R1040
Contig ID
5'-most EST
                   leu701146754.hl
                   15465
Seq. No.
                   35824 1.R1040
Contig ID
                   LIB3072-007-Q1-E1-C10
5'-most EST
                   15466
Seq. No.
                   35835 1.R1040
Contig ID
                   LIB3107-061-Q1-K1-D2
5'-most EST
                   BLASTX
Method
                   q4432836
NCBI GI
BLAST score
                   180
```

Method BLASTX
NCBI GI 94432836
BLAST score 180
E value 3.0e-13
Match length 80
% identity 46

NCBI Description (AC006283) unknown protein [Arabidopsis thaliana]

Seq. No. 15467

2586



Contig ID 35839\_1.R1040 5'-most EST LIB3072-061-Q1-K1-C3

Seq. No. 15468

Contig ID 35857\_1.R1040

5'-most EST LIB3073-006-Q1-K1-G2

Method BLASTN
NCBI GI g343515
BLAST score 50
E value 7.0e-19
Match length 313
% identity 92

NCBI Description Tobacco chloroplast Gly-tRNA and Arg-tRNA genes and the 3'

end of the proton-translocating ATPase alpha-subunit

Seq. No. 15469

Contig ID 35879\_1.R1040

5'-most EST LIB3072-060-Q1-K1-F11

Seq. No. 15470

Contig ID 35900\_1.R1040 5'-most EST zzp700834185.h1

Seq. No. 15471

Contig ID 35920\_1.R1040

5'-most EST LIB3072-060-Q1-K1-A10

Method BLASTX
NCBI GI g3123295
BLAST score 325
E value 5.0e-30
Match length 130
% identity 35

NCBI Description CALMODULIN-RELATED PROTEIN 2, TOUCH-INDUCED >gi\_2583169

(AF026473) calmodulin-related protein [Arabidopsis

thaliana]

Seq. No. 15472

Contig ID 35946 2.R1040 5'-most EST hrw701057284.h1

Method BLASTX
NCBI GI g4191788
BLAST score 289
E value 3.0e-26
Match length 82
% identity 66

NCBI Description (AC005917) putative 1-aminocyclopropane-1-carboxylate

oxidase [Arabidopsis thaliana]

Seq. No. 15473

Contig ID 35947\_1.R1040

5'-most EST LIB3074-011-Q1-E1-E1

Seq. No. 15474

Contig ID 35952\_1.R1040

5'-most EST LIB3072-059-Q1-K1-A1



Contig ID 35957\_1.R1040

5'-most EST LIB3072-059-Q1-K1-A4

Method BLASTN
NCBI GI g256428
BLAST score 319
E value 1.0e-179
Match length 537
% identity 90

NCBI Description KTi3 (KTi3+)=Kunitz trypsin inhibitor [soybeans, Dare and

Forrest, mRNA, 1259 nt]

Seq. No. 15476

Contig ID 35958\_1.R1040

5'-most EST jC-gmro02910006b08a1

Method BLASTX
NCBI GI g2245135
BLAST score 178
E value 6.0e-13
Match length 98
% identity 44

NCBI Description (Z97344) hypothetical protein [Arabidopsis thaliana]

Seq. No. 15477

Contig ID 35962\_1.R1040

5'-most EST LIB3072-015-Q1-E1-F6

Seq. No. 15478

Contig ID 35965\_1.R1040 5'-most EST gsv701048455.h1

Seq. No. 15479

Contig ID 35975\_1.R1040

5'-most EST LIB3072-058-Q1-K1-G10

Seq. No. 15480

Contig ID 35980\_1.R1040

5'-most EST LIB3106-066-P1-K1-A8

Method BLASTN
NCBI GI g343996
BLAST score 122
E value 5.0e-62
Match length 220
% identity 89

NCBI Description Pea chloroplast psbM gene for photosystem II polypeptide M

Seq. No. 15481

Contig ID 35995\_1.R1040 5'-most EST kl1701205966.h1

Seq. No. 15482

Contig ID 36003 1.R1040

5'-most EST LIB3072-058-Q1-K1-A7

Seq. No. 15483

Contig ID 36003\_2.R1040 5'-most EST wrg700788992.h2



Seq. No. 1548

Contig ID 36012 1.R1040

5'-most EST LIB3072-058-Q1-K1-C1

Seq. No. 15485

Contig ID 36016\_1.R1040 5'-most EST pcp700990982.h1

Method BLASTX
NCBI GI g3650033
BLAST score 167
E value 2.0e-11
Match length 105
% identity 33

NCBI Description (AC005396) unknown protein [Arabidopsis thaliana]

Seq. No. 15486

Contig ID 36017 1.R1040

5'-most EST LIB3072-057-Q1-K1-G5

Seq. No. 15487

Contig ID 36023\_1.R1040 5'-most EST uC-gmropic112g08b1

Method BLASTX
NCBI GI g2244816
BLAST score 282
E value 4.0e-25
Match length 119
% identity 60

NCBI Description (297336) hypothetical protein [Arabidopsis thaliana]

Seq. No. 15488

Contig ID 36058\_1.R1040 5'-most EST leu701150060.h1

Seq. No. 15489

Contig ID 36082\_1.R1040 5'-most EST zzp700835971.h1

Seq. No. 15490

Contig ID 36085\_1.R1040

5'-most EST LIB3106-013-Q1-K1-D5

Method BLASTX
NCBI GI g1495366
BLAST score 665
E value 4.0e-82
Match length 258
% identity 57

NCBI Description (Z69370) nitrite transporter [Cucumis sativus]

Seq. No. 15491

Contig ID 36097 1.R1040

5'-most EST jC-gmst02400001f01a1

Method BLASTX
NCBI GI g3759177
BLAST score 338
E value 2.0e-31
Match length 142



% identity 57

NCBI Description (AB018408) 3-phosphoserine phosphatase [Arabidopsis

thaliana] >gi\_3759179\_dbj\_BAA33807\_ (AB018409) 3-phosphoserin phosphatase [Arabidopsis thaliana]

Seq. No. 15492

Contig ID 36097\_2.R1040 5'-most EST pcp700991045.h1

Seq. No. 15493

Contig ID 36097 3.R1040

5'-most EST LIB3072-055-Q1-K1-F3

Seq. No. 15494

Contig ID 36128 1.R1040

5'-most EST LIB3073-023-Q1-K1-H7

Method BLASTX
NCBI GI 94512627
BLAST score 285
E value 2.0e-25
Match length 98
% identity 63

NCBI Description (AC004793) Similar to gb\_Z29643 protein kinase C inhibitor

(PKCI) from Zea mays and a member of HIT family PF 01230.

[Arabidopsis thaliana]

Seq. No. 15495

Contig ID 36141\_1.R1040 5'-most EST wrg700790508.h2

Method BLASTX
NCBI GI g1706817
BLAST score 179
E value 1.0e-12
Match length 106
% identity 39

NCBI Description 39 KD FK506-BINDING NUCLEAR PROTEIN (PEPTIDYL-PROLYL

CIS-TRANS ISOMERASE) (PPIASE) >gi\_1079072\_pir\_\_JC4090 FK506-binding 39k protein - fruit fly (Drosophila melanogaster) >gi\_600424 emb\_CAA86996 (Z46894) FKBP39

[Drosophila melanogaster]

Seq. No. 15496

Contig ID 36151\_1.R1040

5'-most EST LIB3072-028-Q1-E1-B5

Method BLASTX
NCBI GI g4539364
BLAST score 146
E value 4.0e-09
Match length 74
% identity 51

NCBI Description (AL049525) putative protein [Arabidopsis thaliana]

Seq. No. 15497

Contig ID 36170\_1.R1040 5'-most EST pxt700945508.h1



```
Contig ID
                  36191 1.R1040
5'-most EST
                  LIB3072-053-Q1-E1-F9
Method
                  BLASTX
                  g3128212
NCBI GI
BLAST score
                  216
                  4.0e-17
E value
Match length
                  97
% identity
                  49
NCBI Description
                  (AC004077) putative HMG protein [Arabidopsis thaliana]
                  >gi_3337373 (AC004481) putative HMG protein [Arabidopsis
                  thaliana]
Seq. No.
                  15499
Contia ID
                  36193 1.R1040
5'-most EST
                  LIB3072-050-Q1-K1-C9
Seq. No.
                  15500
Contig ID
                  36208 1.R1040
5'-most EST
                  LIB3107-074-Q1-K1-B11
Seq. No.
                  15501
Contig ID
                  36221 1.R1040
5'-most EST
                  LIB3072-053-Q1-E1-C10
Seq. No.
                  15502
Contig ID
                  36231 1.R1040
5'-most EST
                  LIB3106-112-Q1-K1-F1
Seq. No.
                  15503
Contig ID
                  36241 1.R1040
5'-most EST
                  6HA-01-Q1-E1-G6
Method
                  BLASTX
                  g3608154
NCBI GI
BLAST score
                  243
E value
                  1.0e-20
Match length
                  63
% identity
                  65
NCBI Description (AC005314) unknown protein [Arabidopsis thaliana]
Seq. No.
                  15504
Contig ID
                  36243 1.R1040
5'-most EST
                  LIB3072-051-Q1-E1-G4
Method
                  BLASTX
                  g4220491
NCBI GI
BLAST score
                  215
                  6.0e-17
E value
Match length
                  60
% identity
                  57
NCBI Description (AC006069) hypothetical protein [Arabidopsis thaliana]
Seq. No.
Contig ID
                  36243 2.R1040
```

5'-most EST jC-gmf102220081b05d1

Seq. No. 15506

Contig ID 36253 1.R1040

5'-most EST LIB3072-052-Q1-E1-B7



Seq. No. 15507

Contig ID 36257 1.R1040

5'-most EST LIB3072-051-Q1-E1-E4

Seq. No. 15508

Contig ID 36261 1.R1040

5'-most EST LIB3072-051-Q1-E1-E9

Seq. No. 15509

Contig ID 36283 2.R1040

5'-most EST LIB3072-050-Q1-K1-H8

Seq. No. 15510

Contig ID 36298\_1.R1040 5'-most EST zhf700957025.h1

Method BLASTX
NCBI GI g462264
BLAST score 681
E value 1.0e-71
Match length 274
% identity 52

NCBI Description

GTP-BINDING PROTEIN HFLX >gi\_1361024\_pir\_\_S56398 GTPase homolog protein hflX - Escherichia coli >gi\_436156 (U00005) putative GTPase required for high frequency lysogenization by bacteriophage lambda [Escherichia coli] >gi\_537014 (U14003) putative GTPase required for high frequency lysogenization by bacteriophage lambda; TTG start codon [Escherichia coli] >gi\_1790615 (AE000489) GTP - binding subunit of protease specific for phage lambda cII repressor

[Escherichia coli]

Seq. No. 15511

Contig ID 36315 1.R1040

5'-most EST LIB3072-050-Q1-K1-E10

Seq. No. 15512

Contig ID 36320\_1.R1040 5'-most EST rlr700902161.h1

Seq. No. 15513

Contig ID 36320\_2.R1040 5'-most EST rlr700897160.h1

Seq. No. 15514

Contig ID 36348 2.R1040

5'-most EST LIB3106-047-Q1-K1-H4

Method BLASTX
NCBI GI g2911043
BLAST score 278
E value 2.0e-24
Match length 122
% identity 52

NCBI Description (AL021961) putative protein [Arabidopsis thaliana]

Seq. No. 15515

Contig ID 36348\_3.R1040

2592



```
5'-most EST
                  wrg700791887.h1
                  15516
Seq. No.
                  36353 1.R1040
Contig ID
5'-most EST
                  kl1701211505.h1
Method
                  BLASTX
NCBI GI
                  q586099
BLAST score
                  220
E value
                  1.0e-17
Match length
                  110
% identity
                  40
                  THIOREDOXIN H-TYPE 2 (TRX-H2) >gi 486690 pir S34812
NCBI Description
                  thioredoxin h2 - common tobacco >gi 297519 emb CAA77847_
                  (Z11803) THIOREDOXIN [Nicotiana tabacum]
                  >gi 447151 prf 1913431A thioredoxin [Nicotiana tabacum]
                  15517
Seq. No.
Contig ID
                  36367 1.R1040
                  awf700836602.h1
5'-most EST
                  15518
Seq. No.
                  36390 1.R1040
Contig ID
5'-most EST
                  LIB3072-009-Q1-E1-H6
                  15519
Seq. No.
Contig ID
                  36393 1.R1040
5'-most EST
                  LIB3072-047-Q1-K1-A4
                  15520
Seq. No.
                  36398 1.R1040
Contig ID
5'-most EST
                  LIB3106-093-Q1-K1-C7
Method
                  BLASTX
                  g2501647
NCBI GI
BLAST score
                  963
                  1.0e-104
E value
Match length
                  245
                  77
% identity
                  UROPORPHYRINOGEN DECARBOXYLASE PRECURSOR (UPD)
NCBI Description
                  >gi 1362120 pir S55732 uroporphyrinogen decarboxylase -
                  common tobacco >gi 1009429 emb CAA58040 (X82833)
                  uroporphyrinogen decarboxylase [Nicotiana tabacum]
                  15521
Seq. No.
Contig ID
                  36401 1.R1040
5'-most EST
                  ssr700557824.hl
Method
                  BLASTX
                  q4006867
NCBI GI
```

BLAST score 404
E value 2.0e-39
Match length 139
% identity 65

NCBI Description (Z99707) putative protein [Arabidopsis thaliana]

Seq. No. 15522

Contig ID 36410\_1.R1040

5'-most EST LIB3072-028-Q1-E1-C4



Seq. No. 15523

Contig ID 36441\_1.R1040

5'-most EST uC-gmrominsoy194h12b1

Method BLASTX
NCBI GI g3047101
BLAST score 244
E value 1.0e-20
Match length 121
% identity 41

NCBI Description (AF058919) Similar to protein kinase; coded for by A.

thaliana cDNA H36947; coded for by A. thaliana cDNA H37158

[Arabidopsis thaliana]

Seq. No. 15524

Contig ID 36441 2.R1040

5'-most EST uC-gmrominsoy280e02b1

Seq. No. 15525

Contig ID 36451\_1.R1040

5'-most EST LIB3072-046-Q1-K1-B3

Method BLASTX
NCBI GI g4164408
BLAST score 858
E value 3.0e-92
Match length 203
% identity 75

NCBI Description (AJ132228) amino acid carrier [Ricinus communis]

Seq. No. 15526

Contig ID 36458 1.R1040

5'-most EST LIB3072-044-Q1-K1-G2

Seq. No. 15527

Contig ID 36464\_1.R1040

5'-most EST LIB3072-044-Q1-K1-H10

Method BLASTX
NCBI GI g2183221
BLAST score 220
E value 1.0e-17
Match length 64
% identity 61

NCBI Description (AF001954) p33ING1 [Homo sapiens]

Seq. No. 15528

Contig ID 36490 1.R1040

5'-most EST jC-gmf102220130c03d1

Method BLASTX
NCBI GI g3599491
BLAST score 392
E value 8.0e-38
Match length 101
% identity 70

NCBI Description (AF085149) putative aminotransferase [Capsicum chinense]

Seq. No. 15529

Contig ID 36509 1.R1040 5'-most EST taw700660377.h1



Method BLASTX
NCBI GI g4580463
BLAST score 183
E value 2.0e-13
Match length 37
% identity 89

NCBI Description (AC006081) unknown protein [Arabidopsis thaliana]

Seq. No.

Contig ID 36537 1.R1040

5'-most EST LIB3106-010-Q1-K1-G10

15530

Method BLASTN
NCBI GI g22028
BLAST score 33
E value 8.0e-09
Match length 81
% identity 85

NCBI Description V.faba mRNA for polyphenol oxidase

Seq. No. 15531

Contig ID 36548 1.R1040

5'-most EST LIB3072-034-Q1-E1-D6

Seq. No. 15532

Contig ID 36548\_5.R1040

5'-most EST LIB3072-039-Q1-E1-A11

Seq. No. 15533

Contig ID 36549 1.R1040

5'-most EST LIB3072-038-Q1-E1-B7

Seq. No. 15534

Contig ID 36549 2.R1040

5'-most EST LIB3072-030-Q1-E1-C5

Seq. No. 15535

Contig ID 36549\_3.R1040

5'-most EST LIB3072-034-Q1-E1-A10

Seq. No. 15536

Contig ID 36549\_4.R1040

5'-most EST LIB3072-039-Q1-E1-A10

Seq. No. 15537

Contig ID 36549 7.R1040

5'-most EST LIB3072-033-Q1-E1-C2

Seq. No. 15538

Contig ID 36549\_8.R1040

5'-most EST LIB3072-033-Q1-E1-G10

Seq. No. 15539

Contig ID 36549 10.R1040

5'-most EST LIB3072-036-Q1-E1-G12

Seq. No. 15540

Contig ID 36550\_1.R1040



5'-most EST

LIB3072-031-Q1-E1-F10

Seq. No.

15541

Contig ID 5'-most EST

36550 2.R1040 LIB3072-031-Q1-E1-D6

Seq. No.

15542

Contig ID 5'-most EST

36550 3.R1040 LIB3072-030-Q1-E1-B5

Seq. No.

15543

Contig ID 5'-most EST

36550 6.R1040 LIB3072-029-Q1-E1-G6

Seq. No.

15544

Contig ID 5'-most EST 36550 7.R1040

LIB3072-036-Q1-E1-E5

Seq. No. Contig ID 15545

36550 8.R1040

5'-most EST

LIB3072-032-Q1-E1-D4

Seq. No.

15546

Contig ID 5'-most EST 36551 1.R1040

LIB3072-040-Q1-E1-H2

Seq. No.

15547

BLASTX

Contig ID

36555 1.R1040

5'-most EST

LIB3072-043-Q1-K1-A11

Method NCBI GI BLAST score E value

q4455234 172 5.0e-12

Match length % identity

81

NCBI Description (AL035523) putative protein [Arabidopsis thaliana]

Seq. No. Contig ID 15548

5'-most EST

36566 1.R1040

LIB3072-035-Q1-E1-B2

Seq. No.

15549

Contig ID 5'-most EST 36566 2.R1040

LIB3072-032-Q1-E1-F2

Seq. No.

15550

Contig ID

36566 3.R1040

5'-most EST

LIB3072-040-Q1-E1-C11

Seq. No. Contig ID 15551

5'-most EST

36566 4.R1040 LIB3072-037-Q1-E1-D9

Method NCBI GI

BLASTX q3676826

BLAST score E value Match length 168 2.0e-11 100

2596



% identity 6
NCBI Description (AF092449) mucin-like protein [Heterodera glycines]

Seq. No. 15552

Contig ID 36566\_5.R1040

5'-most EST LIB3072-034-Q1-E1-B8

Seq. No. 15553

Contig ID 36566 6.R1040

5'-most EST LIB3072-032-Q1-E1-E6

Seq. No. 15554

Contig ID 36566 10.R1040

5'-most EST LIB3072-038-Q1-E1-A10

Seq. No. 15555

Contig ID 36566\_11.R1040

5'-most EST LIB3072-040-Q1-E1-E1

Seq. No. 15556

Contig ID 36566 23.R1040

5'-most EST LIB3106-069-P1-K1-E10

Seq. No. 15557

Contig ID 36566 24.R1040

5'-most EST LIB3072-040-Q1-E1-A12

Seq. No. 15558

Contig ID 36566 35.R1040

5'-most EST LIB3072-030-Q1-E1-D3

Seq. No. 15559

Contig ID 36582\_1.R1040

5'-most EST LIB3072-030-Q1-E1-E10

Method BLASTX
NCBI GI g3914472
BLAST score 150
E value 1.0e-09
Match length 93
% identity 42

NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR (PII10)

>gi\_322764\_pir\_\_S32021 photosystem II 10K protein - common tobacco >gi\_22669 emb CAA49693 (X70088) NtpII10 [Nicotiana

tabacum]

Seq. No. 15560

Contig ID 36615 1.R1040

5'-most EST LIB3072-031-Q1-E1-A1

Seq. No. 15561

Contig ID 36618\_1.R1040

5'-most EST LIB3072-029-Q1-E1-C6

Seq. No. 15562

Contig ID 36620 1.R1040

5'-most EST LIB3072-029-Q1-E1-E3



Seq. No.	15563
Contig ID	36624_1.R1040
5'-most EST	LIB3072-033-Q1-E1-H9
Seq. No. Contig ID 5'-most EST	15564 36641 1.R1040 LIB3072-036-Q1-E1-D6

Seq. No. 15565 Contig ID 36641\_3.R1040 5'-most EST LIB3072-038-Q1-E1-H5

 Seq. No.
 15566

 Contig ID
 36655\_1.R1040

 5'-most EST
 LIB3072-038-Q1-E1-F4

 Seq. No.
 15567

 Contig ID
 36672\_1.R1040

 5'-most EST
 LIB3072-039-Q1-E1-F4

 Seq. No.
 15568

 Contig ID
 36677 1.R1040

 5'-most EST
 LIB3072-033-Q1-E1-F9

 Seq. No.
 15569

 Contig ID
 36685\_1.R1040

 5'-most EST
 LIB3072-039-Q1-E1-D1

 Seq. No.
 15570

 Contig ID
 36713 1.R1040

 5'-most EST
 LIB3072-038-Q1-E1-H2

 Seq. No.
 15571

 Contig ID
 36729 1.R1040

 5'-most EST
 LIB3072-036-Q1-E1-G8

 Seq. No.
 15572

 Contig ID
 36739 1.R1040

 5'-most EST
 LIB3072-032-Q1-E1-F3

 Seq. No.
 15573

 Contig ID
 36761\_1.R1040

 5'-most EST
 LIB3072-036-Q1-E1-A8

 Seq. No.
 15574

 Contig ID
 36766\_1.R1040

 5'-most EST
 LIB3072-038-Q1-E1-A2

 Seq. No.
 15575

 Contig ID
 36767\_1.R1040

 5'-most EST
 LIB3072-035-Q1-E1-F5

 Seq. No.
 15576

 Contig ID
 36778\_1.R1040

 5'-most EST
 LIB3072-038-Q1-E1-A6



Contig ID 36780\_1.R1040 5'-most EST LIB3072-031-Q1-E1-B2

Seq. No. 15578

Contig ID 36781\_1.R1040 5'-most EST LIB3072-038-Q1-E1-A9

Seq. No. 15579

Contig ID 36787 1.R1040

5'-most EST LIB3072-032-Q1-E1-B6

Seq. No. 15580

Contig ID 36791\_1.R1040 5'-most EST bth700848662.h1

Seq. No. 15581

Contig ID 36831 1.R1040

5'-most EST LIB3072-034-Q1-E1-F1

Seq. No. 15582

Contig ID 36834 1.R1040

5'-most EST LIB3072-037-Q1-E1-A1

Seq. No. 15583

Contig ID 36844 1.R1040

5'-most EST LIB3072-030-Q1-E1-E6

Method BLASTX
NCBI GI g2500353
BLAST score 155
E value 4.0e-10
Match length 120

% identity 39

NCBI Description 60S RIBOSOMAL PROTEIN L10-3 (QM/R22) >gi\_1293784 (U55048)

similar to human QM protein, a putative tumor supressor, and to maize ubiquinol-cytochrome C reductase complex

subunit VI requiring protein SC34 [Oryza sativa]

Seq. No. 15584

Contig ID 36855\_1.R1040

5'-most EST LIB3072-030-Q1-E1-H8

Seq. No. 15585

Contig ID 36855 2.R1040

5'-most EST LIB3072-030-Q1-E1-B2

Seq. No. 15586

Contig ID 36945\_1.R1040

5'-most EST LIB3072-035-Q1-E1-C3

Seq. No. 15587

Contig ID 37006 1.R1040

5'-most EST LIB3072-032-Q1-E1-F4

Seq. No. 15588

Contig ID 37025 1.R1040

5'-most EST LIB3072-029-Q1-E1-E4



15589 Seq. No. 37062 1.R1040 Contig ID LIB3072-031-Q1-E1-D4 5'-most EST Seq. No. 15590 37092 1.R1040 Contig ID LIB3072-033-Q1-E1-F11 5'-most EST 15591 Seq. No. 37094 1.R1040 Contig ID LIB3072-033-Q1-E1-F2 5'-most EST

15592 Seq. No. 37118 1.R1040 Contig ID LIB3072-031-Q1-E1-G1 5'-most EST

15593 Seq. No. 37127 1.R1040 Contig ID LIB3072-033-Q1-E1-A4 5'-most EST

15594 Seq. No. 37341 1.R1040 Contig ID LIB3072-030-Q1-E1-D9 5'-most EST

15595 Seq. No. 37360 1.R1040 Contig ID LIB3072-030-Q1-E1-C2 5'-most EST

15596 Seq. No. 37389 1.R1040 Contig ID LIB3072-029-Q1-E1-H2 5'-most EST

15597 Seq. No. 37523 1.R1040 Contig ID wrg700788148.hl 5'-most EST BLASTX Method

g1780757 NCBI GI 245 BLAST score 8.0e-21 E value 73 Match length 58 % identity

(Y10291) highly expressed in proliferating cells NCBI Description [Arabidopsis thaliana]

15598 Seq. No. 37531\_1.R1040 Contig ID sat701011576.hl 5'-most EST BLASTX Method q3252825 NCBI GI 332 BLAST score 2.0e-30 E value

186

Match length 49 % identity (AC004382) Unknown gene product [Homo sapiens] NCBI Description

15599 Seq. No. Contig ID

37531 2.R1040



5'-most EST asn701133382.h1

Seq. No. 15600

Contig ID 37540 1.R1040

5'-most EST LIB3072-027-Q1-E1-A7

Seq. No. 15601

Contig ID 37553\_1.R1040

5'-most EST LIB3072-026-Q1-E1-G2

Seq. No. 15602

Contig ID 37583 1.R1040

5'-most EST LIB3093-006-Q1-K1-H11

Seq. No. 15603

Contig ID 37605\_1.R1040

5'-most EST LIB3106-095-Q1-K1-B7

Method BLASTX
NCBI GI g4512696
BLAST score 311
E value 4.0e-28
Match length 99
% identity 68

NCBI Description (AC006569) hypothetical protein [Arabidopsis thaliana]

Seq. No. 15604

Contig ID 37632 1.R1040

5'-most EST jC-gmro02800040a04a1

Seq. No. 15605

Contig ID 37633 1.R1040

5'-most EST jC-gmle01810020b11d1

Seq. No. 15606

Contig ID 37645 1.R1040

5'-most EST jC-gmro02910006f11a1

Method BLASTX
NCBI GI g3608137
BLAST score 160
E value 2.0e-13
Match length 128
% identity 41

NCBI Description (AC005314) unknown protein [Arabidopsis thaliana]

Seq. No. 15607

Contig ID 37645 2.R1040

5'-most EST uC-gmrominsoy049d05b1

Seq. No. 15608

Contig ID 37645 3.R1040

5'-most EST uC-gmrominsoy206e04b1

Seq. No. 15609

Contig ID 37661\_1.R1040

5'-most EST LIB3072-024-Q1-E1-B4

Seq. No. 15610

2601

```
37666 1.R1040
```

Contig ID 37666\_1.R1040 5'-most EST zsg701120625.h1

Method BLASTX
NCBI GI g4455324
BLAST score 252
E value 1.0e-21
Match length 72
% identity 56

NCBI Description (AL035525) putative protein [Arabidopsis thaliana]

Seq. No. 15611

Contig ID 37675\_1.R1040

5'-most EST LIB3072-021-Q1-E1-A12

Seq. No. 15612

Contig ID 37675\_2.R1040 5'-most EST kl1701204517.h2

Seq. No. 15613

Contig ID 37684 1.R1040 5'-most EST leu701146690.h1

Method BLASTX
NCBI GI g3121852
BLAST score 231
E value 1.0e-18
Match length 199
% identity 30

NCBI Description CHLORIDE INTRACELLULAR CHANNEL PROTEIN 1 (NUCLEAR CHLORIDE

ION CHANNEL 27) (P64 CLCP) >gi\_2073569 (U93205) nuclear

chloride ion channel protein [Homo sapiens]

>gi\_4502881\_ref\_NP\_001279.1\_pCLIC1\_ chloride intracellular

channel

Seq. No. 15614

Contig ID 37698\_1.R1040

5'-most EST LIB3092-039-Q1-K1-E6

Seq. No. 15615

Contig ID 37712 1.R1040

5'-most EST LIB3072-022-Q1-E1-H3

Seq. No. 15616

Contig ID 37721\_1.R1040

NCBI Description (U84888) phosphoglucomutase [Mesembryanthemum crystallinum]

Seq. No. 15617

Contig ID 37723 1.R1040 5'-most EST g4304543 Method BLASTX NCBI GI g461729



```
BLAST score
                  388
E value
                  2.0e-37
                  95
Match length
                  75
% identity
                  10 KD CHAPERONIN (PROTEIN CPN10) (PROTEIN GROES)
NCBI Description
                  >gi 2146744 pir__S65597 probable chaperonin, 10K -
                  Arabidopsis thaliana >gi 166662 (L02843) 10 kDa chaperonin
                  [Arabidopsis thaliana]
                  15618
Seq. No.
                  37727 1.R1040
Contig ID
5'-most EST
                  fua701039549.h1
                  15619
Seq. No.
                  37737 1.R1040
Contig ID
                  ncj700983303.hl
5'-most EST
Method
                  BLASTX
NCBI GI
                  q461532
                  234
BLAST score
E value
                  5.0e-21
Match length
                  71
                  72
% identity
                  ADP-RIBOSYLATION FACTOR >gi_1362500_pir__D49993
NCBI Description
                  ADP-ribosylation factor - Ajellomyces capsulata >gi_407693
                   (L25117) ADP-ribosylation factor [Histoplasma capsulatum]
                  15620
Seq. No.
                  37737 2.R1040
Contig ID
5'-most EST
                  fua701037055.h1
                  BLASTX
Method
NCBI GI
                  g461532
BLAST score
                  187
                  3.0e-14
E value
Match length
                  50
                   68
% identity
                  ADP-RIBOSYLATION FACTOR >gi_1362500_pir__D49993
NCBI Description
                   ADP-ribosylation factor - Ajellomyces capsulata >gi_407693
                   (L25117) ADP-ribosylation factor [Histoplasma capsulatum]
                   15621
Seq. No.
                   37749 1.R1040
Contig ID
                   LIB3074-018-Q1-E1-G9
5'-most EST
                  BLASTN
Method
                   g2564044
NCBI GI
BLAST score
                   39
                   2.0e-12
E value
Match length
                   59
                   92
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                   K19P17, complete sequence [Arabidopsis thaliana]
```

Seq. No. 15622

Contig ID 37759\_1.R1040

5'-most EST LIB3106-032-Q1-K1-E1

Seq. No. 15623

Contig ID 37769\_1.R1040



```
5'-most EST crh700852347.h1

Seq. No. 15624
Contig ID 37784_1.R1040
5'-most EST LIB3072-021-Q1-E1-C10
```

Seq. No. 15625 Contig ID 37786\_1.R1040 5'-most EST LIB3072-020-Q1-E1-H11

 Seq. No.
 15626

 Contig ID
 37796\_1.R1040

 5'-most EST
 rlr700897470.h1

 Method
 BLASTX

 NCBI GI
 q3695408

NCBI GI g3695408
BLAST score 146
E value 6.0e-09
Match length 80
% identity 42

NCBI Description (AF096373) contains similarity to Solanum lycopersicum (tomato) wound-induced protein (GB:X59882) [Arabidopsis thaliana] >gi\_4538956\_emb\_CAB39780.1\_ (AL049488) probable

wound-induced protein [Arabidopsis thaliana]

Seq. No. 15627

Contig ID 37796\_2.R1040

5'-most EST LIB3107-057-Q1-K1-B1

Seq. No. 15628

Contig ID 37817\_1.R1040

5'-most EST LIB3072-020-Q1-E1-E11

Method BLASTN
NCBI GI g255572
BLAST score 374
E value 0.0e+00
Match length 407
% identity 98

NCBI Description small auxin up RNA gene cluster: orf 15A [Glycine

max=soybeans, cv. Wayne, Genomic, 637 nt]

Seq. No. 15629

Contig ID 37817\_2.R1040 5'-most EST jsh701066132.h1

Method BLASTN
NCBI GI g255576
BLAST score 99
E value 2.0e-48
Match length 250
% identity 86

NCBI Description small auxin up RNA gene cluster: orf 6B [Glycine

max=soybeans, cv. Wayne, Genomic, 665 nt]

Seq. No. 15630

Contig ID 37818 1.R1040

5'-most EST LIB3072-020-Q1-E1-E12



37848 1.R1040 Contig ID jC-gmro02910055e02a1 5'-most EST Seq. No. 15632 37928 1.R1040 Contig ID jC-gmro02910009a10a1 5'-most EST BLASTX Method g2739046 NCBI GI 229 BLAST score 1.0e-18 E value 163 Match length 33 % identity (AF024652) polyphosphoinositide binding protein Ssh2p NCBI Description [Glycine max] 15633 Seq. No. 37928 2.R1040 Contig ID leu701150844.h1 5'-most EST BLASTN Method g2618600 NCBI GI 33 BLAST score 6.0e-09 E value 73 Match length 86 % identity Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MDC12, complete sequence [Arabidopsis thaliana] 15634 Seq. No. 37931 1.R1040 Contig ID LIB3072-017-Q1-E1-H11 5'-most EST BLASTX Method q3582002 NCBI GI BLAST score 248 E value 5.0e-21164 Match length % identity 38 (AJ010943) tomato invertase inhibitor [Lycopersicon NCBI Description esculentum] 15635 Seq. No. 37939 1.R1040 Contig ID LIB3072-018-Q1-E1-A5 5'-most EST Seq. No. 15636 37945 1.R1040 Contig ID LIB3072-017-Q1-E1-F2 5'-most EST 15637 Seq. No. 37946 1.R1040 Contig ID LIB3072-007-Q1-E1-C12

5'-most EST

15638 Seq. No.

38002 1.R1040 Contig ID

LIB3109-010-Q1-K1-F8 5'-most EST

Seq. No. 15639

38014\_1.R1040 Contig ID



5'-most EST kl1701208691.h1

Method BLASTX
NCBI GI g4467157
BLAST score 184
E value 2.0e-13
Match length 138
% identity 34

NCBI Description (AL035540) disease resistance response like protein

[Arabidopsis thaliana]

Seq. No. 15640

Contig ID 38033\_1.R1040

5'-most EST LIB3072-015-Q1-E1-C3

Method BLASTX
NCBI GI g2827657
BLAST score 311
E value 4.0e-28
Match length 104
% identity 60

NCBI Description (AL021637) putative protein [Arabidopsis thaliana]

Seq. No. 15641

Contig ID 38036\_1.R1040 5'-most EST fua701043025.h1

Method BLASTX
NCBI GI g3355626
BLAST score 455
E value 4.0e-45
Match length 221
% identity 62

NCBI Description (Y09204) histidinol-phosphate aminotransferase [Nicotiana

tabacum]

Seq. No. 15642

Contig ID 38040\_1.R1040

5'-most EST LIB31 $\overline{3}$ 9-045-P1-N1-F6

Seq. No. 15643

Contig ID 38041\_1.R1040

5'-most EST LIB30 $\overline{9}2$ -010-Q1-K1-B12

Seq. No. 15644

Contig ID 38041\_2.R1040

5'-most EST LIB3072-014-Q1-E1-H12

Seq. No. 15645

Contig ID 38054\_1.R1040

5'-most EST LIB3072-014-Q1-E1-E2

Seq. No. 15646

Contig ID 38065\_1.R1040

5'-most EST LIB3073-025-Q1-K1-C10

Method BLASTX
NCBI GI g3540193
BLAST score 467
E value 6.0e-47
Match length 99



```
% identity
                  (AC004122) Unknown protein [Arabidopsis thaliana]
NCBI Description
                  15647
Seq. No.
                  38065 2.R1040
Contig ID
                  leu701148234.h1
5'-most EST
                  BLASTX
Method
                  g3540193
NCBI GI
                  291
BLAST score
                  1.0e-26
E value
                  61
Match length
                  84
% identity
                  (AC004122) Unknown protein [Arabidopsis thaliana]
NCBI Description
                  15648
Seq. No.
                  38087_1.R1040
Contig ID
                  jC-gmst02400053a07d1
5'-most EST
                  15649
Seq. No.
                   38087 2.R1040
Contig ID
                  uC-gmrominsoy175e02b1
5'-most EST
                  BLASTX
Method
                   g4469025
NCBI GI
BLAST score
                   313
                   2.0e-28
E value
                   98
Match length
                   55
% identity
                  (AL035602) putative protein [Arabidopsis thaliana]
NCBI Description
                   15650
Seq. No.
                   38087 3.R1040
Contig ID
                   LIB3073-024-Q1-K1-F10
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4469025
                   299
BLAST score
E value
                   8.0e-27
Match length
                   98
                   53
% identity
NCBI Description (AL035602) putative protein [Arabidopsis thaliana]
Seq. No.
                   15651
                   38087 4.R1040
Contig ID
                   g4287589
5'-most EST
Method
                   BLASTX
                   q4469025
NCBI GI
                   302
BLAST score
E value
                   3.0e-27
Match length
                   98
                   53
% identity
NCBI Description (AL035602) putative protein [Arabidopsis thaliana]
                   15652
Seq. No.
                   38087 5.R1040
Contig ID
```

jsh701068533.hl 5'-most EST

15653 Seq. No.

38087\_6.R1040 Contig ID



kl1701214922.hl 5'-most EST

BLASTX Method q3094014 NCBI GI 157 BLAST score 1.0e-10 E value Match length 60

47 % identity (AF060862) unknown [Homo sapiens] NCBI Description

Seq. No. 15654

38088 1.R1040 Contig ID LIB3072-012-Q1-E1-G12 5'-most EST

15655 Seq. No. 38091 1.R1040

Contig ID LIB3072-012-Q1-E1-G5 5'-most EST

15656 Seq. No.

38101 1.R1040 Contig ID

LIB3072-010-Q1-E1-A11 5'-most EST

15657 Seq. No.

38101 2.R1040 Contig ID

 $uC-gm\overline{f}lminsoy011c07b1$ 5'-most EST

15658 Seq. No.

38107 1.R1040 Contig ID

LIB3074-022-Q1-E1-A11 5'-most EST

15659 Seq. No.

38122 1.R1040 Contig ID awf700841115.h15'-most EST

BLASTX Method g140701 NCBI GI 211 BLAST score 1.0e-16 E value 132 Match length 36 % identity

NCBI Description

HYPOTHETICAL 26.5 KD PROTEIN IN TOLC-RIBB INTERGENIC REGION (ORFB) (O265) >gi\_96076\_pir\_\_S22363 hypothetical protein B - Escherichia coli >gi\_146680 (M77129) ORFB [Escherichia coli] >gi\_1789419 (AEOO0386) orf, hypothetical protein

[Escherichia coli]

15660 Seq. No.

38122 2.R1040 Contig ID hrw701059941.hl 5'-most EST

15661 Seq. No.

38125 2.R1040 Contig ID zhf700953888.h1 5'-most EST

15662 Seq. No.

38129 1.R1040 Contig ID

LIB3072-012-Q1-E1-B8 5'-most EST

BLASTX Method g4538962 NCBI GI



BLAST score 149 E value 2.0e-09 Match length 133 % identity 30

NCBI Description (AL049488) hypothetical protein [Arabidopsis thaliana]

Seq. No. 15663

Contig ID 38136\_1.R1040 5'-most EST xzy700966722.h1 Method BLASTX

NCBI GI g3868857
BLAST score 497
E value 2.0e-96
Match length 303
% identity 64

NCBI Description (AB013886) RAV1 [Arabidopsis thaliana]

Seq. No. 15664

Contig ID 38136 2.R1040 5'-most EST epx701105014.h1

Method BLASTX
NCBI GI g3868859
BLAST score 276
E value 2.0e-24
Match length 77
% identity 73

NCBI Description (AB013887) RAV2 [Arabidopsis thaliana]

Seq. No. 15665

Contig ID 38136\_3.R1040 5'-most EST uC-gmropic010d08b1

Method BLASTX
NCBI GI g3868859
BLAST score 472
E value 2.0e-47
Match length 155
% identity 66

NCBI Description (AB013887) RAV2 [Arabidopsis thaliana]

Seq. No. 15666

Contig ID 38141\_1.R1040 5'-most EST LIB3072-011-Q1-E1-F1

Seq. No. 15667

Contig ID 38143\_1.R1040 5'-most EST trc700566061.h1

Seq. No. 15668

Contig ID 38143\_3.R1040 5'-most EST jsh701069222.h1

Seq. No. 15669

Contig ID 38143\_5.R1040 5'-most EST uaw700666625.h1

Seq. No. 15670

Contig ID 38148 1.R1040



```
LIB3170-037-Q1-K1-C3
5'-most EST
                  15671
Seq. No.
                  38148 2.R1040
Contig ID
                  vzy700752483.hl
5'-most EST
Seq. No.
                  15672
                  38162 1.R1040
Contig ID
                  trc700561670.hl
5'-most EST
                  15673
Seq. No.
                  38185 1.R1040
Contig ID
                  LIB3072-010-Q1-E1-F12
5'-most EST
Method
                  BLASTX
                  q4220484
NCBI GI
                  211
BLAST score
E value
                  2.0e-16
Match length
                  130
                  42
% identity
                  (AC006069) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  15674
Seq. No.
                  38185 2.R1040
Contig ID
                  pxt700943644.hl
5'-most EST
                   15675
Seq. No.
                   38187 1.R1040
Contig ID
                  wrq700786281.h2
5'-most EST
                  BLASTX
Method
                   g4432834
NCBI GI
                   243
BLAST score
                   2.0e-20
E value
Match length
                   79
                   66
% identity
                  (AC006283) unknown protein [Arabidopsis thaliana]
NCBI Description
                   15676
Seq. No.
                   38191 1.R1040
Contiq ID
                   uC-gmflminsoy109g07b1
5'-most EST
                   BLASTX
Method
                   g3096949
NCBI GI
                   1163
BLAST score
                   1.0e-128
E value
                   308
Match length
                   73
 % identity
                   (Y16328) putative cyclic nucleotide-regulated ion channel
NCBI Description
                   [Arabidopsis thaliana] >gi_3894399 (AF067798) cyclic
                   nucleotide-gated cation channel [Arabidopsis thaliana]
                   15677
 Seq. No.
                   38202 1.R1040
 Contig ID
 5'-most EST
                   vwf700674326.hl
```

38237\_1.R1040

5'-most EST LIB3072-009-Q1-E1-F11

Seq. No.

Contig ID

15678



```
Seq. No.
                   38259 1.R1040
Contig ID
                   zhf70\overline{0}955591.h1
5'-most EST
                  BLASTX
Method
                   g1685005
NCBI GI
                   442
BLAST score
                   1.0e-43
E value
                   137
Match length
                   59
% identity
                  (U32644) immediate-early salicylate-induced
NCBI Description
                   glucosyltransferase [Nicotiana tabacum]
                   15680
Seq. No.
                   38272 1.R1040
Contig ID
                   txt70\overline{0}732307.h1
5'-most EST
                   BLASTX
Method
                   g2145023
NCBI GI
                   284
BLAST score
                   3.0e-25
E value
                   135
Match length
                   47
% identity
                   (U97700) 15.5 kDa oleosin [Sesamum indicum]
NCBI Description
                   15681
Seq. No.
                   38283 1.R1040
Contig ID
                   LIB3106-095-Q1-K1-C10
5'-most EST
                   BLASTX
Method
                   a3980406
NCBI GI
                   230
BLAST score
                   6.0e-19
E value
                   61
Match length
                   69
% identity
                   (AC004561) putative tropinone reductase [Arabidopsis
NCBI Description
                   thaliana]
                   15682
Seq. No.
                   38298 1.R1040
Contig ID
                   LIB3106-097-Q1-K1-D3
5'-most EST
                   15683
Seq. No.
                    38298 2.R1040
Contig ID
                   LIB3167-023-P4-K4-E4
 5'-most EST
                   BLASTX
Method
                    g2464852
NCBI GI
                    250
BLAST score
                    6.0e-21
E value
                    164
Match length
                    40
 % identity
 NCBI Description (Z99707) putative protein [Arabidopsis thaliana]
                    15684
 Seq. No.
```

38310 1.R1040 Contig ID

5'-most EST LIB3072-008-Q1-E1-B9

15685 Seq. No.

38315 1.R1040 Contig ID g5677393 5'-most EST



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15686
Seq. No.
Contig ID
                   38338 1.R1040
5'-most EST
                  g5057466
                   15687
Seq. No.
                   38354 1.R1040
Contig ID
                   LIB3074-003-Q1-K1-G11
5'-most EST
                   15688
Seq. No.
                   38367_1.R1040
Contig ID
                   jC-gmle01810086d10d1
5'-most EST
                   BLASTN
Method
                   g343022
NCBI GI
BLAST score
                   663
                   0.0e + 00
E value
                   911
Match length
                   94
% identity
NCBI Description Pea chloroplast photosystem II gene encoding the D2 and
                   44kd chlorophyll a-binding proteins, complete cds
                   15689
Seq. No.
                   38386 1.R1040
Contig ID
                   LIB3072-003-Q1-K1-H11
5'-most EST
                   15690
Seq. No.
                   38417 1.R1040
Contig ID
5'-most EST
                   LIB3170-018-Q1-J1-B7
                   BLASTX
Method
                   q2464880
NCBI GI
                   342
BLAST score
                   5.0e-32
E value
                   138
Match length
                   51
% identity
NCBI Description (Z99707) putative protein [Arabidopsis thaliana]
                   15691
 Seq. No.
                   38418 1.R1040
 Contig ID
 5'-most EST
                   LIB3170-030-Q1-K1-B7
                   15692
 Seq. No.
                   38467 1.R1040
 Contig ID
                   jC-gmf102220142a02a1
 5'-most EST
                   BLASTX
Method
 NCBI GI
                   g2245125
 BLAST score
                   153
 E value
                   2.0e-22
 Match length
                   130
                   41
```

% identity

NCBI Description (Z97343) hypothetical protein [Arabidopsis thaliana]

15693 Seq. No.

38467 2.R1040 Contig ID

LIB3072-014-Q1-E1-H1 5'-most EST

15694 Seq. No.

38475\_1.R1040 Contig ID



```
q5606538
5'-most EST
Method
                   BLASTX
                   q2982243
NCBI GI
BLAST score
                   303
                   2.0e-27
E value
                   113
Match length
% identity
                  (AF051204) hypothetical protein [Picea mariana]
NCBI Description
                   15695
Seq. No.
                   38475 2.R1040
Contig ID
                   LIB3072-017-Q1-E1-D3
5'-most EST
                   BLASTX
Method
                   a2982243
NCBI GI
                   184
BLAST score
                   2.0e-13
E value
                   70
Match length
                   54
% identity
NCBI Description (AF051204) hypothetical protein [Picea mariana]
                   15696
Seq. No.
                   38511 1.R1040
Contig ID
5'-most EST
                   LIB3072-022-Q1-E1-G2
                   15697
Seq. No.
                   38516 1.R1040
Contig ID
                   LIB3072-023-Q1-E1-C9
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3044212
                   438
BLAST score
                   2.0e-43
E value
                   125
Match length
% identity
                   (AF057043) acyl-CoA oxidase [Arabidopsis thaliana]
NCBI Description
                    15698
Seq. No.
                    38546 1.R1040
 Contig ID
                    LIB3139-050-P1-N1-C2
 5'-most EST
                    BLASTX
Method
                    g4105794
 NCBI GI
                    204
 BLAST score
                    6.0e-16
 E value
                    69
 Match length
                    51
 % identity
 NCBI Description (AF049928) PGP224 [Petunia x hybrida]
 Seq. No.
                    15699
                    38550 1.R1040
 Contig ID
                    LIB3092-001-Q1-K1-G6
 5'-most EST
                    15700
 Seq. No.
                    38550 2.R1040
 Contig ID
                    6HC - 0\overline{2} - Q1 - E1 - F4
 5'-most EST
```

15701 Seq. No.

38572 1.R1040 Contig ID zhf700959357.h1 5'-most EST



Seq. No. 15702

Contig ID 38608 1.R1040

5'-most EST LIB3072-054-Q1-E1-E11

Seq. No. 15703

Contig ID 38617 1.R1040

5'-most EST LIB3072-056-Q1-K1-B12

Seq. No. 15704

Contig ID 38624\_1.R1040

5'-most EST LIB3072-057-Q1-K1-D2

Seq. No. 15705

Contig ID 38654\_1.R1040 5'-most EST fC-gmse700673271f2

Method BLASTN
NCBI GI g2735255
BLAST score 85

E value 1.0e-39
Match length 185

% identity 86

NCBI Description Lycopersicon esculentum protein kinase (LePK6) gene,

partial cds

Seq. No. 15706

Contig ID 38658 1.R1040

5'-most EST jC-gmle01810087g11a1

Seq. No. 15707

Contig ID 38690\_1.R1040

5'-most EST LIB3073-026-Q1-K1-D3

Method BLASTX
NCBI GI g1684851
BLAST score 176
E value 1.0e-12
Match length 68
% identity 56

NCBI Description (U77935) DnaJ-like protein [Phaseolus vulgaris]

Seq. No. 15708

Contig ID 38692\_1.R1040 5'-most EST uaw700661987.h1

Seq. No. 15709

Contig ID 38708\_1.R1040

5'-most EST LIB3073-026-Q1-K1-C7

Seq. No. 15710

Contig ID 38708 2.R1040

5'-most EST LIB3109-003-Q1-K1-B3

Seq. No. 15711

Contig ID 38713 1.R1040

5'-most EST LIB3109-042-Q1-K1-C1



Contig ID 38725 1.R1040

5'-most EST LIB3074-039-Q1-K1-E10

Seq. No. 15713

Contig ID 38725\_2.R1040 5'-most EST LIB3106-032-Q1-K1-E5

Seq. No. 15714

Contig ID 38725\_3.R1040 5'-most EST wrg700788527.h1

Seq. No. 15715

Contig ID 38725\_4.R1040 5'-most EST asn701138079.h1

Seq. No. 15716

Contig ID 38733\_1.R1040 5'-most EST seb700651947.h1 Method BLASTX

Method BLASTX
NCBI GI g4510424
BLAST score 752
E value 2.0e-84
Match length 340

% identity 52

NCBI Description (AC006929) putative carboxypeptidase [Arabidopsis thaliana]

Seq. No. 15717

Contig ID 38733\_2.R1040

5'-most EST uC-gmrominsoy025f08b1

Method BLASTX
NCBI GI g3876299
BLAST score 195
E value 7.0e-15
Match length 90

% identity 46

NCBI Description (Z71180) similar to BPTI/KUNITZ inhibitor domain; cDNA EST EMBL:D68293 comes from this gene; cDNA EST yk448h4.5 comes

from this gene; cDNA EST yk249e6.5 comes from this gene; cDNA EST yk448h4.3 comes from this gene [Caenorhabdi... >gi\_3880760\_emb\_CAA16311\_ (AL021474) similar to BPTI/KUNITZ inhibitor domain; cDNA EST EMBL:D68293 comes from this gene; cDNA EST yk448h4.5 comes from this gene; cDNA EST yk448h4.3 comes

from this gene [Caenorhab

Seq. No. 15718

Contig ID 38775\_1.R1040 5'-most EST pmv700894977.h1

Method BLASTX
NCBI GI g2827992
BLAST score 211
E value 1.0e-16
Match length 77
% identity 52

% identity 52
NCBI Description (AF034743) UDP-glucuronosyltransferase [Pisum sativum]



Contig ID 38781\_1.R1040 5'-most EST LIB3073-024-Q1-K1-H2

Seq. No. 15720

Contig ID 38786\_1.R1040

5'-most EST LIB3073-024-Q1-K1-E12

Method BLASTX
NCBI GI g2367429
BLAST score 179
E value 1.0e-12
Match length 114
% identity 43

NCBI Description (AF000402) Nlj21 [Lotus japonicus]

Seq. No. 15721

Contig ID 38788\_1.R1040

5'-most EST LIB3073-024-Q1-K1-E3

Method BLASTX
NCBI GI g125020
BLAST score 340
E value 1.0e-31
Match length 178
% identity 48

NCBI Description TRYPSIN INHIBITORS A AND C PRECURSOR (KUNITZ)

>gi 99955 pir JQ0968 trypsin inhibitor KTi3+ (Kunitz) - soybean >gi 256429 bbs 114634 (S45092) Kunitz trypsin inhibitor, KTi [soybeans, Dare and Forrest, Peptide, 216

aa] [Glycine max]

Seq. No. 15722

Contig ID 38863\_1.R1040

5'-most EST LIB3073-023-Q1-K1-F10

Seq. No. 15723

Contig ID 38895\_1.R1040

5'-most EST LIB3073-022-Q1-K1-C11

Seq. No. 15724

Contig ID 38927\_1.R1040

5'-most EST LIB3107-003-Q1-K1-F5

Seq. No. 15725

Contig ID 38934\_1.R1040 5'-most EST xpa700795977.h1

Seq. No. 15726

Contig ID 38934\_2.R1040

5'-most EST LIB3138-049-Q1-N1-C12

Seq. No. 15727

Contig ID 38934\_3.R1040

5'-most EST jC-gmle01810068d05a1

Seq. No. 15728

Contig ID 38934\_4.R1040

5'-most EST LIB3073-021-Q1-K1-D2



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15729
Seq. No.
                  38989 1.R1040
Contig ID
                  epx701107895.hl
5'-most EST
                  15730
Seq. No.
                  38993 1.R1040
Contig ID
                  LIB3074-011-Q1-E1-H12
5'-most EST
                  BLASTX
Method
                  g1362056
NCBI GI
                  228
BLAST score
                  1.0e-18
E value
                  92
Match length
                  54
% identity
                  trypsin inhibitor precursor (clone ATI21) - alfalfa
NCBI Description
                  >gi_509374_emb_CAA56254_ (X79880) serine proteinase
                   inhibitor [Medicago sativa]
                   15731
Seq. No.
                   39012 1.R1040
Contig ID
                   jsh701063892.h1
5'-most EST
Method
                   BLASTX
                   g2764992
NCBI GI
                   462
BLAST score
                   4.0e-46
E value
                   144
Match length
% identity
                   64
                  (Y08609) plasma membrane polypeptide [Nicotiana tabacum]
NCBI Description
                   15732
Seq. No.
                   39017 1.R1040
Contig ID
                   LIB3073-020-Q1-K1-A10
5'-most EST
                   BLASTX
Method
                   g99957
NCBI GI
                   330
BLAST score
                   1.0e-30
E value
                   131
Match length
% identity
                   trypsin inhibitor B (Kunitz) precursor - soybean
NCBI Description
                   >qi 18772 emb CAA45778 (X64448) trypsin inhibitor subtype
                   B [Glycine max]
                   15733
Seq. No.
                   39020 1.R1040
Contig ID
                   LIB3073-020-Q1-K1-A3
5'-most EST
                   BLASTX
Method
                   g140299
NCBI GI
                   1074
BLAST score
                   1.0e-117
E value
Match length
                   322
 % identity
```

NCBI Description

CYTOCHROME C BIOGENESIS PROTEIN CCSA >gi\_82213\_pir\_\_A05213 hypothetical protein 313 - common tobacco chloroplast

>gi\_1223666\_emb\_CAA77395\_ (Z00044) c-type cytochrome

synthesis protein [Nicotiana tabacum]

>gi\_225254\_prf\_\_1211235CN ORF 313 [Nicotiana tabacum]



Contig ID 39021\_1.R1040

5'-most EST LIB3074-031-Q1-K1-B3

Method BLASTX
NCBI GI g2144584
BLAST score 290
E value 6.0e-26
Match length 154
% identity 44

NCBI Description trypsin inhibitor A (Kunitz) precursor - soybean

>qi 18770 emb CAA45777 (X64447) trypsin inhibitor subtype

A [Glycine max]

Seq. No. 15735

Contig ID 39040\_1.R1040 5'-most EST fua701043368.h1

Method BLASTX
NCBI GI g4105798
BLAST score 460
E value 5.0e-46
Match length 124
% identity 60

NCBI Description (AF049930) PGP237-11 [Petunia x hybrida]

Seq. No. 15736

Contig ID 39045\_1.R1040

5'-most EST LIB3170-009-Q2-J1-A12

Method BLASTX
NCBI GI g2618702
BLAST score 277
E value 2.0e-24
Match length 87
% identity 64

NCBI Description (AC002510) unknown protein [Arabidopsis thaliana]

Seq. No.

Contig ID 39059 1.R1040

5'-most EST LIB3073-019-Q1-K1-C11

15737

Seq. No. 15738

Contig ID 39087\_1.R1040 5'-most EST zhf700956344.h1

Method BLASTX
NCBI GI g4522009
BLAST score 467
E value 8.0e-47
Match length 136
% identity 69

NCBI Description (AC007069) unknown protein [Arabidopsis thaliana]

Seq. No. 15739

Contig ID 39103 1.R1040

5'-most EST LIB3107-003-Q1-K1-B1

Seq. No. 15740

Contig ID 39141 1.R1040 5'-most EST pcp700995510.h1

Method BLASTX



q3080415 NCBI GI 1348 BLAST score 1.0e-149 E value 349 Match length 71 % identity

(AL022604) cysteine proteinase - like protein [Arabidopsis NCBI Description

thaliana]

15741 Seq. No.

39187 1.R1040 Contig ID

LIB3106-013-Q1-K1-H1 5'-most EST

15742 Seq. No.

39200 1.R1040 Contig ID

uC-gmflminsoy074d03b1 5'-most EST

15743 Seq. No.

39211 1.R1040 Contig ID

LIB3073-016-Q1-K1-D6 5'-most EST

BLASTX Method g2829751 NCBI GI 165 BLAST score 2.0e-11 E value 110 Match length 31 % identity

MACROPHAGE MIGRATION INHIBITORY FACTOR HOMOLOG (BMMIF) NCBI Description

>gi 1850559 (U88035) macrophage migration inhibitory factor [Brugia malayi] >gi\_2190976 (AF002699) macrophage migration

inhibitory factor [Brugia malayi]

15744 Seq. No.

39214 1.R1040 Contig ID zsg701127539.h1 5'-most EST

BLASTX Method g2501555 NCBI GI 900 BLAST score 4.0e-97 E value 211 Match length 77 % identity

POSSIBLE APOSPORY-ASSOCIATED PROTEIN C >gi 549984 (U13148) NCBI Description

possible apospory-associated protein [Pennisetum ciliare]

15745 Seq. No.

39225 1.R1040 Contig ID hrw701062078.h1 5'-most EST

15746 Seq. No.

39337 1.R1040 Contig ID

LIB3073-013-Q1-K1-F8 5'-most EST

Seq. No. 15747

39341 1.R1040 Contia ID

uC-gmrominsoy217e05b1 5'-most EST

15748 Seq. No.

39368 1.R1040 Contig ID pcp700994174.h1 5'-most EST



```
Method
                  BLASTX
NCBI GI
                  g4098517
BLAST score
                  620
E value
                  2.0e-64
Match length
                  194
% identity
                  62
                  (U79114) auxin-binding protein ABP19 [Prunus persica]
NCBI Description
                  15749
Seq. No.
                  39368 2.R1040
Contig ID
5'-most EST
                  LIB3167-077-P1-K2-C11
                  BLASTX
Method
NCBI GI
                  g4098517
BLAST score
                  246
                  9.0e-40
E value
Match length
                  139
% identity
                  57
NCBI Description (U79114) auxin-binding protein ABP19 [Prunus persica]
Seq. No.
                  15750
```

39382 1.R1040 Contig ID 5'-most EST g5606856

Seq. No. 15751

Contig ID 39383 1.R1040 5'-most EST zhf700960857.h1

Method BLASTN NCBI GI g21004 728 BLAST score 0.0e+00E value 1008 Match length % identity 93

NCBI Description French Bean mRNA for plastid-located glutamine synthetase (EC 6.3.1.2)

Seq. No. 15752

Contig ID 39383 2.R1040 5'-most EST asn701132950.hl

Method BLASTN NCBI GI g21004 BLAST score 51 E value 7.0e-20 Match length 130 85 % identity

NCBI Description French Bean mRNA for plastid-located glutamine synthetase (EC 6.3.1.2)

Seq. No. 15753

Contig ID 39385 1.R1040 5'-most EST pxt700941706.h1

Seq. No. 15754

39385 2.R1040 Contig ID

5'-most EST LIB3107-060-Q1-K1-B5

Seq. No. 15755

Contig ID 39390\_1.R1040

2620



5'-most EST LIB3073-012-Q1-K1-H5
Method BLASTX
NCBI GI g2462834
BLAST score 307
E value 5.0e-28
Match length 110

% identity 51
NCBI Description (AF000657) hypothetical protein [Arabidopsis thaliana]

Seq. No. 15756

Contig ID 39395\_1.R1040 5'-most EST taw700655563.h1

Method BLASTN
NCBI GI g2623245
BLAST score 124
E value 4.0e-63
Match length 310
% identity 89

NCBI Description Pisum sativum poly(A) polymerase mRNA, nuclear gene

encoding chloroplast protein, complete cds

Seq. No. 15757

Contig ID 39400\_1.R1040 5'-most EST leu701149631.h1

Method BLASTX
NCBI GI g20725
BLAST score 470
E value 6.0e-47
Match length 137
% identity 69

NCBI Description (X65154) GA [Pisum sativum]

Seq. No. 15758

Contig ID 39400\_2.R1040

5'-most EST LIB3093-053-Q1-K1-F8

Method BLASTX
NCBI GI g493636
BLAST score 313
E value 1.0e-28
Match length 91
% identity 52

NCBI Description (D29684) predicted polypeptide for cytokinin-repressed mRNA

[Cucumis sativus] >gi\_746031\_prf\_\_2016504A

cytokinin-repressed protein CR9 [Cucumis sativus]

Seq. No. 15759

Contig ID 39400\_3.R1040 5'-most EST bth700846523.h1

Method BLASTX
NCBI GI g20725
BLAST score 340
E value 7.0e-32
Match length 113
% identity 64

NCBI Description (X65154) GA [Pisum sativum]

Match length

% identity

109



```
39400 5.R1040
Contig ID
                  LIB3106-009-Q1-K1-H12
5'-most EST
                  BLASTX
Method
                  g20725
NCBI GI
BLAST score
                  243
E value
                  6.0e-27
Match length
                  103
% identity
NCBI Description (X65154) GA [Pisum sativum]
Seq. No.
                  15761
                  39405 1.R1040
Contig ID
5'-most EST
                  LIB3073-012-Q1-K1-D3
Seq. No.
                  15762
                  39424 1.R1040
Contig ID
5'-most EST
                  LIB3073-012-Q1-K1-B11
Seq. No.
                  15763
                  39426 1.R1040
Contig ID
5'-most EST
                  ssr700559275.h1
Method
                  BLASTX
NCBI GI
                  g3776572
BLAST score
                  624
E value
                  5.0e-65
Match length
                  136
% identity
NCBI Description
                  (AC005388) ESTs qb R65052, qb AA712146, qb H76533,
                  gb_H76282, gb_AA650771, gb_H76287, gb_AA650887, gb_N37383,
                  gb Z29721 and gb Z29722 come from this gene. [Arabidopsis
                  thaliana]
                  15764
Seq. No.
                  39444 1.R1040
Contig ID
5'-most EST
                  jC-qmst02400029c06d1
Method
                  BLASTX
NCBI GI
                  q82200
BLAST score
                  376
                  8.0e-36
E value
Match length
                  210
% identity
                  47
NCBI Description hypothetical protein 1244 - common tobacco chloroplast
Seq. No.
                  15765
                  39480 1.R1040
Contig ID
5'-most EST
                  LIB3073-011-Q1-K1-A8
Seq. No.
                  15766
                  39481 2.R1040
Contig ID
5'-most EST
                  LIB3170-038-Q1-K1-A4
Method
                  BLASTX
NCBI GI
                  g4249388
BLAST score
                  447
E value
                  2.0e-44
```

NCBI Description (AC005966) Similar to gb\_AF025438 Opa-interacting protein



(OIP2) from Homo sapiens. [Arabidopsis thaliana]

Seq. No. 15767

Contig ID 39481\_3.R1040 5'-most EST bth700848343.h1

Method BLASTX
NCBI GI 94249388
BLAST score 309
E value 2.0e-28
Match length 81
% identity 73

NCBI Description (AC005966) Similar to gb\_AF025438 Opa-interacting protein

(OIP2) from Homo sapiens. [Arabidopsis thaliana]

Seq. No. 15768

Contig ID 39487\_1.R1040 5'-most EST uC-gmropic026g05b1

Seq. No. 15769

Contig ID 39504 1.R1040

5'-most EST LIB3094-011-Q1-K1-C10

Method BLASTX
NCBI GI g4467123
BLAST score 428
E value 8.0e-42
Match length 178
% identity 57

NCBI Description (AL035538) hypothetical protein [Arabidopsis thaliana]

Seq. No. 15770

Contig ID 39504 2.R1040

5'-most EST LIB3094-004-Q1-K1-A9

Method BLASTX
NCBI GI g4467123
BLAST score 228
E value 4.0e-21
Match length 156
% identity 49

NCBI Description (AL035538) hypothetical protein [Arabidopsis thaliana]

Seq. No. 15771

Contig ID 39506\_1.R1040

5'-most EST LIB3107-018-Q1-K1-F9

Method BLASTX
NCBI GI g404690
BLAST score 477
E value 8.0e-48
Match length 197
% identity 50

NCBI Description (L19075) cytochrome P450 [Catharanthus roseus]

Seq. No. 15772

Contig ID 39513 1.R1040

5'-most EST LIB3073-010-Q1-K1-D3

Seq. No. 15773

Contig ID 39556\_1.R1040



```
5'-most EST
                  epx701107134.h1
                  15774
Seq. No.
Contig ID
                  39557 1.R1040
5'-most EST
                  LIB3073-009-Q1-K1-H7
Method
                  BLASTX
                  q1652105
NCBI GI
BLAST score
                  182
                  1.0e-13
E value
Match length
                  60
% identity
NCBI Description (D90902) hypothetical protein [Synechocystis sp.]
Seq. No.
                  15775
Contig ID
                  39575 1.R1040
5'-most EST
                  6HA-02-Q1-E1-H3
Method
                  BLASTX
NCBI GI
                  q1174498
BLAST score
                  158
                  1.0e-10
E value
Match length
                  59
% identity
                  51
NCBI Description
                  SYNAPTOBREVIN-RELATED PROTEIN >gi_600710 (M90418) formerly
                  called HAT24; synaptobrevin-related protein [Arabidopsis
                  thaliana]
                  15776
Seq. No.
Contig ID
                  39598 1.R1040
                  LIB3073-009-Q1-K1-C8
5'-most EST
                  15777
Seq. No.
                  39606_1.R1040
Contig ID
5'-most EST
                  LIB3073-009-Q1-K1-A3
Method
                  BLASTX
NCBI GI
                  a2281103
BLAST score
                  266
E value
                  6.0e-23
Match length
                  77
% identity
                  53
NCBI Description (AC002333) Glucan endo-1,3-beta glucosidase isolog
                  [Arabidopsis thaliana]
                  15778
Seq. No.
Contig ID
                  39638 1.R1040
5'-most EST
                  g4287246
Method
                  BLASTX
NCBI GI
                  g2642450
BLAST score
                  372
E value
                  2.0e-38
Match length
                  122
% identity
                  70
NCBI Description
                  (AC002391) putative metal ion transporter (Nramp)
                   [Arabidopsis thaliana] >qi 3169188 (AC004401) putative
                  metal ion transporter (Nramp) [Arabidopsis thaliana]
```

Seq. No. 15779

Contig ID 39647 1.R1040



```
LIB3073-008-Q1-K1-A7
5'-most EST
                  15780
Seq. No.
                  39661 1.R1040
Contig ID
                  LIB31\overline{3}8-129-Q1-N1-A10
5'-most EST
                  BLASTX
Method
                  g4062574
NCBI GI
                  200
BLAST score
                   5.0e-15
E value
                   157
Match length
                   36
% identity
                  (D90738) Hypothetical protein [Escherichia coli]
NCBI Description
                   15781
Seq. No.
                   39661 2.R1040
Contig ID
                   qbt700547986.hl
5'-most EST
                   15782
Seq. No.
                   39680 1.R1040
Contig ID
                   jC-gmst02400060d07a1
5'-most EST
                   BLASTX
Method
                   g4455365
NCBI GI
                   370
BLAST score
                   3.0e-35
E value
                   78
Match length
                   85
% identity
NCBI Description (AL035524) putative protein [Arabidopsis thaliana]
                   15783
Seq. No.
                   39714 1.R1040
Contig ID
                   LIB3073-006-Q1-K1-G4
5'-most EST
Seq. No.
                   15784
                   39716 1.R1040
Contig ID
                   taw700657964.h1
5'-most EST
                   BLASTX
Method
                   q3355476
NCBI GI
                   419
BLAST score
                   5.0e-41
E value
                   148
Match length
 % identity
                   (AC004218) unknown protein [Arabidopsis thaliana]
NCBI Description
                   15785
Seq. No.
                   39735 1.R1040
 Contig ID
                   LIB3073-006-Q1-K1-F3
 5'-most EST
                   BLASTX
Method
                   g2129752
 NCBI GI
                   437
 BLAST score
                   2.0e-43
 E value
                   128
 Match length
                   62
 % identity
 NCBI Description thioredoxin - Arabidopsis thaliana >gi_992964_emb_CAA84612_
                    (Z35475) thioredoxin [Arabidopsis thaliana]
```

15786

39752 1.R1040

Seq. No.

Contig ID



5'-most EST bnc700605501.h2

Seq. No. 15787

Contig ID 39769\_1.R1040

5'-most EST LIB31 $\overline{3}$ 8-013-Q1-N1-E4

Seq. No. 15788

Contig ID 39772\_1.R1040

5'-most EST LIB3073-005-Q1-K1-F8

Seq. No. 15789

Contig ID 39801\_1.R1040

5'-most EST LIB3073-005-Q1-K1-C5

Method BLASTX
NCBI GI g543565
BLAST score 206
E value 3.0e-16
Match length 69
% identity 52

NCBI Description hypothetical 10.0K protein - Zinnia elegans

>gi\_493721\_dbj\_BAA06462\_ (D30802) TED4 [Zinnia elegans]
>gi\_641903 (U19266) putative nonspecific lipid transfer;

auxin induced gene [Zinnia elegans]

Seq. No. 15790

Contig ID 39806\_1.R1040

5'-most EST LIB3073-005-Q1-K1-A10

Method BLASTX
NCBI GI g4262146
BLAST score 244
E value 2.0e-20
Match length 181
% identity 32

NCBI Description (AC005275) predicted protein of unknown function

[Arabidopsis thaliana]

Seq. No. 15791

Contig ID 39811\_1.R1040 5'-most EST taw700660505.h1

Seq. No. 15792

Contig ID 39822\_1.R1040

5'-most EST LIB3073-004-Q1-K1-E8

Seq. No. 15793

Contig ID 39823\_1.R1040

5'-most EST LIB3073-004-Q1-K1-G9

Seq. No. 15794

Contig ID 39931\_1.R1040 5'-most EST txt700733127.h1

Seq. No. 15795

Contig ID 39935\_1.R1040

5'-most EST LIB3073-002-Q1-K1-H10

Seq. No. 15796

2626



39951 1.R1040 Contig ID epx701108488.hl 5'-most EST BLASTX Method

q2191128 NCBI GI BLAST score 882 6.0e-95 E value 211 Match length 80 % identity

(AF007269) belongs to the L5P family of ribosomal proteins NCBI Description

[Arabidopsis thaliana]

15797 Seq. No.

39955 1.R1040 Contig ID

LIB3073-002-Q1-K1-C3 5'-most EST

Seq. No. 15798

39969 1.R1040 Contig ID wrq700788338.hl 5'-most EST

BLASTX Method g119931 NCBI GI BLAST score 494 1.0e-49 E value 146 Match length 67 % identity

FERREDOXIN I PRECURSOR >gi\_65740\_pir\_\_FEPM1 ferredoxin [2Fe-2S] I precursor - garden pea >gi\_169087 (M31713) NCBI Description

ferredoxin I precursor [Pisum sativum]

15799 Seq. No.

39981 1.R1040 Contig ID

LIB3073-001-Q1-K1-G11 5'-most EST

15800 Seq. No.

40003 1.R1040 Contig ID

LIB3092-016-Q1-K1-D8 5'-most EST

BLASTX Method g2129454 NCBI GI 179 BLAST score 6.0e-13 E value 61 Match length 16 % identity

chlorophyll a/b-binding protein (clone GC18 and others) -NCBI Description

Euglena gracilis (var. bacillaris) (fragment)

>gi\_510388\_emb\_CAA43633\_ (X61361) light harvesting

chlorophyll a /b binding protein of PSII [Euglena gracilis]

15801 Seq. No.

40048 1.R1040 Contig ID 5'-most EST g5126684

Seq. No. 15802

40085 1.R1040 Contig ID rlr700898782.hl 5'-most EST

15803 Seq. No.

40099 1.R1040 Contig ID

LIB3073-007-Q1-K1-E7 5'-most EST



```
BLASTX
Method
NCBI GI
                  q4262140
                  289
BLAST score
                  5.0e-26
E value
                  72
Match length
                  74
% identity
NCBI Description (AC005275) putative C-type U1 snRNP [Arabidopsis thaliana]
                  15804
Seq. No.
                  40099 2.R1040
Contig ID
5'-most EST
                  leu70\overline{1}149779.h1
                  BLASTX
Method
NCBI GI
                  g4262140
BLAST score
                  249
                  1.0e-21
E value
                  44
Match length
                  98
% identity
                 (AC005275) putative C-type U1 snRNP [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  15805
                  40108 1.R1040
Contig ID
5'-most EST
                  LIB3073-008-Q1-K1-D1
                  BLASTX
Method
                  g3128175
NCBI GI
BLAST score
                  174
                  3.0e-12
E value
                  141
Match length
                  33
% identity
NCBI Description (AC004521) unknown protein [Arabidopsis thaliana]
                  15806
Seq. No.
                   40152 1.R1040
Contig ID
5'-most EST
                  LIB3106-092-Q1-K1-C7
                  BLASTX
Method
                   q3212862
NCBI GI
BLAST score
                   296
E value
                   1.0e-26
                   81
Match length
                   70
% identity
                  (AC004005) putative riboflavin synthase [Arabidopsis
NCBI Description
                   thalianal
                   15807
Seq. No.
Contig ID
                   40172 1.R1040
5'-most EST
                   wvk700685988.h1
Method
                   BLASTX
NCBI GI
                   g1169186
BLAST score
                   468
E value
                   1.0e-46
Match length
                   180
% identity
                   51
                  THIOL PROTEASE SEN102 PRECURSOR >gi 1085732 pir S36421
NCBI Description
                   cysteine proteinase - Hemerocallis sp
                   >gi 1364024 pir S57777 cysteine protease precursor -
                   Hemerocallis x hybrida >gi 396568_emb_CAA52425_ (X74406)
```

thiol-protease [Hemerocallis sp.]



```
Seq. No.
                   15808
Contig ID
                   40230 1.R1040
5'-most EST
                   LIB3074-041-Q1-K1-H6
                   15809
Seq. No.
Contig ID
                   40244 1.R1040
5'-most EST
                   LIB3139-114-P1-N1-C9
Method
                   BLASTX
NCBI GI
                   g2832618
BLAST score
                   428
                   5.0e-42
E value
Match length
                   208
% identity
                   37
NCBI Description
                  (AL021711) putative protein [Arabidopsis thaliana]
                   15810
Seq. No.
                   40291 1.R1040
Contig ID
5'-most EST
                   LIB3074-041-Q1-K1-A1
Seq. No.
                   15811
Contig ID
                   40326 1.R1040
                   seb70\overline{0}653650.h1
5'-most EST
Method
                   BLASTX
                   g1170897
NCBI GI
BLAST score
                   1550
E value
                   1.0e-173
Match length
                   355
% identity
                   86
NCBI Description
                  MALATE DEHYDROGENASE, GLYOXYSOMAL PRECURSOR
                   >gi_1076276_pir__S52039 NAD-malate dehydrogenase - cucumber
                   >gi 695311 (L31900) glyoxysomal malate dehydrogenase
                   [Cucumis sativus]
Seq. No.
                   15812
Contig ID
                   40326 3.R1040
5'-most EST
                   q5676893
Seq. No.
                   15813
Contig ID
                   40336 1.R1040
5'-most EST
                   LIB3074-039-Q1-K1-B2
Seq. No.
                   15814
                   40474 1.R1040
Contig ID
                   LIB3074-036-Q1-K1-C1
5'-most EST
Seq. No.
                   15815
                   40511_1.R1040
Contig ID
                   pcp70\overline{0}995144.h1
Method
                   BLASTX
```

5'-most EST

NCBI GI q2673913 BLAST score 502 7.0e-51 E value Match length 145 % identity 64

(AC002561) hypothetical protein [Arabidopsis thaliana] NCBI Description



```
40511 2.R1040
Contig ID
5'-most EST
                    epx701105504.hl
                    BLASTX
Method
                    q2673913
NCBI GI
                    346
BLAST score
                    1.0e-32
E value
Match length
                    94
                    70
% identity
NCBI Description (AC002561) hypothetical protein [Arabidopsis thaliana]
                    15817
Seq. No.
                    40542 1.R1040
Contig ID
5'-most EST
                    LIB3074-033-Q1-K1-D12
                    15818
Seq. No.
Contig ID
                    40565 1.R1040
                    jsh70\overline{1}069867.h1
5'-most EST
Method
                    BLASTX
                    g2494034
NCBI GI
                    964
BLAST score
                    1.0e-104
E value
Match length
                    215
% identity
                    84
                    DIACYLGLYCEROL KINASE 1 (DIGLYCERIDE KINASE) (DGK 1) (DAG
NCBI Description
                    KINASE 1) >gi_2129573_pir__S71467 diacylglycerol kinase - Arabidopsis thaliana >gi_1374772_dbj_BAA09856_ (D63787)
                    diacylglycerol kinase [Arabidopsis thaliana]
Seq. No.
                    15819
                    40726 1.R1040
Contig ID
                    leu70\overline{1}149578.h1
5'-most EST
                    15820
Seq. No.
                    40726 2.R1040
Contig ID
5'-most EST
                    LIB3106-098-Q1-K1-C8
Method
                    BLASTN
                    g3821780
NCBI GI
                    36
BLAST score
                    9.0e-11
E value
                    49
Match length
% identity
                    51
NCBI Description Xenopus laevis cDNA clone 27A6-1
                    15821
Seq. No.
                    40726 3.R1040
Contig ID
                    k1170\overline{1}204832.h1
5'-most EST
                    15822
Seq. No.
                    40751 2.R1040
Contig ID
                    uC-gmflminsoy035g04b1
5'-most EST
                    BLASTX
Method
                    g2811014
NCBI GI
```

Method BLASTX
NCBI GI g2811014
BLAST score 173
E value 4.0e-12
Match length 78
% identity 44

NCBI Description DYNEIN LIGHT CHAIN LC6, FLAGELLAR OUTER ARM



>gi\_2208914\_dbj\_BAA20525\_ (AB004830) outer arm dynein LC6
[Anthocidaris crassispina]

15823 Seq. No. 40751 3.R1040 Contig ID 5'-most EST g4300275 BLASTX Method g2494221 NCBI GI 150 BLAST score 2.0e-09 E value 77 Match length 40 % identity

NCBI Description

DYNEIN LIGHT CHAIN 1, CYTOPLASMIC (PROTEIN INHIBITOR OF NEURONAL NITRIC OXIDE SYNTHASE) (PIN) >gi\_4558123\_pdb\_1BKQ\_Solution Nmr Structure Of Pin: A Protein Inhibitor Of Neuronal Nitric Oxide Synthase, 20 Structures >gi\_1209061 (U32944) cytoplasmic dynein light chain 1 [Homo sapiens] >gi\_1654355 (U66461) protein inhibitor of neuronal nitric oxide synthase [Rattus norvegicus] >gi\_2654600 (AF008304) protein inhibitor of neuronal nitric oxide synthase [Oryctolagus cuniculus] >gi\_2655057 (AF020710) protein inhibitor of neuronal nitric oxide synthase [Oryctolagus cuniculus] >gi\_4103059 (AF020185) protein inhibitor of nitric oxide synthase [Mus musculus] >gi\_4505813\_ref\_NP\_003737.1\_pPIN\_ dynein, cytoplasmic, light polypeptide

Seq. No. 15824

Contig ID 40760 1.R1040

5'-most EST LIB3074-029-Q1-K1-F8

Seq. No. 15825

Contig ID 40770 1.R1040

5'-most EST LIB3074-029-Q1-K1-C6

Method BLASTX
NCBI GI g3228666
BLAST score 218
E value 1.0e-17
Match length 112
% identity 38

NCBI Description (AF069987) nitrilase 1 [Homo sapiens] >gi\_3242978

(AF069984) nitrilase homolog 1 [Homo sapiens]

Seq. No. 15826

Contig ID 40785\_1.R1040

5'-most EST LIB3074-029-Q1-K1-A8

Seq. No. 15827

Contig ID 40787\_1.R1040 5'-most EST zhf700962929.h1

Method BLASTX
NCBI GI g114009
BLAST score 145
E value 1.0e-08
Match length 54
% identity 52

NCBI Description APAG PROTEIN >gi 72927\_pir\_\_BVECAG apaG protein -



Escherichia coli >gi\_40918\_emb\_CAA28418\_ (X04711) URF (apaG) (AA 1-375) [Escherichia coli] >gi\_216475\_dbj\_BAA01326\_ (D10483) apaG protein [Escherichia  $col\overline{i}] > gi_{1786235}$  (AE000115) orf, hypothetical protein [Escherichia coli]

15828 Seq. No.

40787 2.R1040 Contig ID wvk700682208.hl 5'-most EST

15829 Seq. No.

40794 1.R1040 Contig ID

LIB3170-077-Q1-K1-A6 5'-most EST

BLASTX Method g3287270 NCBI GI 539 BLAST score 5.0e-55 E value 205 Match length 54 % identity

(Y09533) involved in starch metabalism [Solanum tuberosum] NCBI Description

15830 Seq. No.

40812\_1.R1040 Contig ID

jC-gmro02800031g08a1 5'-most EST

BLASTX Method q3135277 NCBI GI 240 BLAST score 6.0e-20 E value 113 Match length % identity

(AC003058) hypothetical protein [Arabidopsis thaliana] NCBI Description

>gi 4191776 (AC005917) hypothetical protein [Arabidopsis

thaliana]

15831 Seq. No.

40812 2.R1040 Contig ID

LIB3074-028-Q1-K1-E3 5'-most EST

BLASTX Method q3135277 NCBI GI BLAST score 210 1.0e-16 E value 120 Match length 42 % identity

(AC003058) hypothetical protein [Arabidopsis thaliana] NCBI Description

>gi\_4191776 (AC005917) hypothetical protein [Arabidopsis

thaliana]

15832 Seq. No.

40813 1.R1040 Contig ID rlr700896847.h1 5'-most EST

15833 Seq. No.

40859 1.R1040 Contig ID

LIB3074-026-Q1-E1-F8 5'-most EST

15834 Seq. No.

40892 1.R1040 Contig ID



```
q5688095
5'-most EST
                  BLASTX
Method
                  q2808420
NCBI GI
                  179
BLAST score
                  4.0e-13
E value
Match length
                  100
% identity
                  37
NCBI Description (Z97632) HIV-1 transcriptional elongation factor TAT
                  cofactor TAT-SF1 [Homo sapiens]
                  15835
Seq. No.
                   40906 1.R1040
Contig ID
                  LIB3074-025-Q1-E1-F11
5'-most EST
                  15836
Seq. No.
                   40934 1.R1040
Contig ID
5'-most EST
                  LIB3170-015-Q1-K1-A2
                  BLASTN
Method
NCBI GI
                   q343344
                   606
BLAST score
                   0.0e + 00
E value
                   665
Match length
                   98
% identity
                   Soybean chloroplast 16S rRNA (3' end), 18S rRNA (5' end),
NCBI Description
                   Ile-tRNA, and Ala-tRNA genes
                   15837
Seq. No.
                   40935 1.R1040
Contig ID
                   pmv700893664.h1
5'-most EST
                   BLASTX
Method
                   q1351359
NCBI GI
                   289
BLAST score
E value
                   1.0e-25
                   69
Match length
                   75
% identity
                   UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 7.8 KD PROTEIN
NCBI Description
                   (MITOCHONDRIAL HINGE PROTEIN) (CR7) >gi_1071788_pir__S48690
                   ubiquinol--cytochrome-c reductase (EC 1.10.2.2) 11K protein
                   - potato >gi_488712_emb_CAA55860_ (X79273)
                   ubiquinol--cytochrome c reductase [Solanum tuberosum]
Seq. No.
                   15838
                   40958 1.R1040
Contig ID
                   LIB3106-062-Q1-K1-D5
 5'-most EST
                   BLASTN
Method
                   g505584
NCBI GI
                   325
BLAST score
                   0.0e+00
E value
                   613
Match length
                   88
 % identity
 NCBI Description G.max mRNA for Glyoxalase I
                   15839
 Seq. No.
                   40967 1.R1040
 Contig ID
                   kmv700743448.h1
 5'-most EST
```

BLASTX

g2511693

Method NCBI GI



```
BLAST score
                  573
                  4.0e-59
E value
                  159
Match length
                  71
% identity
NCBI Description (Z99954) cysteine proteinase precursor [Phaseolus vulgaris]
                  15840
Seq. No.
Contig ID
                  40973 1.R1040
5'-most EST
                  smc700745029.h1
                  BLASTX
Method
NCBI GI
                  g461812
BLAST score
                  1364
E value
                  1.0e-151
Match length
                  497
% identity
                  50
NCBI Description CYTOCHROME P450 72 (CYPLXXII) (PROBABLE
                  GERANIOL-10-HYDROXYLASE) (GE10H) >gi 167484 (L10081)
                  Cytochrome P-450 protein [Catharanthus roseus]
                  >gi 445604 prf 1909351A cytochrome P450 [Catharanthus
                  roseus]
Seq. No.
                  15841
                  40973 2.R1040
Contig ID
5'-most EST
                  zzp700831951.h1
Method
                  BLASTX
                  g404688
NCBI GI
BLAST score
                  2 5
                  : Je-18
E value
                  82
Match length
                  54
% identity
NCBI Description (L19074) cytochrome P450 [Catharanthus roseus]
Seq. No.
                  15842
                  40998 1.R1040
Contig ID
5'-most EST
                  leu701153111.h1
                  15843
Seq. No.
Contig ID
                  40998 2.R1040
5'-most EST
                  LIB3074-023-Q1-E1-G10
                  15844
Seq. No.
Contig ID
                  41112 1.R1040
5'-most EST
                  bth700847980.h1
Method
                  BLASTX
                  g4455236
NCBI GI
BLAST score
                  480
E value
                  5.0e-48
                  143
Match length
% identity
                  66
NCBI Description (AL035523) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  15845
```

Contig ID 41123\_1.R1040

5'-most EST LIB3074-018-Q1-E1-E9

Method BLASTX
NCBI GI g3335366
BLAST score 395



E value 2.0e-38
Match length 105
% identity 70

NCBI Description (AC003028) unknown protein [Arabidopsis thaliana]

Seq. No. 15846

Contig ID 41124 1.R1040 5'-most EST fC-gmle700870920f3

Method BLASTX
NCBI GI g1653089
BLAST score 234
E value 2.0e-19
Match length 72
% identity 57

NCBI Description (D90911) hypothetical protein [Synechocystis sp.]

Seq. No. 15847

Contig ID 41142\_1.R1040

5'-most EST LIB3074-018-Q1-E1-D10

Method BLASTX
NCBI GI g3399767
BLAST score 255
E value 1.0e-21
Match length 119
% identity 39

NCBI Description (U76298) uclacyanin I [Arabidopsis thaliana] >gi\_3831466

C005700) uclacyanin I [Arabidopsis thaliana]

Seq. No. 15848

Contig ID 41198\_1.R1040

5'-most EST LIB3093-004-Q1-K1-E3

Method BLASTX
NCBI GI g4415930
BLAST score 167
E value 1.0e-11
Match length 58
% identity 53

NCBI Description (AC006418) unknown protein [Arabidopsis thaliana]

>gi\_4559389\_gb\_AAD23049.1\_AC006526\_14 (AC006526) unknown

protein [Arabidopsis thaliana]

Seq. No. 15849

Contig ID 41244\_1.R1040

5'-most EST LIB3074-012-Q1-E1-B11

Seq. No. 15850

Contig ID 41278\_1.R1040 5'-most EST wrg700790644.h2

Method BLASTX
NCBI GI g2344892
BLAST score 285
E value 2.0e-25
Match length 118
% identity 53

NCBI Description (AC002388) unknown protein [Arabidopsis thaliana]



Contig ID 41278\_2.R1040 5'-most EST wvk700681031.h1

Method BLASTX
NCBI GI g2344892
BLAST score 250
E value 1.0e-21
Match length 58
% identity 83

NCBI Description (AC002388) unknown protein [Arabidopsis thaliana]

Seq. No. 15852

Contig ID 41278\_3.R1040 5'-most EST pcp700991320.h1

Method BLASTX
NCBI GI g2344892
BLAST score 290
E value 7.0e-26
Match length 154
% identity 53

NCBI Description (AC002388) unknown protein [Arabidopsis thaliana]

Seq. No. 15853

Contig ID 41301 1.R1040

5'-most EST LIB3109-038-Q1-K1-C4

Seq. No. 15854

1.R1040 Contig ID . 677525 5'-most EST Method BLASTX NCB1 GI g4218115 BLAST score 353 3.0e-33 E value Match length 116 62 % identity

NCBI Description (AL035353) putative protein [Arabidopsis thaliana]

Seq. No. 15855

Contig ID 41334 1.R1040 5'-most EST seb700650771.h1

Seq. No. 15856

Contig ID 41359\_1.R1040

5'-most EST LIB3074-009-Q1-E1-A3

Method BLASTN
NCBI GI g20880
BLAST score 180
E value 2.0e-96
Match length 372
% identity 87

NCBI Description Pea mRNA for plastid ribosomal protein CL9

Seq. No. 15857

Contig ID 41461 1.R1040

5'-most EST LIB3074-004-Q1-K1-D11

Seq. No. 15858

Contig ID 41461\_2.R1040

E value

Match length

% identity



```
5'-most EST
                  g4313788
                  15859
Seq. No.
Contig ID
                  41517 1.R1040
5'-most EST
                  xzy700966814.h1
Method
                  BLASTX
NCBI GI
                  q3738285
BLAST score
                  542
E value
                  3.0e-55
Match length
                  162
% identity
NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]
                  15860
Seq. No.
Contig ID
                  41519 1.R1040
5'-most EST
                  LIB3074-019-Q1-E1-H10
Method
                  BLASTX
NCBI GI
                  g461453
BLAST score
                  162
                  1.0e-11
E value
Match length
                  57
% identity
                  63
NCBI Description AUXIN-BINDING PROTEIN 1 PRECURSOR (ABP)
                  >gi_322467_pir__S31584 auxin-binding protein precursor -
                  Arabidopsis thaliana >gi_16201_emb_CAA49526_ (X69901)
                  auxin-binding protein [Arabidopsis thaliana]
                    i_251899_bbs_109280 (S40550) At-ERabp1=endoplasmic
                   eticulum auxin binding protein 1 [Arabidopsis thaliana,
                   Peptide, 198 aa] [Arabidopsis thaliana] >gi 3924607
                   (AF069442) auxin-binding protein 1 precursor [Arabidopsis
                  thaliana]
Seq. No.
                  15861
                  41653 2.R1040
Contig ID
5'-most EST
                  ujr70\overline{0}646671.h1
                  BLASTX
Method
                  g4056478
NCBI GI
BLAST score
                  230
E value
                  7.0e-19
Match length
                  62
% identity
NCBI Description
                  (AC005896) unknown protein [Arabidopsis thaliana]
Seq. No.
                  15862
Contig ID
                  41660 1.R1040
5'-most EST
                  LIB3087-012-Q1-K1-G9
Seq. No.
                  15863
                  41664 2.R1040
Contig ID
5'-most EST
                  jex70\overline{0}906561.h1
Method
                  BLASTX
                  g3183377
NCBI GI
BLAST score
                  141
```

2637

NCBI Description HYPOTHETICAL 79.3 KD PROTEIN C24C9.05C IN CHROMOSOME I

1.0e-08

88 20



>gi\_2330788\_emb\_CAB11262\_ (Z98601) hypothetical protein.
[Schizosaccharomyces pombe]

15864 Seq. No. 41669 1.R1040 Contig ID LIB3087-012-Q1-K1-H1 5'-most EST 15865 Seq. No. 41673 1.R1040 Contig ID LIB3087-012-Q1-K1-H3 5'-most EST 15866 Seq. No. 41682 1.R1040 Contig ID gsv701044957.hl 5'-most EST

Seq. No. 15867

Contig ID 41683\_1.R1040

5'-most EST LIB3087-012-Q1-K1-E8

Seq. No. 15868

Contig ID 41687\_1.R1040

5'-most EST LIB3087-012-Q1-K1-F3

Seq. No. 15869

Contig ID 41690 1.R1040 5'-most EST asn701143247.h1

Method B. ASTX
NCBI GI g2 739046
BLAST score 601
E value 3.0e-62
Match length 166
% identity 66

NCBI Description (AF024652) polyphosphoinositide binding protein Ssh2p

[Glycine max]

Seq. No. 15870

Contig ID 41690\_2.R1040

5'-most EST LIB3087-012-Q1-K1-F6

Method BLASTN
NCBI GI g2739045
BLAST score 56
E value 1.0e-22
Match length 152
% identity 84

NCBI Description Glycine max polyphosphoinositide binding protein Ssh2p

(SSH2) mRNA, complete cds

Seq. No. 15871

Contig ID 41697\_1.R1040

5'-most EST LIB3106-032-Q1-K1-H3

Method BLASTN
NCBI GI g2264312
BLAST score 42
E value 3.0e-14
Match length 46
% identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:



## MOK16, complete sequence [Arabidopsis thaliana]

15872 Seq. No. Contig ID 41697 2.R1040 5'-most EST ssr700554496.h1 Method BLASTN NCBI GI g2264312 BLAST score 38 4.0e-12 E value Match length 46 % identity 96 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MOK16, complete sequence [Arabidopsis thaliana] Seq. No. 15873 Contig ID 41704 1.R1040 5'-most EST zsq701119162.h1 Method BLASTX NCBI GI g4544409 BLAST score 523 5.0e-53 E value Match length 161 % identity 65 NCBI Description (AC006955) putative transcription factor [Arabidopsis thaliana] 1-874 Seq. No. Contig ID - 711 1.R1040 pmv700895290.h1 5'-most EST Method BLASTX NCBI GI g3688173 BLAST score 784 E value 1.0e-83 219 Match length % identity 65 (AL031804) putative protein [Arabidopsis thaliana] NCBI Description 15875 Seq. No. 41712 1.R1040 Contig ID 5'-most EST LIB3087-012-Q1-K1-B3 Seq. No. 15876 Contig ID 41713 1.R1040 5'-most EST leu701146552.h1 Seq. No. 15877 41715 1.R1040 Contig ID 5'-most EST LIB3087-012-Q1-K1-B6 Method BLASTX NCBI GI g4467125

NCBI GI g4467125
BLAST score 448
E value 2.0e-44
Match length 114
% identity 75

NCBI Description (AL035538) putative protein [Arabidopsis thaliana]



```
41724 1.R1040
Contig ID
                  LIB3087-011-Q1-K1-H11
5'-most EST
Method
                  BLASTX
NCBI GI
                  g4038057
BLAST score
                  145
                  5.0e-09
E value
                  79
Match length
                  41
% identity
                  (AC005897) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  15879
Seq. No.
                  41727 1.R1040
Contig ID
5'-most EST
                  fC-gmle700743051a1
Method
                  BLASTX
NCBI GI
                  q1911166
BLAST score
                  1537
E value
                  1.0e-171
Match length
                  320
% identity
                  88
                  (X94400) soluble-starch-synthase [Solanum tuberosum]
NCBI Description
                  15880
Seq. No.
Contig ID
                  41731_1.R1040
5'-most EST
                  fC-gmst700653807f1
                  BLASTX
Method
NCBI GI
                  q541824
                  2134
BLAST score
                  0 Je+00
E value
                  476
Match length
                  83
% identity
                  protein kinase - spinach >gi 457709 emb CAA82991 (Z30330)
NCBI Description
                  protein kinase [Spinacia oleracea]
                  15881
Seq. No.
Contig ID
                  41734 1.R1040
5'-most EST
                  LIB3087-012-Q1-K1-A7
Seq. No.
                  15882
Contig ID
                  41737 1.R1040
5'-most EST
                  asn701139503.h1
Method
                  BLASTX
NCBI GI
                  q3600036
BLAST score
                  670
                  3.0e-70
E value
Match length
                  257
% identity
                  60
                  (AF080119) contains similarity to protein kinase domains
NCBI Description
                  (Pfam: pkinase.hmm, score: 227.04) [Arabidopsis thaliana]
Seq. No.
                  15883
                  41739 1.R1040
Contig ID
5'-most EST
                  LIB3087-012-Q1-K1-F11
Method
                  BLASTN
```

NCBI GI g170643
BLAST score 94
E value 3.0e-45
Match length 282



% identity 86

NCBI Description Vigna aconitifolia

5'-phosphoribosyl-4-(N-succinocarboxamide)-5-

aminoimidazole synthetase mRNA

Seq. No. 15884

Contig ID 41741 1.R1040

5'-most EST LIB3087-011-Q1-K1-F7

Method BLASTX
NCBI GI g629654
BLAST score 246
E value 8.0e-21
Match length 118
% identity 51

NCBI Description 5'-phosphoribosyl-4-(N-succinocarboxamide)-5-ami

noimidazole synthetase - moth bean

Seq. No. 15885

Contig ID 41744 1.R1040

5'-most EST LIB3087-011-Q1-K1-G10

Seq. No. 15886

Contig ID 41755\_1.R1040 5'-most EST asn701132483.h1

Seq. No. 15887

Contig ID (766 1.R1040

5'-most EST \(\(\)\\_\B30\\\87-011-\Q1-\K1-\A7\\)

Method BLASTX
NCBI GI g3080397
BLAST score 659
E value 5.0e-69
Match length 193

% identity 67

NCBI Description (AL022603) hypothetical protein [Arabidopsis thaliana]

Seq. No. 15888

Contig ID 41770\_1.R1040 5'-most EST uC-gmropic108g10b1

Method BLASTX
NCBI GI g2827554
BLAST score 330
E value 9.0e-47
Match length 230
% identity 51

NCBI Description (AL021635) putative DNA binding protein [Arabidopsis

thaliana]

Seq. No. 15889

Contig ID 41772\_1.R1040

5'-most EST LIB3109-046-Q1-K1-H3

Seq. No. 15890

Contig ID 41774 1.R1040

5'-most EST LIB3087-010-01-K1-F7



Contig ID	41774 2.R1040
5'-most EST	$gsv70\overline{1}051312.h1$

Seq. No. 15892

Contig ID 41777 1.R1040

5'-most EST LIB3107-061-Q1-K1-A10

Seq. No. 15893

Contig ID 41778\_1.R1040

5'-most EST uC-gmrominsoy112b03b1

Seq. No. 15894

Contig ID 41778\_2.R1040

5'-most EST LIB3087-010-Q1-K1-G12

Seq. No. 15895

Contig ID 41778\_3.R1040

5'-most EST jC-gmst02400046c01a1

Seq. No. 15896

Contig ID 41779\_1.R1040

5'-most EST LIB3087-010-Q1-K1-G3

Seq. No. 15897

Contig ID 41807\_1.R1040

5'-most EST LIB3087-010-Q1-K1-A11

Seq. No. 1,398

Contig ID 41808\_1.R1040

5'-most EST LIB3087-010-Q1-K1-A12

Method BLASTX
NCBI GI g4558556
BLAST score 553
E value 1.0e-56
Match length 211

% identity 52

NCBI Description (AC007138) predicted protein of unknown function

[Arabidopsis thaliana]

Seq. No. 15899

Contig ID 41809\_1.R1040 5'-most EST uaw700662444.h1

Seq. No. 15900

Contig ID 41812\_1.R1040 5'-most EST rca700996964.h1

Seq. No. 15901

Contig ID 41814\_1.R1040 5'-most EST wvk700681344.h2

Seq. No. 15902

Contig ID 41815\_1.R1040

5'-most EST LIB3087-009-Q1-K1-H5

Method BLASTN NCBI GI g1335861 BLAST score 225



E value 1.0e-123 Match length 353 % identity 91

NCBI Description Glycine max clathrin heavy chain mRNA, complete cds

Seq. No. 15903

Contig ID 41825 1.R1040

5'-most EST LIB3087-009-Q1-K1-H2

Method BLASTX
NCBI GI g832876
BLAST score 584
E value 4.0e-60
Match length 197
% identity 55

NCBI Description (L41345) ascorbate free radical reductase [Solanum

lycopersicum] >gi\_1097368\_prf\_\_2113407A ascorbate free

radical reductase [Lycopersicon esculentum]

Seq. No. 15904

Contig ID 41834\_1.R1040 5'-most EST kll701211187.h1

Method BLASTX
NCBI GI g4008446
BLAST score 239
E value 6.0e-20
Match length 113
% identity 4?

NCBI Description (ALO34488) predicted using Genefinder; cDNA EST EMBL:C08771

comes from this gene; cDNA EST EMBL: C07412 comes from this

gene [Caenorhabditis elegans]

Seq. No. 15905

Contig ID 41848\_1.R1040

5'-most EST LIB3087-009-Q1-K1-C10

Seq. No. 15906

Contig ID 41849 1.R1040

5'-most EST LIB3087-009-Q1-K1-A8

Seq. No. 15907

Contig ID 41864 1.R1040 5'-most EST trc700567308.h1

Method BLASTX
NCBI GI g120669
BLAST score 370
E value 1.0e-35
Match length 81
% identity 84

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC

>gi\_66014\_pir\_\_DEJMG glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora
>gi\_19566\_emb\_CAA42905\_(X60347) glyceraldehyde
3-phosphate\_dehydrogenase [Magnolia liliiflora]

Seq. No. 15908

Contig ID 41876\_1.R1040

5'-most EST LIB3087-008-Q1-K1-D11



Method BLASTX
NCBI GI g2911040
BLAST score 322
E value 6.0e-30
Match length 125
% identity 25

NCBI Description (AL021961) receptor protein kinase - like protein

[Arabidopsis thaliana]

Seq. No. 15909

Contig ID 41887\_1.R1040 5'-most EST uC-gmropic056h08b1

Method BLASTX
NCBI GI g3914600
BLAST score 178
E value 6.0e-13
Match length 55
% identity 55

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi\_3168587\_dbj\_BAA28610.1\_

(AB004883) ribulose 1,5-bisphosphate carboxylase/oxygenase

small subunit [Marchantia paleacea]

Seq. No. 15910

Contig ID 41887 2.R1040

5'-most EST LIB3087-008-Q1-K1-C5

Method BIASTX
NCBI GI GD914600
BLAST score 194
E value 7.0e-15
Match length 56
% identity 57

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi\_3168587\_dbj\_BAA28610.1

(AB004883) ribulose 1,5-bisphosphate carboxylase/oxygenase

small subunit [Marchantia paleacea]

Seq. No. 15911

Contig ID 41893 1.R1040

5'-most EST LIB3106-066-P1-K1-C7

Method BLASTX
NCBI GI g3894173
BLAST score 526
E value 3.0e-53
Match length 129
% identity 74

NCBI Description (AC005312) hypothetical protein [Arabidopsis thaliana]

Seq. No. 15912

Contig ID 41893\_3.R1040 5'-most EST leu701153729.h1

Seq. No. 15913

Contig ID 41895\_1.R1040 5'-most EST sat701009362.h1

Method BLASTX NCBI GI q3128168



BLAST score 1301 E value 1.0e-144 Match length 344 % identity 67

NCBI Description (AC004521) putative carboxyl-terminal peptidase

[Arabidopsis thaliana]

Seq. No. 15914

Contig ID 41895\_2.R1040

5'-most EST LIB3087-008-Q1-K1-B3

Seq. No. 15915

Contig ID 41895\_3.R1040 5'-most EST pxt700943033.h1

Seq. No. 15916

Contig ID 41897\_1.R1040

5'-most EST LIB3167-029-P1-K1-E8

Method BLASTX
NCBI GI g2129630
BLAST score 494
E value 7.0e-50
Match length 117
% identity 71

NCBI Description lamin - Arabidopsis thaliana >gi\_1262754\_emb\_CAA65750\_

(X97023) lamin [Arabidopsis thaliana] >gi 3395760 (U77721)

urknown [Arabidopsis thaliana]

Seq. No. 15917

Contig ID 41901\_1.R1040 5'-most EST gsv701045903.h1

Method BLASTX
NCBI GI g3650032
BLAST score 289
E value 5.0e-26
Match length 60
% identity 73

NCBI Description (AC005396) gibberellin-regulated protein GAST1-like

[Arabidopsis thaliana]

Seq. No. 15918

Contig ID 41901\_2.R1040 5'-most EST gsv701044721.h1

Method BLASTX
NCBI GI g3650032
BLAST score 148
E value 1.0e-09
Match length 33
% identity 64

NCBI Description (AC005396) gibberellin-regulated protein GAST1-like

[Arabidopsis thaliana]

Seq. No. 15919

Contig ID 41907\_1.R1040 5'-most EST zhf700952814.h1

Method BLASTX NCBI GI g2275210



BLAST score E value 1.0e-08 Match length 44 % identity

NCBI Description (AC002337) peptidyl-prolyl cis-trans isomerase isolog

[Arabidopsis thaliana]

Seq. No. 15920

41911 1.R1040 Contig ID 5'-most EST pcp700990887.h1

Method BLASTX NCBI GI g1871187 BLAST score 277 E value 2.0e-24 Match length 162 43 % identity

(U90439) unknown protein [Arabidopsis thaliana] NCBI Description

Seq. No. 15921

Contig ID 41914 1.R1040

5'-most EST uC-gmflminsoy026f11b1

Seq. No. 15922

41914 2.R1040 Contig ID

5'-most EST jC-gmro02910052g02a1

Seq. No. 15923

41916 1.R1040 Contig ID

5'-most EST LIB3087-005-Q1-K1-H12

Method BLASTX NCBI GI g1352904 BLAST score 145 E value 5.0e-09 Match length 128 35 % identity

NCBI Description

HYPOTHETICAL 37.5 KD PROTEIN IN YUH1-URA8 INTERGENIC REGION

>gi 1077903 pir S57121 hypothetical protein YJR100c yeast (Saccharomyces cerevisiae) >gi 1015804 emb CAA89630

(Z49600) ORF YJR100c [Saccharomyces cerevisiae]

Seq. No. 15924

41920 1.R1040 Contig ID

5'-most EST LIB3087-007-Q1-K1-A10

Seq. No. 15925

Contig ID 41925 1.R1040

5'-most EST LIB3138-122-Q1-N1-F8

Seq. No. 15926

Contig ID 41930 1.R1040 5'-most EST awf700836871.h1

Method BLASTX NCBI GI q2618702 BLAST score 340 E value 7.0e-32 Match length 81 % identity 80



(AC002510) unknown protein [Arabidopsis thaliana] NCBI Description

Seq. No.

15927

Contig ID

41935 1.R1040

5'-most EST Method

uC-gmrominsoy093d09b1 BLASTX

NCBI GI BLAST score g282994 343

E value Match length % identity

5.0e-32 140 47

NCBI Description Sip1 protein - barley >gi 167100 (M77475) seed imbibition

protein [Hordeum vulgare]

Seq. No.

15928

Contig ID 5'-most EST 41935 2.R1040 fua701037316.h1

Method NCBI GI BLAST score E value

BLASTX q282994 222 5.0e-18

Match length % identity

NCBI Description Sipl protein - barley >gi 167100 (M77475) seed imbibition

protein [Hordeum vulgare]

Seq. No.

15929

84 49

Contig ID 5'-most EST

41938 1.R1040 uC-gmronoir048c10b1

Seq. No.

15930

Contig ID

41943 1.R1040

5'-most EST

fC-qmse7000754894f1

Method NCBI GI BLASTX g3928758

BLAST score

512

E value

6.0e-52

Match length % identity

152 68

NCBI Description

(AB007987) Lipoic acid synthase [Arabidopsis thaliana]

>gi\_4454462 gb AAD20909 (AC006234) putative lipoic acid

synthase [Arabidopsis thaliana]

Seq. No.

15931

Contig ID

41948 1.R1040

5'-most EST

LIB3087-004-Q1-K1-B3

Seq. No.

15932

Contig ID

41951 1.R1040

5'-most EST

LIB3087-006-Q1-K1-F11

Seq. No.

15933

Contig ID 5'-most EST 41953 1.R1040 sat701011579.h1

Method NCBI GI BLASTX q4220535

BLAST score

696



```
2.0e-73
E value
                  157
Match length
% identity
                  (AL035356) clathrin coat assembly like protein [Arabidopsis
NCBI Description
                  thaliana]
                  15934
Seq. No.
                  41959 1.R1040
Contig ID
                  LIB3087-006-Q1-K1-C9
5'-most EST
                  BLASTX
Method
                  q4567302
NCBI GI
                   370
BLAST score
                   3.0e-35
E value
                   97
Match length
% identity
NCBI Description (AC005956) unknown protein [Arabidopsis thaliana]
                   15935
Seq. No.
                   41960 1.R1040
Contig ID
                   g5753243
5'-most EST
                   15936
Seq. No.
                   41961 1.R1040
Contig ID
                   g5677026
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3402722
BLAST score
                   469
                   6.0e-47
E value
                   102
Match length
                   87
% identity
NCBI Description (AC004261) CPDK-related protein [Arabidopsis thaliana]
Seq. No.
                   15937
                   41961 2.R1040
Contig ID
                   LIB3109-045-Q1-K1-A10
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3402722
                   1284
BLAST score
                   1.0e-142
E value
                   326
Match length
 % identity
                   75
                   (AC004261) CPDK-related protein [Arabidopsis thaliana]
NCBI Description
                   15938
 Seq. No.
                   41963 1.R1040
 Contig ID
                   LIB3087-006-Q1-K1-D3
 5'-most EST
                   BLASTX
 Method
                   g1903034
 NCBI GI
                   234
 BLAST score
                   2.0e-19
 E value
                   86
 Match length
 % identity
                   59
                   (X94625) amp-binding protein [Brassica napus]
 NCBI Description
```

2648

15939

41964 1.R1040

rca701001351.hl

Seq. No.

Contig ID

5'-most EST



Method BLASTX
NCBI GI 94539303
BLAST score 723
E value 2.0e-76
Match length 248
% identity 56

NCBI Description (AL049480) putative protein [Arabidopsis thaliana]

Seq. No. 15940

Contig ID 41966\_1.R1040 5'-most EST fC-gmst700889725f2

Method BLASTX
NCBI GI g2980770
BLAST score 556
E value 3.0e-60
Match length 308
% identity 45

NCBI Description (AL022198) putative protein kinase [Arabidopsis thaliana]

Seq. No. 15941

Contig ID 41975 1.R1040

5'-most EST LIB3087-006-Q1-K1-B7

Seq. No. 15942

Contig ID 41980\_1.R1040 5'-most EST zsg701126907.h1

Method BLASTX
NCBI GI g4239879
BLAST score 696
E value 2.0e-73
Match length 229
% identity 62

NCBI Description (AB016780) Glutamine:fructose-6-phosphate amidotransferase

2 [Mus musculus]

Seq. No. 15943

Contig ID 41992 1.R1040

5'-most EST uC-gmflminsoy084e10b1

Method BLASTX
NCBI GI g992917
BLAST score 2018
E value 0.0e+00
Match length 392
% identity 99

NCBI Description (L42814) acetyl CoA carboxylase [Glycine max]

Seq. No. 15944

Contig ID 41993 1.R1040 5'-most EST leu701146556.h1

Seq. No. 15945

Contig ID 42001\_1.R1040

5'-most EST LIB3087-005-Q1-K1-F6

Seq. No. 15946

Contig ID 42002 1.R1040 5'-most EST gsv701044040.h1

2649



```
Method
                  BLASTX
                  g3122703
NCBI GI
BLAST score
                  592
                  3.0e-61
E value
                  148
Match length
                  80
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L23A >gi 2641201 (AF031542) ribosomal
                  protein L23a [Fritillaria agrestis]
Seq. No.
                  15947
Contig ID
                  42003 1.R1040
5'-most EST
                  q5509280
Method
                  BLASTX
NCBI GI
                  q3033398
```

Method BLASTX
NCBI GI g303339
BLAST score 555
E value 7.0e-57
Match length 145
% identity 76

NCBI Description (AC004238) putative phosphoribosylaminoimidazolecarboxamide

formyltransferase [Arabidopsis thaliana]

Seq. No. 15948
Contig ID 42006 2.R1040
5'-most EST asn701139772.h1
Method BLASTX
NCBI GI 92257530

NCBI GI g2257530
BLAST score 330
E value 1.0e-30
Match length 180
% identity 39

NCBI Description (AB004537) hypothetical protein YPL063w

[Schizosaccharomyces pombe]

Seq. No. 15949

Contig ID 42008\_1.R1040 5'-most EST gsv701046929.h1

Method BLASTX
NCBI GI g4191788
BLAST score 386
E value 2.0e-37
Match length 119
% identity 62

NCBI Description (AC005917) putative 1-aminocyclopropane-1-carboxylate

oxidase [Arabidopsis thaliana]

Seq. No. 15950

Contig ID 42010 1.R1040

5'-most EST LIB3087-005-Q1-K1-C4

Seq. No. 15951

Contig ID 42023\_1.R1040 5'-most EST V4R-01-Q1-E1-B10

Seq. No. 15952

Contig ID 42036\_1.R1040

5'-most EST LIB3087-005-Q1-K1-C11



```
Seq. No. 15953
```

Contig ID 42044 1.R1040 5'-most EST wrg700789986.h2

Method BLASTX
NCBI GI g3367534
BLAST score 1318
E value 1.0e-146
Match length 321
% identity 78

NCBI Description (AC004392) Strong similarity to coatamer alpha subunit (HEPCOP) homolog gb U24105 from Homo sapiens. [Arabidopsis

thaliana]

Seq. No. 15954

Contig ID 42055\_1.R1040 5'-most EST seb700653705.h1

Method BLASTX
NCBI GI g3928142
BLAST score 2455
E value 0.0e+00
Match length 508
% identity 58

NCBI Description (AJ131045) protein phosphatase [Cicer arietinum]

Seq. No. 15955

Contig ID 42058\_1.R1040

5'-most EST jC-gmle01810009d05a1

Method BLASTX
NCBI GI g2225948
BLAST score 149
E value 2.0e-09
Match length 120
% identity 30

NCBI Description (Z97193) fadB5 [Mycobacterium tuberculosis]

Seq. No. 15956

Contig ID 42068 1.R1040

5'-most EST uC-gmflminsoy028f06b1

Seq. No. 15957

Contig ID 42069 1.R1040

5'-most EST LIB3087-004-Q1-K1-G10

Method BLASTX
NCBI GI 94567267
BLAST score 288
E value 2.0e-37
Match length 94
% identity 57

NCBI Description (AC006841) putative zinc finger protein [Arabidopsis

thaliana]

Seq. No. 15958

Contig ID 42105\_1.R1040 5'-most EST fua701042585.h1

Seq. No. 15959

Contig ID 42105 2.R1040



```
5'-most EST
                  LIB3087-004-Q1-K1-C11
Seq. No.
                  15960
                  42112 1.R1040
Contig ID
5'-most EST
                  LIB3087-003-Q1-K1-H3
Seq. No.
                  15961
                  42113 1.R1040
Contig ID
5'-most EST
                  LIB3094-046-Q1-K1-B10
                  15962
Seq. No.
Contig ID
                  42118 1.R1040
                  LIB3087-004-Q1-K1-A2
5'-most EST
                  15963
Seq. No.
Contig ID
                  42123 1.R1040
5'-most EST
                  jC-gmle01810028a06d1
Method
                  BLASTX
NCBI GI
                  q4539383
BLAST score
                  193
E value
                  1.0e-14
Match length
                  65
% identity
                  51
                 (AL035526) putative protein (fragment) [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  15964
Contig ID
                  42124 1.R1040
                  LIB3087-003-Q1-K1-F7
5'-most EST
                  15965
Seq. No.
Contig ID
                  42138 1.R1040
5'-most EST
                  crh700856174.h1
Seq. No.
                  15966
                  42142 1.R1040
Contig ID
5'-most EST
                  uaw700666719.h1
Method
                  BLASTX
NCBI GI
                  g1110502
BLAST score
                  446
E value
                  3.0e-44
Match length
                  139
% identity
                  67
NCBI Description (U40387) coil protein [Medicago sativa]
Seq. No.
                  15967
                  42146 1.R1040
Contig ID
5'-most EST
                  zhf700964610.h1
                  15968
Seq. No.
```

Contig ID 42151\_1.R1040 5'-most EST zsg701129584.h1

Seq. No. 15969

Contig ID 42153\_1.R1040

5'-most EST LIB3087-003-Q1-K1-C12



Seq. No. 15970

Contig ID 42163\_1.R1040 5'-most EST g5677772 Method BLASTX NCBI GI g1220453 BLAST score 433 E value 2.0e-42

E value 2.00 Match length 142 % identity 55

NCBI Description (M79328) alpha-amylase [Solanum tuberosum]

Seq. No. 15971

Contig ID 42176 1.R1040

5'-most EST LIB3087-002-Q1-K1-G5

Method BLASTX
NCBI GI g4204310
BLAST score 455
E value 3.0e-45
Match length 168
% identity 60

NCBI Description (AC003027) lcl prt seq No definition line found

[Arabidopsis thaliana]

Seq. No. 15972

Contig ID 42188 1.R1040

5'-most EST LIB3087-002-Q1-K1-H8

Seq. No. 15973

Contig ID 42194\_1.R1040 5'-most EST wvk700685652.h1

Seq. No. 15974

Contig ID 42194 2.R1040

5'-most EST LIB3107-035-Q1-K1-C5

Seq. No. 15975

Contig ID 42195 1.R1040

5'-most EST LIB3093-027-Q1-K1-F11

Seq. No. 15976

Contig ID 42200\_1.R1040

5'-most EST LIB3087-002-Q1-K1-G3

Seq. No. 15977

Contig ID 42203\_1.R1040

5'-most EST LIB3087-002-Q1-K1-D4

Seq. No. 15978

Contig ID 42206\_1.R1040

5'-most EST uC-gmflminsoy040d11b1

Seq. No. 15979

Contig ID 42207 1.R1040

5'-most EST uC-gmrominsoy226b03b1

Method BLASTX
NCBI GI g3219151
BLAST score 512



E value 5.0e-52 Match length 118 % identity 88

NCBI Description (AB015181) cdc2 related [Mesembryanthemum crystallinum]

Seq. No. 15980

Contig ID 42211 1.R1040

5'-most EST uC-gmrominsoy106f10b1

Seq. No. 15981

Contig ID 42213\_1.R1040 5'-most EST LIB3094-005-Q1-K1-B1

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 2.0e-10

Match length 36 % identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 15982

Contig ID 42215 1.R1040

5'-most EST LIB3087-002-Q1-K1-C11

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 1.0e-10
Match length 48
% identity 67

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 15983

Contig ID 42219 1.R1040

5'-most EST LIB3093-028-Q1-K1-D10

Seq. No. 15984

Contig ID 42227 1.R1040

5'-most EST LIB3087-002-Q1-K1-C10

Seq. No. 15985

Contig ID 42234\_1.R1040 5'-most EST dpv701103656.h1

Method BLASTX
NCBI GI g2459417
BLAST score 1403
E value 1.0e-156
Match length 403
% identity 69

NCBI Description (AC002332) putative pre-mRNA splicing factor PRP19

[Arabidopsis thaliana]

Seq. No. 15986

Contig ID 42234 2.R1040

5'-most EST LIB3139-084-P1-N1-F11

Method BLASTX
NCBI GI g2459417
BLAST score 1153



E value 1.0e-127 Match length 289 % identity 77

NCBI Description (AC002332) putative pre-mRNA splicing factor PRP19

[Arabidopsis thaliana]

Seq. No. 15987

Contig ID 42234\_3.R1040 5'-most EST fC-gmro700867273d1

Seq. No. 15988

Contig ID 42242\_1.R1040 5'-most EST awf700838938.h1

Method BLASTX
NCBI GI g4455351
BLAST score 276
E value 2.0e-24
Match length 76
% identity 70

NCBI Description (AL035524) putative protein [Arabidopsis thaliana]

Seq. No. 15989

Contig ID 42250\_1.R1040 5'-most EST trc700563193.h1

Method BLASTX
NCBI GI g2160166
BLAST score 520
E value 1.0e-52
Match length 247
% identity 47

NCBI Description (AC000132) No definition line found [Arabidopsis thaliana]

Seq. No. 15990

Contig ID 42250\_3.R1040 5'-most EST zhf700955402.h1

Seq. No. 15991

Contig ID 42251\_1.R1040 5'-most EST kl1701206621.h1

Method BLASTX
NCBI GI g4490727
BLAST score 164
E value 3.0e-11
Match length 43

% identity 67

NCBI Description (AL035709) putative protein [Arabidopsis thaliana]

Seq. No. 15992

Contig ID 42256 1.R1040

5'-most EST LIB3087-002-Q1-K1-A5

Seq. No. 15993

Contig ID 42260\_1.R1040

5'-most EST uC-gmronoir0001h10b1

Method BLASTX
NCBI GI g3327868
BLAST score 355



1.0e-33 E value Match length 145 % identity (AB012912) COP1-Interacting Protein 7 (CIP7) [Arabidopsis NCBI Description thaliana] 15994 Seq. No. 42262 1.R1040 Contig ID LIB3087-001-Q1-K1-G11 5'-most EST BLASTX Method q2980806 NCBI GI BLAST score 356 3.0e-33 E value 107 Match length 63 % identity NCBI Description (AL022197) putative protein [Arabidopsis thaliana] 15995 Seq. No. 42268 1.R1040 Contig ID LIB3087-001-Q1-K1-G7 5'-most EST 15996 Seq. No. 42269 1.R1040 Contig ID LIB3087-001-Q1-K1-G8 5'-most EST BLASTX Method q2314805 NCBI GI BLAST score 464 E value 2.0e-46114 Match length % identity 79 (U85045) 2-oxoglutarate-dependent dioxygenase [Pisum NCBI Description sativum] >gi 2316036 (AF001219) gibberellin 3 beta-hydroxylase [Pisum sativum] 15997 Seq. No. 42285 1.R1040 Contig ID gsv701044820.h1 5'-most EST 15998 Seq. No. 42286 1.R1040 Contig ID LIB3087-001-Q1-K1-F4 5'-most EST 15999 Seq. No. 42286 2.R1040 Contig ID LIB3106-005-Q1-K1-B1 5'-most EST BLASTX Method g4006926 NCBI GI 383 BLAST score 5.0e-37 E value Match length 141 % identity 52 (Z99708) putative protein (fragment) [Arabidopsis thaliana] NCBI Description

Seq. No. 16000

Contig ID 42306\_1.R1040

5'-most EST LIB3087-001-Q1-K1-B6

Method BLASTX

2656



NCBI GI g3805854
BLAST score 195
E value 4.0e-23
Match length 130
% identity 42

NCBI Description (AL031986) putative protein [Arabidopsis thaliana]

Seq. No. 16001

Contig ID 42314\_1.R1040 5'-most EST cle700967819.h1

Seq. No. 16002

Contig ID 42325\_1.R1040

5'-most EST LIB3087-001-Q1-K1-A4

Method BLASTX
NCBI GI 94490310
BLAST score 1454
E value 1.0e-162
Match length 315
% identity 90

NCBI Description (AL035678) somatic embryogenesis receptor-like kinase-like

protein [Arabidopsis thaliana]

Seq. No. 16003

Contig ID 42326 1.R1040 5'-most EST 6HA-01-Q1-B1-H10

Seq. No. 16004

Contig ID 42327 1.R1040

5'-most EST LIB3087-001-Q1-K1-A6

Method BLASTX
NCBI GI g2982452
BLAST score 581
E value 5.0e-60
Match length 161
% identity 71

NCBI Description (AL022223) receptor protein kinase-like protein

[Arabidopsis thaliana]

Seq. No. 16005

Contig ID 42333\_1.R1040

5'-most EST LIB3087-001-Q1-K1-B12

Method BLASTX
NCBI GI g2648032
BLAST score 1863
E value 0.0e+00
Match length 475
% identity 70

NCBI Description (AJ001374) alpha-glucosidase [Solanum tuberosum]

Seq. No. 16006

Contig ID 42337\_1.R1040

5'-most EST LIB3087-001-Q1-K1-B2

Method BLASTX
NCBI GI g4580468
BLAST score 169
E value 1.0e-11



Match length 80 % identity 42

NCBI Description (AC006081) putative protein kinase; similar to human PKX1

and Drosophila DC2 [Arabidopsis thaliana]

Seq. No. 16007

Contig ID 42358\_2.R1040 5'-most EST yz1700967060.h1

Method BLASTX
NCBI GI g3687230
BLAST score 198
E value 2.0e-15
Match length 57
% identity 67

NCBI Description (AC005169) hypothetical protein [Arabidopsis thaliana]

Seq. No.

16008

Contig ID 42375 1.R1040

5'-most EST LIB3087-005-Q1-K1-E3

Method BLASTX
NCBI GI g4455316
BLAST score 259
E value 3.0e-22
Match length 117
% identity 43

NCBI Description (AL035528) putative protein [Arabidopsis thaliana]

Seq. No. 16009

Contig ID 42375\_2.R1040 5'-most EST sat701013007.h1

Method BLASTX
NCBI GI g3757518
BLAST score 144
E value 5.0e-09
Match length 109
% identity 32

NCBI Description (AC005167) putative immediate-early salicylate-induced

glucosyltransferase [Arabidopsis thaliana]

Seq. No. 16010

42377 1.R1040 Contig ID 5'-most EST g4297627 Method BLASTX g3927831 NCBI GI BLAST score 414 3.0e-40E value Match length 128 28 % identity

NCBI Description (AC005727) similar to mouse ankyrin 3 [Arabidopsis

thaliana]

Seq. No. 16011

Contig ID 42377\_3.R1040 5'-most EST smc700746924.h1

Seq. No. 16012

Contig ID 42380 1.R1040

2658



...5'-most EST leu701154302.h1

Method BLASTX
NCBI GI g3033396
BLAST score 378
E value 4.0e-36
Match length 121
% identity 59

NCBI Description (AC004238) unknown protein [Arabidopsis thaliana]

Seq. No. 16013

Contig ID 42380 2.R1040

5'-most EST LIB3087-005-Q1-K1-H7

Method BLASTX
NCBI GI g3033396
BLAST score 204
E value 7.0e-19
Match length 75
% identity 58

NCBI Description (AC004238) unknown protein [Arabidopsis thaliana]

Seq. No. 16014

Contig ID 42381 1.R1040

5'-most EST LIB3087-005-Q1-K1-H8

Method BLASTX
NCBI GI g4335724
BLAST score 149
E value 2.0e-09
Match length 114
% identity 33

NCBI Description (AC006248) putative RING-H2 finger protein [Arabidopsis

thaliana]

Seq. No. 16015

Contig ID 42385\_1.R1040 5'-most EST gsv701052536.h1

Seq. No. 16016

Contig ID 42389 1.R1040

5'-most EST jC-gmf102220061h12a1

Method BLASTX
NCBI GI g4191785
BLAST score 694
E value 8.0e-73
Match length 252
% identity 57

NCBI Description (AC005917) putative hydrolase [Arabidopsis thaliana]

Seq. No. 16017

Contig ID 42403\_1.R1040

5'-most EST LIB3109-035-Q1-K6-B12

Method BLASTN
NCBI GI g560503
BLAST score 59
E value 2.0e-24
Match length 159
% identity 84

NCBI Description V.faba mRNA for guanine nucleotide regulatory protein



## (1226bp)

Seq. No. 16018

Contig ID 42403\_2.R1040 5'-most EST sat701009684.h1

Seq. No. 16019

Contig ID 42404 1.R1040

5'-most EST LIB3087-007-Q1-K1-F11

Method BLASTN
NCBI GI g2511688
BLAST score 124
E value 4.0e-63
Match length 286
% identity 86

NCBI Description Phaseolus vulgaris Moldavian encoding cysteine proteinase

precursor (clone cp6a)

Seq. No. 16020

Contig ID 42404\_4.R1040 5'-most EST ssr700560148.h1

Method BLASTN
NCBI GI g1256829
BLAST score 74
E value 1.0e-33
Match length 146
% identity 88

NCBI Description Phaseolus vulgaris cysteine endopeptidase 1 (PvCEP-1) mRNA,

complete cds >gi 2959417 emb AJ224766 PVA224766 Phaseolus

vulgaris mRNA cotyledon cysteine protease

Seq. No. 16021

Contig ID 42406 1.R1040

5'-most EST LIB3087-007-Q1-K1-H8

Method BLASTX
NCBI GI g4249380
BLAST score 292
E value 3.0e-26
Match length 122
% identity 49

NCBI Description (AC005966) ESTs gb Z37637, gb AA042498 and gb AA042269 come

from this gene. [Arabidopsis thaliana]

Seq. No. 16022

Contig ID 42406\_2.R1040 5'-most EST hrw701058386.h1

Method BLASTX
NCBI GI 94249380
BLAST score 164
E value 1.0e-11
Match length 46
% identity 63

NCBI Description (AC005966) ESTs gb\_Z37637, gb\_AA042498 and gb\_AA042269 come

from this gene. [Arabidopsis thaliana]

Seq. No. 16023

Contig ID 42412 1.R1040

2660



```
LIB3087-008-Q1-K1-C11
5'-most EST
                  BLASTX
Method
                  q4512698
NCBI GI
                  208
BLAST score
                  2.0e-16
E value
Match length
                  98
% identity
                  (AC006569) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  16024
Seq. No.
                   42412 3.R1040
Contig ID
                  zsq701127342.hl
5'-most EST
                  16025
Seq. No.
                   42414 1.R1040
Contig ID
                  LIB3087-008-Q1-K1-C9
5'-most EST
Method
                  BLASTX
NCBI GI
                   q1110502
                   639
BLAST score
E value
                   5.0e-67
                   224
Match length
% identity
                   62
                  (U40387) coil protein [Medicago sativa]
NCBI Description
                   16026
Seq. No.
                   42417 1.R1040
Contig ID
                   LIB3087-008-Q1-K1-E9
5'-most EST
                   BLASTX
Method
                   g1171577
NCBI GI
                   382
BLAST score
                   7.0e-37
E value
                   104
Match length
                   71
% identity
                   (X95343) hypersensitivity-related gene [Nicotiana tabacum]
NCBI Description
                   16027
Seq. No.
                   42418 1.R1040
Contig ID
                   LIB3087-008-Q1-K1-F10
5'-most EST
                   16028
Seq. No.
                   42424 1.R1040
Contig ID
                   LIB3087-008-Q1-K1-G11
5'-most EST
                   BLASTX
Method
                   g465740
NCBI GI
                   151
BLAST score
                   7.0e-10
E value
                   84
Match length
 % identity
                   HYPOTHETICAL 54.9 KD PROTEIN C02F5.7 IN CHROMOSOME III
NCBI Description
                   >gi 630513 pir__S44609 hypothetical protein C02F5.7 -
                   Caenorhabditis elegans >gi_289614 (L14745) homology with
                   glucose induced repressor, GRR1; putative [Caenorhabditis
                   elegans]
```

Seq. No. 16029

Contig ID 42436\_1.R1040

5'-most EST LIB3087-009-Q1-K1-B9



Method BLASTN
NCBI GI g3832511
BLAST score 226
E value 1.0e-124
Match length 374
% identity 90

NCBI Description Astragalus membranaceus granule-bound glycogen (starch)

synthase mRNA, complete cds

Seq. No. 16030

Contig ID 42438\_1.R1040 5'-most EST kl1701214025.h1

Method BLASTX
NCBI GI g3687654
BLAST score 1370
E value 1.0e-152
Match length 402
% identity 70

NCBI Description (AF047975) putative ethylene receptor; ETR2 [Arabidopsis

thaliana]

Seq. No. 16031

Contig ID 42438 2.R1040

5'-most EST LIB3087-009-Q1-K1-C2

Method BLASTX
NCBI GI g1762947
BLAST score 323
E value 3.0e-29
Match length 113
% identity 58

NCBI Description (U66270) ORF; able to induce HR-like lesions [Nicotiana

tabacum]

Seq. No. 16032

Contig ID 42438\_3.R1040 5'-most EST epx701107081.h1

Seq. No. 16033

Contig ID 42438\_4.R1040 5'-most EST smc700748218.h1

Seq. No. 16034

Contig ID 42448 1.R1040

5'-most EST LIB3087-009-Q1-K1-F4

Method BLASTX
NCBI GI g3775987
BLAST score 246
E value 1.0e-20
Match length 105
% identity 60

NCBI Description (AJ010457) RNA helicase [Arabidopsis thaliana]

Seq. No. 16035

Contig ID 42448\_2.R1040 5'-most EST zpv700760107.h1

Method BLASTX NCBI GI g3775987



BLAST score 379
E value 3.0e-36
Match length 176
% identity 55

NCBI Description (AJ010457) RNA helicase [Arabidopsis thaliana]

Seq. No. 16036

Contig ID 42454\_1.R1040 5'-most EST g5510209

Seq. No. 16037

Contig ID 42463\_1.R1040 5'-most EST bth700844173.h1

Method BLASTX
NCBI GI g2129550
BLAST score 1838
E value 0.0e+00
Match length 466
% identity 71

NCBI Description calcium-dependent protein kinase (EC 2.7.1.-) CDPK6 -

Arabidopsis thaliana >gi\_2129554\_pir\_\_S71901

calcium-dependent protein kinase 6 - Arabidopsis thaliana

>gi\_836940 (U20623) calcium-dependent protein kinase

[Arabidopsis thaliana] >gi\_836944 (U20625)

calcium-dependent protein kinase [Arabidopsis thaliana] >gi\_4454034\_emb\_CAA23031.1\_ (AL035394) calcium-dependent

protein kinase (CDPK6) [Arabidopsis thaliana]

Seq. No. 16038

Contig ID 42470\_1.R1040

5'-most EST LIB3093-003-Q1-K1-G2

Method BLASTN
NCBI GI g437994
BLAST score 242
E value 1.0e-133
Match length 726
% identity 83

NCBI Description F.pringlei mRNA for glycine hydroxymethyltransferase

Seq. No. 16039

Contig ID 42470\_2.R1040

5'-most EST LIB3087-010-Q1-K1-D3

Method BLASTX
NCBI GI g462187
BLAST score 447
E value 1.0e-44
Match length 118
% identity 78

NCBI Description SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL PRECURSOR (SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE)

(SHMT) >qi 282928 pir A42906 serine

hydroxymethyltransferase - garden pea >gi\_169158 (M87649)

serine hydroxymethyltransferase [Pisum sativum]

Seq. No. 16040

Contig ID 42470 3.R1040 5'-most EST gsv701047711.h1



Method BLASTN NCBI GI q438246 BLAST score 70 E value 7.0e-31 Match length 146 % identity 87

NCBI Description S.tuberosum mRNA for glycine hydroxymethyltransferase

Seq. No.

16041

Contig ID 5'-most EST

42472 1.R1040 LIB3087-010-Q1-K1-D5

Seq. No.

16042

Contig ID

42482 1.R1040

5'-most EST

LIB3087-010-Q1-K1-F2

Seq. No.

16043

Contig ID 5'-most EST

42485 1.R1040 sat701007627.h1

Seq. No.

16044

Contig ID 5'-most EST

42491 1.R1040 pmv700893903.h1

Method BLASTX NCBI GI g4510381 290 BLAST score 3.0e-26 E value 117 Match length

% identity 57

NCBI Description (AC007017) unknown protein [Arabidopsis thaliana]

Seq. No.

16045

Contig ID

42527 1.R1040

5'-most EST

LIB3092-062-Q1-K1-H10

Seq. No.

16046

Contig ID

42530 1.R1040

5'-most EST

jC-gmle01810044f12a1

Seq. No.

16047

Contig ID 5'-most EST 42537 1.R1040 fua701041783.h1

Seq. No.

16048

Contig ID

42540 1.R1040

5'-most EST

LIB3092-062-Q1-K1-F2

Seq. No.

16049

Contig ID

42545\_1.R1040

5'-most EST

LIB3092-062-Q1-K1-F5

Method NCBI GI BLASTX g1039355

BLAST score

445

E value Match length 8.0e-44

% identity

229 48

NCBI Description (X92179) alcohol dehydrogenase [Solanum tuberosum]



```
16050
Seq. No.
                  42548 1.R1040
Contig ID
                  dpv701097128.hl
5'-most EST
Method
                  BLASTN
                  q3434972
NCBI GI
                  55
BLAST score
                   6.0e-22
E value
                   213
Match length
                   84
% identity
                  Arabidopsis thaliana AtERF-4 mRNA for ethylene responsive
NCBI Description
                   element binding factor 4, complete cds
                   16051
Seq. No.
                   42549 1.R1040
Contig ID
                   LIB3107-020-Q1-K1-G11
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3063469
                   145
BLAST score
                   5.0e-09
E value
                   53
Match length
% identity
NCBI Description (AC003981) F22013.31 [Arabidopsis thaliana]
                   16052
Seq. No.
                   42557 1.R1040
Contig ID
                   wrg700787578.hl
5'-most EST
                   BLASTX
Method
                   g4206200
NCBI GI
                   235
BLAST score
                   1.0e-19
E value
                   148
Match length
% identity
                   21
                   (AF071527) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   16053
Seq. No.
                   42568 1.R1040
Contig ID
                   sat701012225.h1
5'-most EST
                   16054
Seq. No.
                   42574 1.R1040
Contig ID
                   LIB3092-062-Q1-K1-C1
5'-most EST
                   16055
 Seq. No.
                   42601 1.R1040
 Contig ID
                   LIB31\overline{3}8-091-Q1-N1-E11
 5'-most EST
                   BLASTX
Method
                   g1652649
 NCBI GI
                    381
 BLAST score
                   2.0e-36
 E value
                   130
 Match length
                    55
 % identity
 NCBI Description (D90907) hypothetical protein [Synechocystis sp.]
```

Contig ID

Seq. No.

LIB3092-062-Q1-K1-B12 5'-most EST

16056

42604 2.R1040

2665



```
16057
Seq. No.
                  42612 1.R1040
Contig ID
5'-most EST
                  pmv700888633.hl
Method
                  BLASTX
                  q2344889
NCBI GI
                  392
BLAST score
                  6.0e-38
E value
                  155
Match length
                  48
% identity
                  (AC002388) unknown protein [Arabidopsis thaliana]
NCBI Description
                  16058
Seq. No.
                   42613 1.R1040
Contig ID
5'-most EST
                  LIB3092-061-Q1-K1-E6
                   16059
Seq. No.
Contig ID
                   42624 1.R1040
                   pmv700890259.hl
5'-most EST
                   BLASTX
Method
                   q3757523
NCBI GI
BLAST score
                   545
                   6.0e-56
E value
Match length
                   155
                   69
% identity
                   (AC005167) putative transportin [Arabidopsis thaliana]
NCBI Description
                   16060
Seq. No.
                   42636_1.R1040
Contig ID
                   uC-gmrominsoy248e04b1
5'-most EST
                   BLASTN
Method
                   q1684850
NCBI GI
                   257
BLAST score
                   1.0e-142
E value
                   548
Match length
                   85
% identity
NCBI Description Phaseolus vulgaris DnaJ-like protein mRNA, partial cds
                   16061
Seq. No.
                   42643 1.R1040
Contig ID
                   LIB3092-049-Q1-K1-F2
5'-most EST
                   16062
Seq. No.
                   42646 1.R1040
Contig ID
5'-most EST
                   asn701142478.h1
                   BLASTX
Method
                   g4490738
NCBI GI
                   150
BLAST score
                   3.0e-09
E value
Match length
                   180
% identity
                   37
```

Seq. No. 16063

NCBI Description

Contig ID 42647\_1.R1040

5'-most EST LIB3092-060-Q1-K1-G11

(AL035708) putative protein [Arabidopsis thaliana]



Seq. No. 16064

Contig ID 42653 1.R1040

5'-most EST jC-gmro02910074g01a1

Seq. No. 16065

Contig ID 42653 2.R1040

5'-most EST LIB3109-010-Q1-K1-C2

Method BLASTN
NCBI GI g2264318
BLAST score 37
E value 3.0e-11

Match length 53 % identity 92

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MUP24, complete sequence [Arabidopsis thaliana]

Seq. No. 16066

Contig ID 42659 1.R1040

5'-most EST LIB3106-109-Q1-K1-C12

Seq. No. 16067

Contig ID 42662 1.R1040 5'-most EST epx701109007.h1

Seq. No. 16068

Contig ID 42665\_1.R1040

5'-most EST uC-gmrominsoy217b11b1

Method BLASTX
NCBI GI g2462835
BLAST score 322
E value 2.0e-29
Match length 200
% identity 38

NCBI Description (AF000657) hypothetical protein [Arabidopsis thaliana]

Seq. No. 16069

Contig ID 42669\_1.R1040 5'-most EST fua701040990.h1

Seq. No. 16070

Contig ID 42695 1.R1040

5'-most EST LIB30 $\overline{9}2$ -058-Q1-K1-E4

Method BLASTX
NCBI GI g3540199
BLAST score 232
E value 1.0e-39
Match length 152
% identity 55

NCBI Description (AC004260) Putative monosaccharide transport protein

[Arabidopsis thaliana]

Seq. No. 16071

Contig ID 42701\_1.R1040

5'-most EST LIB3092-058-Q1-K1-F2

Seq. No. 16072

Contig ID 42701 2.R1040

2667



```
5'-most EST
                  LIB3093-002-Q1-K1-D12
                  16073
Seq. No.
                  42710 1.R1040
Contig ID
5'-most EST
                  LIB3092-058-Q1-K1-B10
Method
                  BLASTX
NCBI GI
                  g1929998
BLAST score
                  217
E value
                  1.0e-18
Match length
                  144
% identity
                  41
                  (U77463) NADPH-dependent HC-toxin reductase [Hordeum
NCBI Description
                  vulgare]
Seq. No.
                  16074
Contig ID
                  42714 1.R1040
5'-most EST
                  jC-gmf102220086e06d1
                  16075
Seq. No.
                  42714 2.R1040
Contig ID
5'-most EST
                  LIB3092-058-Q1-K1-B5
Seq. No.
                  16076
Contig ID
                  42727 1.R1040
5'-most EST
                  jC-gmro02910003b02a1
Seq. No.
                  16077
                  42743 1.R1040
Contig ID
5'-most EST
                  wvk700685369.h1
                  16078
Seq. No.
Contig ID
                  42762 1.R1040
5'-most EST
                  LIB3092-057-Q1-K1-A2
Method
                  BLASTX
NCBI GI
                  q719291
                  331
BLAST score
E value
                  4.0e-31
                  108
Match length
                  66
% identity
                  (U19134) unknown [Arabidopsis thaliana]
NCBI Description
                  >gi_1095007_prf__2107236A SABRE gene [Arabidopsis thaliana]
Seq. No.
                  16079
Contig ID
                  42779 1.R1040
5'-most EST
                  kmv700741358.h1
Method
                  BLASTX
NCBI GI
                  q2245066
BLAST score
                  1942
                  0.0e+00
E value
Match length
                  486
% identity
                  74
NCBI Description
                 (Z97342) Beta-Amylase [Arabidopsis thaliana]
```

Contig ID 42779\_2.R1040 5'-most EST LIB3138-122-Q1-N1-H8

16080

Method BLASTX

Seq. No.

```
g2245066
NCBI GI
BLAST score
                  310
                  3.0e-28
E value
                  112
Match length
% identity
                   58
NCBI Description (Z97342) Beta-Amylase [Arabidopsis thaliana]
                  16081
Seq. No.
                   42790 1.R1040
Contig ID
5'-most EST
                   g5606152
Method
                   BLASTX
                   g3426043
NCBI GI
BLAST score
                   442
                   4.0e-79
E value
                   248
Match length
% identity
                   63
                  (AC005168) putative choline kinase [Arabidopsis thaliana]
NCBI Description
                   16082
Seq. No.
                   42804 1.R1040
Contig ID
                   gsv701051882.hl
5'-most EST
                   BLASTX
Method
                   g2827702
NCBI GI
                   687
BLAST score
                   2.0e-72
E value
                   181
Match length
% identity
                   (AL021684) predicted protein [Arabidopsis thaliana]
NCBI Description
                   16083
Seq. No.
                   42805 1.R1040
Contig ID
                   LIB3092-056-Q1-K1-E6
5'-most EST
Seq. No.
                   16084
                   42829 1.R1040
Contig ID
                   uaw700661872.hl
5'-most EST
                   16085
Seq. No.
                   42831 1.R1040
Contig ID
                   leu701152033.hl
5'-most EST
Seq. No.
                   16086
                   42845 1.R1040
 Contig ID
                   LIB3092-055-Q1-K1-C8
 5'-most EST
                   BLASTX
Method
                   g2435521
 NCBI GI
                   308
 BLAST score
                   4.0e-28
 E value
                   140
 Match length
                   17
 % identity
                   (AF024504) contains similarity to Nicotiana tabacum
 NCBI Description
                   membrane-associated salt-inducible protein (GB:U08285)
                   [Arabidopsis thaliana]
```

16087 Seq. No. Contig ID 42850 1.R1040

LIB3138-129-Q1-N1-F6 5'-most EST



Method BLASTX NCBI GI g1778093 BLAST score 303 9.0e-28 E value Match length 116 56 % identity

NCBI Description (U64902) putative sugar transporter; member of major facilitative superfamily; integral membrane protein [Beta

vulgaris]

Seq. No.

16088 Contig ID 42856 1.R1040

5'-most EST LIB3106-078-P1-K1-G1

Seq. No.

16089

Contig ID 42864 1.R1040

5'-most EST LIB3092-055-Q1-K1-B10

16090 Seq. No.

Contig ID 42865 1.R1040 5'-most EST sat701013743.hl

Seq. No.

16091

16092

Contig ID 42884 1.R1040

5'-most EST LIB3092-054-Q1-K1-G7

Seq. No.

Contig ID 42885 1.R1040

5'-most EST LIB3106-089-Q1-K1-H3

16093 Seq. No.

Contig ID 42893 1.R1040 5'-most EST dpv701102366.h1

Method BLASTX NCBI GI g4262234 BLAST score 498 1.0e-107 E value 305 Match length

62 % identity

(AC006200) unknown protein [Arabidopsis thaliana] NCBI Description

Seq. No. 16094

Contig ID 42898 1.R1040 5'-most EST fua701039020.11

Seq. No. 16095

Contig ID 42899 1.R1040

5'-most EST LIB3107-078-Q1-K1-C3

Method BLASTX NCBI GI g3341695 BLAST score 495 7.0e-50 E value Match length 138 % identity 67

(AC003672) putative thiamin pyrophosphokinase [Arabidopsis NCBI Description

thaliana]



```
Seq. No.
                   42899 2.R1040
Contig ID
                  gsv701046159.hl
5'-most EST
                  BLASTX
Method
                  g3341695
NCBI GI
BLAST score
                   694
                   4.0e-73
E value
                   179
Match length
% identity
                   (AC003672) putative thiamin pyrophosphokinase [Arabidopsis
NCBI Description
                  thaliana]
                   16097
Seq. No.
                   42902 1.R1040
Contig ID
                   LIB3092-054-Q1-K1-E2
5'-most EST
                   BLASTN
Method
NCBI GI
                   g2653401
BLAST score
                   352
                   0.0e + 00
E value
                   392
Match length
                   97
% identity
NCBI Description Homo sapiens mRNA for Ins(1,3,4,5)P4-binding protein
                   16098
Seq. No.
                   42909 1.R1040
Contig ID
                   uC-qmropic035h02b1
5'-most EST
Method
                   BLASTX
                   q2642435
NCBI GI
BLAST score
                   383
                   6.0e-37
E value
Match length
                   89
                   78
% identity
                   (AC002391) MYB-related protein [Arabidopsis thaliana]
NCBI Description
                   16099
Seq. No.
                   42910_1.R1040
Contig ID
                   jC-gmle01810068h12d1
5'-most EST
                   BLASTX
Method
                   g2829918
NCBI GI
                   391
BLAST score
                   2.0e-37
E value
                   106
Match length
                   77
% identity
                   (AC002291) similar to "tub" protein gp_U82468_2072162
NCBI Description
                   [Arabidopsis thaliana]
                   16100
 Seq. No.
                   42911 1.R1040
Contig ID
                   dpv701096968.h1
5'-most EST
                   16101
 Seq. No.
                   42911_2.R1040
```

Contig ID 42911\_2.R1040 5'-most EST dpv701101074.h1

Seq. No. 16102

Contig ID 42931 1.R1040

5'-most EST LIB3092-053-Q1-K1-G7



Seq. No. 16103

Contig ID 42937\_1.R1040 5'-most EST dpv701103316.h1

Method BLASTX
NCBI GI g4490309
BLAST score 212
E value 7.0e-17
Match length 65
% identity 57

NCBI Description (AL035678) peroxidase ATP17a-like protein [Arabidopsis

thaliana]

Seq. No. 16104

Contig ID 42946\_1.R1040

5'-most EST LIB3092-053-Q1-K1-H1

Method BLASTN
NCBI GI g187701
BLAST score 300
E value 1.0e-168
Match length 372
% identity 95

NCBI Description Human MHC protein homologous to chicken B complex protein

mRNA, complete cds

Seq. No. 16105

Contig ID 42957\_1.R1040 5'-most EST rlr700899310.h1

Seq. No. 16106

Contig ID 42957 2.R1040 5'-most EST bth700846261.h1

Seq. No. 16107

Contig ID 42961 1.R1040

5'-most EST LIB3092-052-Q1-K1-A11

Method BLASTX
NCBI GI 94510377
BLAST score 227
E value 2.0e-36
Match length 96
% identity 83

NCBI Description (AC007017) putative RNA helicase A [Arabidopsis thaliana]

Seq. No. 16108

Contig ID 42961\_2.R1040 5'-most EST uaw700661360.h1

Method BLASTX
NCBI GI g4510377
BLAST score 438
E value 1.0e-43
Match length 96
% identity 88

NCBI Description (AC007017) putative RNA helicase A [Arabidopsis thaliana]

Seq. No. 16109

Contig ID 42962 1.R1040



5'-most EST zsg701130005.h1

Seq. No. 16110

Contig ID 42964\_1.R1040 5'-most EST LIB3092-053-Q1-K1-B2

Method BLASTX
NCBI GI g2735841
BLAST score 343
E value 4.0e-32
Match length 173
% identity 40

NCBI Description (AF010283) No definition line found [Sorghum bicolor]

Seq. No. 16111

Contig ID 42970 1.R1040

5'-most EST LIB3107-002-Q1-K1-A2

Method BLASTX
NCBI GI 94097573
BLAST score 162
E value 8.0e-11
Match length 72
% identity 43

NCBI Description (U64917) GMFP7 [Glycine max]

Seq. No. 16112

Contig ID 42973\_1.R1040 5'-most EST uC-gmropic064e12b1

Method BLASTX
NCBI GI g2494736
BLAST score 434
E value 2.0e-67
Match length 201
% identity 65

NCBI Description GLUCOSE INHIBITED DIVISION PROTEIN A

>gi\_1001595\_dbj\_BAA10223\_ (D64000) glucose inhibited

division protein A [Synechocystis sp.]

Seq. No. 16113

Contig ID 42982 1.R1040 5'-most EST uC-gmropic059d01b1

Method BLASTX
NCBI GI g2347098
BLAST score 1224
E value 1.0e-135
Match length 317
% identity 80

NCBI Description (U76845) ubiquitin-specific protease [Arabidopsis thaliana]

>qi 4490742 emb CAB38904.1 (AL035708) ubiquitin-specific

protease (AtUBP3) [Arabidopsis thaliana]

Seq. No. 16114

Contig ID 42982\_2.R1040

5'-most EST jC-gmst02400001e10a1

Method BLASTX
NCBI GI g2347098
BLAST score 189
E value 4.0e-20



```
95
Match length
                  62
% identity
                  (U76845) ubiquitin-specific protease [Arabidopsis thaliana]
NCBI Description
                  >qi 4490742 emb CAB38904.1 (AL035708) ubiquitin-specific
                  protease (AtUBP3) [Arabidopsis thaliana]
                  16115
Seq. No.
                  42982 3.R1040
Contig ID
                  LIB3139-096-P1-N1-H2
5'-most EST
Method
                  BLASTX
                  g2347098
NCBI GI
                  763
```

BLAST score 763
E value 3.0e-87
Match length 189
% identity 85

NCBI Description (U76845) ubiquitin-specific protease [Arabidopsis thaliana] >gi 4490742\_emb CAB38904.1\_ (AL035708) ubiquitin-specific

protease (AtUBP3) [Arabidopsis thaliana]

Seq. No. 16116

Contig ID 42982\_4.R1040 5'-most EST gsv701055113.h1

Method BLASTN
NCBI GI g2347097
BLAST score 97
E value 5.0e-47
Match length 269
% identity 84

NCBI Description Arabidopsis thaliana ubiquitin-specific protease (AtUBP3)

mRNA, complete cds

Seq. No. 16117

Contig ID 42986 1.R1040

5'-most EST LIB3107-035-Q1-K1-B8

Method BLASTX
NCBI GI g3775987
BLAST score 1579
E value 1.0e-176
Match length 485
% identity 66

NCBI Description (AJ010457) RNA helicase [Arabidopsis thaliana]

Seq. No.

16118

Contig ID 42988\_1.R1040

5'-most EST jC-gmf102220062a07a1

Method BLASTX
NCBI GI g4038055
BLAST score 539
E value 6.0e-55
Match length 188
% identity 54

NCBI Description (AC005897) putative cytochrome P450 [Arabidopsis thaliana] >gi 4557077 gb AAD22516.1 AC007045\_16 (AC007045) putative

cytochrome p450 [Arabidopsis thaliana]

Seq. No. 16119

Contig ID 42990 1.R1040



5'-most EST LIB3093-015-Q1-K2-B5

Method BLASTX
NCBI GI g3434975
BLAST score 281
E value 1.0e-24
Match length 200
% identity 45

NCBI Description (AB008107) ethylene responsive element binding factor 5

[Arabidopsis thaliana]

Seq. No. 16120

Contig ID 42992\_1.R1040 5'-most EST awf700839279.h1

Method BLASTX
NCBI GI g2980767
BLAST score 203
E value 1.0e-15
Match length 70
% identity 49

NCBI Description (AL022198) putative protein [Arabidopsis thaliana]

Seq. No. 16121

Contig ID 42995 1.R1040 5'-most EST leu701146892.h1

Method BLASTX
NCBI GI g3023453
BLAST score 261
E value 3.0e-22
Match length 170
% identity 41

NCBI Description CBBY PROTEIN >gi 1825471 (U67781) CbbY [Rhodobacter

sphaeroides]

Seq. No. 16122

Contig ID 42997 1.R1040

5'-most EST LIB3092-051-Q1-K1-B11

Seq. No. 16123

Contig ID 43001 1.R1040

5'-most EST LIB3092-051-Q1-K1-D10

Seq. No. 16124

Contig ID 43005 1.R1040

5'-most EST LIB3109-032-Q1-K1-B6

Method BLASTX
NCBI GI g2827709
BLAST score 1336
E value 1.0e-148
Match length 306
% identity 84

NCBI Description (AL021684) predicted protein [Arabidopsis thaliana]

Seq. No. 16125

Contig ID 43013 1.R1040

5'-most EST LIB3139-022-P1-N1-B12

Method BLASTX NCBI GI 9627469



BLAST score 301 E value 4.0e-27 Match length 163 % identity 11

NCBI Description hypothetical protein 2 - human (fragment)

Seq. No. 16126

Contig ID 43014\_1.R1040

5'-most EST jC-gmle01810070c02a1

Method BLASTX
NCBI GI g2739382
BLAST score 303
E value 2.0e-27
Match length 138
% identity 33

NCBI Description (AC002505) myosin heavy chain-like protein [Arabidopsis

thaliana]

Seq. No. 16127

Contig ID 43018\_1.R1040

5'-most EST jC-gmle01810029c01d1

Seq. No. 16128

Contig ID 43024\_1.R1040

5'-most EST LIB3092-050-Q1-K1-G5

Seq. No. 16129

Contig ID 43029 1.R1040

5'-most EST LIB3093-034-Q1-K1-F7

Method BLASTX
NCBI GI g3334276
BLAST score 811
E value 1.0e-86
Match length 235
% identity 63

NCBI Description AUTOANTIGEN NGP-1 >gi\_179285 (L05425) autoantigen [Homo

sapiens]

Seq. No. 16130

Contig ID 43029\_2.R1040 5'-most EST g5127023

Seq. No. 16131

Contig ID 43040\_1.R1040 5'-most EST kl1701203766.h2

Method BLASTX
NCBI GI g2983147
BLAST score 253
E value 2.0e-21
Match length 96
% identity 51

NCBI Description (AE000692) hypothetical protein [Aquifex aeolicus]

Seq. No. 16132

Contig ID 43045\_1.R1040 5'-most EST leu701152151.h1

Method BLASTX

```
q2330647
NCBI GI
                  826
BLAST score
                  2.0e-88
E value
                  290
Match length
% identity
NCBI Description (Y14557) ribonucleoprotein [Pisum sativum]
                  16133
Seq. No.
                  43045 2.R1040
Contig ID
                  LIB3092-002-Q1-K1-A4
5'-most EST
                  BLASTX
Method
                  g1076305
NCBI GI
                  117
BLAST score
                   2.0e-11
E value
                  73
Match length
                   45
% identity
                  RNA-binding protein cp31 precursor - Arabidopsis thaliana
NCBI Description
                   >gi 681906 dbj_BAA06520_ (D31712) cp31 [Arabidopsis
                   thaliana]
                   16134
Seq. No.
                   43049 1.R1040
Contig ID
                   LIB3092-050-Q1-K1-B5
5'-most EST
                   16135
Seq. No.
                   43061 1.R1040
Contig ID
                   LIB3092-050-Q1-K1-C11
5'-most EST
                   BLASTX
Method
                   q4337025
NCBI GI
BLAST score
                   521
                   4.0e-53
E value
                   136
Match length
% identity
                   (AF123253) AIM1 protein [Arabidopsis thaliana]
NCBI Description
                   16136
Seq. No.
                   43073 1.R1040
Contig ID
                   fde700872886.hl
 5'-most EST
                   BLASTX
Method
                   g629561
NCBI GI
 BLAST score
                   432
                   1.0e-42
 E value
 Match length
                   162
                   51
 % identity
                   SRG1 protein - Arabidopsis thaliana
 NCBI Description
                   >gi_479047_emb_CAA55654_ (X79052) SRG1 [Arabidopsis
                   thaliana]
                   16137
 Seq. No.
                   43076 1.R1040
 Contig ID
                   uC-gmropic030g03b1
 5'-most EST
                   BLASTX
 Method
                   g3695408
 NCBI GI
```

2677

247

87

55

7.0e-21

BLAST score

Match length % identity

E value



NCBI Description (AF096373) contains similarity to Solanum lycopersicum (tomato) wound-induced protein (GB:X59882) [Arabidopsis thaliana] >gi\_4538956\_emb\_CAB39780.1\_ (AL049488) probable wound-induced protein [Arabidopsis thaliana]

Seq. No. 16138

Contig ID 43080 1.R1040

5'-most EST uC-gmflminsoy030h10b1

Seq. No. 16139

Contig ID 43080 2.R1040

5'-most EST LIB3092-050-Q1-K1-A12

Seq. No. 16140

Contig ID 43091\_1.R1040

5'-most EST LIB3092-049-Q1-K1-F5

Method BLASTX
NCBI GI g2245066
BLAST score 256
E value 5.0e-22
Match length 91
% identity 64

NCBI Description (Z97342) Beta-Amylase [Arabidopsis thaliana]

Seq. No. 16141

Contig ID 43093\_1.R1040 5'-most EST rca700996404.h1

Method BLASTX
NCBI GI g1899175
BLAST score 646
E value 2.0e-67
Match length 198
% identity 68

NCBI Description (U90262) calcium-dependent calmodulin-independent protein

kinase CDPK [Cucurbita pepo]

Seq. No. 16142

Contig ID 43095\_1.R1040 5'-most EST ncj700986970.h1

Method BLASTX
NCBI GI g2245029
BLAST score 403
E value 2.0e-39
Match length 141
% identity 54

NCBI Description (297341) limonene cyclase homolog [Arabidopsis thaliana]

Seq. No. 16143

Contig ID 43102 1.R1040

5'-most EST LIB3139-080-P1-N1-B10

Method BLASTX
NCBI GI g3660548
BLAST score 333
E value 1.0e-30
Match length 214
% identity 41

NCBI Description (AB013815) DREB1A [Arabidopsis thaliana]

Match length

% identity

240 77



```
Seq. No.
                  16144
                  43102 2.R1040
Contig ID
5'-most EST
                  sat701002926.h1
Method
                  BLASTX
NCBI GI
                  q3660548
BLAST score
                  392
E value
                  7.0e-38
Match length
                  99
                  76
% identity
                  (AB013815) DREB1A [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  16145
                  43115 1.R1040
Contig ID
5'-most EST
                  zsg701120772.h1
Method
                  BLASTX
NCBI GI
                  g3549626
BLAST score
                  430
E value
                  2.0e-42
Match length
                  173
% identity
                  (AJ009696) wall-associated kinase 1 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  16146
                  43120 1.R1040
Contig ID
5'-most EST
                  kl1701212704.h1
Method
                  BLASTX
                  g4580398
NCBI GI
BLAST score
                  276
                  4.0e-24
E value
Match length
                  80
                  65
% identity
NCBI Description
                  (AC007171) putative protein kinase APK1A [Arabidopsis
                  thaliana]
                  16147
Seq. No.
                  43130 1.R1040
Contig ID
                  LIB3139-077-P1-N1-E10
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4468986
BLAST score
                  309
E value
                   6.0e-28
Match length
                  133
% identity
                  46
NCBI Description
                  (AL035605) putative protein [Arabidopsis thaliana]
Seq. No.
                  16148
                  43140_1.R1040
Contig ID
5'-most EST
                  xpa700795788.h1
Method
                  BLASTX
NCBI GI
                  q2505870
BLAST score
                  567
E value
                  3.0e-97
```

NCBI Description (Y12227) hypothetical protein [Arabidopsis thaliana]



Seq. No. 16149

Contig ID 43140 2.R1040

5'-most EST jC-gmle01810055d05a1

Method BLASTX
NCBI GI g2505870
BLAST score 871
E value 6.0e-94
Match length 214
% identity 81

NCBI Description (Y12227) hypothetical protein [Arabidopsis thaliana]

Seq. No. 16150

Contig ID 43146 1.R1040

5'-most EST uC-gmrominsoy093c01b1

Method BLASTX
NCBI GI g2244835
BLAST score 238
E value 1.0e-19
Match length 133
% identity 43

NCBI Description (Z97337) protein kinase homolog [Arabidopsis thaliana]

Seq. No. 16151

Contig ID 43149\_1.R1040 5'-most EST ncj700980869.h1

Method BLASTX
NCBI GI g1134882
BLAST score 732
E value 1.0e-77
Match length 186
% identity 74

NCBI Description (Z68291) cysteine protease [Pisum sativum]

Seq. No. 16152

Contig ID 43155 1.R1040

5'-most EST LIB3092-008-Q1-K1-B12

Seq. No. 16153

Contig ID 43163\_1.R1040

5'-most EST LIB3138-048-Q1-N1-G11

Method BLASTX
NCBI GI g2832623
BLAST score 770
E value 6.0e-82
Match length 209
% identity 69

NCBI Description (AL021711) protein kinase - like protein [Arabidopsis

thaliana]

Seq. No. 16154

Contig ID 43166 1.R1040

5'-most EST uC-gmflminsoy067a01b1

Method BLASTX
NCBI GI g4544402
BLAST score 1070
E value 1.0e-117
Match length 441



% identity 52

NCBI Description (AC007047) putative leucine rich repeat protein

[Arabidopsis thaliana]

Seq. No.

16155

Contig ID

43170 1.R1040

5'-most EST

LIB3092-048-Q1-K1-C4

Seq. No.

16156

Contig ID 5'-most EST

43171\_1.R1040 gbt700547909.h1

Method NCBI GI BLASTX q2507229

BLAST score

413

E value Match length 2.0e-40 131

% identity

63

NCBI Description

40 KD PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE)

(ROTAMASE) (CYCLOPHILIN-40) (CYP-40) (CYCLOPHILIN-RELATED

PROTEIN) (ESTROGEN RECEPTOR BINDING CYCLOPHILIN) >gi 423247 pir A46579 estrogen receptor-binding

cyclophilin - bovine >gi 393300 dbj BAA03159 (D14074)

cyclophilin [Bos taurus]

Seq. No.

16157

Contig ID

43171 2.R1040

5'-most EST

jC-gmst02400067h07a1

Method BLASTX
NCBI GI g4049344
BLAST score 363
E value 2.0e-34
Match length 90

% identity 77

NCBI Description (AL

(AL034567) putative protein [Arabidopsis thaliana]

Seq. No.

16158

Contig ID 5'-most EST

43177\_1.R1040 zsg701125830.h1

Seq. No.

16159

Contig ID

43190 1.R1040

5'-most EST

LIB3092-047-Q1-K1-G7

Method BLASTN
NCBI GI g3746902
BLAST score 186
E value 1.0e-100
Match length 333

% identity NCBI Description 89
Pisum sativum signal recognition particle 54 kDa subunit precursor (Ffc) mRNA, nuclear gene encoding chloroplast

protein, partial cds

Seq. No.

16160

16161

Contig ID

43192\_1.R1040

5'-most EST

LIB3092-047-Q1-K1-G9

Seq. No.

2681



Contig ID 43208 1.R1040

5'-most EST LIB3170-058-Q1-K1-F12

16162

Method BLASTX
NCBI GI g4335758
BLAST score 394
E value 5.0e-38
Match length 121
% identity 66

NCBI Description (AC006284) unknown protein [Arabidopsis thaliana]

Seq. No.

Contig ID 43208\_2.R1040 5'-most EST ssr700558362.h1

Method BLASTX
NCBI GI g4335758
BLAST score 177
E value 9.0e-13
Match length 64
% identity 59

NCBI Description (AC006284) unknown protein [Arabidopsis thaliana]

Seq. No. 16163

Contig ID 43224 1.R1040

5'-most EST LIB3092-047-Q1-K1-D3

Seq. No. 16164

Contig ID 43229 1.R1040 5'-most EST ncj700983432.h1

Method BLASTX
NCBI GI g3250697
BLAST score 548
E value 5.0e-56
Match length 127
% identity 77

NCBI Description (AL024486) putative protein [Arabidopsis thaliana]

Seq. No. 16165

Contig ID 43239\_1.R1040 5'-most EST trc700563001.h1

Method BLASTX
NCBI GI g2827139
BLAST score 1133
E value 1.0e-124
Match length 300
% identity 74

NCBI Description (AF027172) cellulose synthase catalytic subunit

[Arabidopsis thaliana] >gi\_4049343\_emb\_CAA22568\_ (AL034567) cellulose synthase catalytic subunit (RSW1) [Arabidopsis

thaliana]

Seq. No. 16166

Contig ID 43243\_1.R1040

5'-most EST jC-gmf102220100b08a1

Method BLASTX
NCBI GI g3249084
BLAST score 744
E value 1.0e-78



Match length 23 % identity

NCBI Description (AC004473) Similar to red-1 (related to thioredoxin) gene

gb X92750 from Mus musculus. ESTs gb AA712687 and gb Z37223 come from this gene [Arabidopsis thaliana]

16167 Seq. No.

Contig ID 43243 2.R1040

5'-most EST jC-gmle01810086h04a1

Method BLASTX NCBI GI g3249084 BLAST score 138 E value 2.0e-11 71 Match length 21 % identity

NCBI Description (AC004473) Similar to red-1 (related to thioredoxin) gene

gb X92750 from Mus musculus. ESTs gb AA712687 and

gb Z37223 come from this gene [Arabidopsis thaliana]

16168 Seq. No.

Contig ID 43243 3.R1040 5'-most EST uC-gmropic037e12b1

Seq. No. 16169

43243 7.R1040 Contig ID 5'-most EST fde700871123.h1

Seq. No. 16170

43251 1.R1040 Contig ID

5'-most EST LIB3106-054-Q1-K1-F7

Seq. No. 16171

Contig ID 43253 1.R1040

5'-most EST LIB3092-046-Q1-K1-H1

16172 Seq. No.

43256 1.R1040 Contig ID 5'-most EST pxt700946016.h1

BLASTX Method NCBI GI g2982991 BLAST score 147 E value 9.0e-09 Match length 111 % identity 32

(AE000682) hypothetical protein [Aquifex aeolicus] NCBI Description

Seq. No. 16173

Contig ID 43259 1.R1040 5'-most EST ssr700553663.hl

BLASTX Method NCBI GI g3335366 499 BLAST score 2.0e-50 E value Match length 131 % identity 73

NCBI Description (AC003028) unknown protein [Arabidopsis thaliana]



```
Seq. No.
                  16174
                  43260 1.R1040
Contig ID
5'-most EST
                  bth700844706.h1
Method
                  BLASTX
NCBI GI
                  q4138265
BLAST score
                  1347
E value
                  1.0e-149
Match length
                  269
% identity
                  90
NCBI Description
                  (AJ006228) Avr9 elicitor response protein [Nicotiana
                  tabacum]
Seq. No.
                  16175
                  43266 1.R1040
Contig ID
5'-most EST
                  jex700903406.hl
Seq. No.
                  16176
Contig ID
                  43279 1.R1040
5'-most EST
                  jC-gmf102220080a12d1
                  16177
Seq. No.
Contig ID
                  43279 2.R1040
                  ssr700556462.hl
5'-most EST
Method
                  BLASTX
                  q4234955
NCBI GI
                  787
BLAST score
E value
                  1.0e-83
                  396
Match length
% identity
                  47
                  (AF098971) NBS-LRR-like protein cD8 [Phaseolus vulgaris]
NCBI Description
                  16178
Seq. No.
Contig ID
                  43279 4.R1040
                  fC-gmle7000740303r1
5'-most EST
Method
                  BLASTX
                  q4234955
NCBI GI
BLAST score
                  253
E value
                  7.0e-22
Match length
                  69
                  67
% identity
NCBI Description
                  (AF098971) NBS-LRR-like protein cD8 [Phaseolus vulgaris]
Seq. No.
                  16179
Contig ID
                   43286 1.R1040
                  LIB3092-046-Q1-K1-B5
5'-most EST
                  16180
Seq. No.
                  43287 1.R1040
Contig ID
5'-most EST
                  jC-gmro02910060h12a1
Method
                  BLASTX
                  g4101473
NCBI GI
BLAST score
                  1257
```

1.0e-139 E value Match length 322

77 % identity

(AF003382) KEA1 [Arabidopsis thaliana] NCBI Description



Contig ID 43288\_1.R1040 5'-most EST hrw701059961.h1

Method BLASTX
NCBI GI g4218010
BLAST score 313
E value 1.0e-28
Match length 101
% identity 57

NCBI Description (AC006135) putative sugar transporter [Arabidopsis thaliana] >gi 4309720 gb AAD15490 (AC006439) putative

sugar transporter [Arabidopsis thaliana]

Seq. No. 16182

Contig ID 43302\_1.R1040

5'-most EST uC-gmrominsoy196c12b1

Method BLASTN
NCBI GI g2062705
BLAST score 35
E value 9.0e-10
Match length 37
% identity 39

NCBI Description Human butyrophilin (BTF5) mRNA, complete cds

Seq. No. 16183

Contig ID 43307\_1.R1040 5'-most EST zzp700830319.h1

Method BLASTX
NCBI GI g3337367
BLAST score 255
E value 8.0e-22
Match length 160
% identity 33

NCBI Description (AC004481) hypothetical protein [Arabidopsis thaliana]

Seq. No. 16184

Contig ID 43309 1.R1040 5'-most EST g5677513

Seq. No. 16185

Contig ID 43311\_1.R1040 5'-most EST eep700865534.h1

Seq. No. 16186

Contig ID 43312\_1.R1040

5'-most EST LIB3092-046-Q1-K1-A8

Method BLASTX
NCBI GI g3063694
BLAST score 476
E value 1.0e-47
Match length 152
% identity 68

NCBI Description (AL022537) putative protein [Arabidopsis thaliana]

Seq. No. 16187

Contig ID 43320\_1.R1040 5'-most EST bth700845086.h1

2685



Method BLASTX
NCBI GI g3075390
BLAST score 222
E value 4.0e-18
Match length 122
% identity 43

NCBI Description (AC004484) protein kinase ARSK1 [Arabidopsis thaliana]

Seq. No. 16188

Contig ID 43322 1.R1040

5'-most EST LIB3092-045-Q1-K1-F6

Seq. No. 16189

Contig ID 43326\_1.R1040 5'-most EST wvk700683873.h1

Method BLASTX
NCBI GI g2190540
BLAST score 614
E value 1.0e-63
Match length 167
% identity 66

NCBI Description (AC001229) Similar to Arabidopsis TFL1 (qb U77674).

[Arabidopsis thaliana]

Seq. No. 16190

Contig ID 43333 1.R1040 5'-most EST pmv700895016.h1

Seq. No. 16191

Contig ID 43334\_1.R1040 5'-most EST xpa700793213.h1

Method BLASTX
NCBI GI g2642451
BLAST score 221
E value 8.0e-18
Match length 157
% identity 35

NCBI Description (AC002391) putative indole-3-acetate

beta-glucosyltransferase [Arabidopsis thaliana]

Seq. No. 16192

Contig ID 43336\_1.R1040

5'-most EST LIB3170-022-Q1-J1-F8

Method BLASTX
NCBI GI g2842490
BLAST score 383
E value 7.0e-37
Match length 107
% identity 66

NCBI Description (AL021749) heat-shock protein [Arabidopsis thaliana]

Seq. No. 16193

Contig ID 43338\_1.R1040

5'-most EST LIB3093-012-Q1-K1-E8

Method BLASTX NCBI GI g3402711 BLAST score 489



E value 6.0e-49 Match length 247 % identity 44

NCBI Description (AC004261) putative RNA-binding protein [Arabidopsis

thaliana]

Seq. No. 16194

Contig ID 43347\_1.R1040 5'-most EST rlr700896179.h1

Seq. No. 16195

Contig ID 43352 1.R1040

5'-most EST LIB3107-054-Q1-K1-B6

Method BLASTX
NCBI GI g3176687
BLAST score 1030
E value 1.0e-112
Match length 266
% identity 71

NCBI Description (AC003671) Strong similarity to trehalose-6-phosphate

synthase homolog from A. thaliana chromosome 4 contig gb\_Z97344. ESTs gb\_H37594, gb\_R65023, gb\_H37578 and gb\_R64855 come from this gene. [Arabidopsis thaliana]

Seq. No. 16196

Contig ID 43357 1.R1040

5'-most EST LIB3092-045-Q1-K1-C4

Seq. No. 16197

Contig ID 43359 1.R1040

5'-most EST LIB3107-004-Q1-K1-C7

Method BLASTX
NCBI GI g2623299
BLAST score 817
E value 4.0e-87
Match length 359
% identity 51

NCBI Description (AC002409) hypothetical protein [Arabidopsis thaliana]

Seq. No. 16198

Contig ID 43359\_3.R1040 5'-most EST ncj700975108.h1

Seq. No. 16199

Contig ID 43366\_1.R1040

5'-most EST LIB3092-044-Q1-K1-H3

Method BLASTX
NCBI GI g2911075
BLAST score 385
E value 4.0e-37
Match length 128
% identity 56

NCBI Description (AL021960) putative protein [Arabidopsis thaliana]

Seq. No. 16200

Contig ID 43383\_1.R1040 5'-most EST rlr700895541.h1



Method BLASTX NCBI GI q3341699 BLAST score 224 E value 3.0e-18 Match length 124 % identity 36

(AC003672) putative giberellin beta-hydroxylase NCBI Description

[Arabidopsis thaliana]

Seq. No. 16201

43387 1.R1040 Contig ID 5'-most EST  $asn70\overline{1}131165.h1$ 

BLASTX Method NCBI GI g2623298 BLAST score 633 E value 3.0e-66 Match length 171 % identity

NCBI Description (AC002409) putative 4-alpha-glucanotransferase [Arabidopsis

16202 Seq. No.

43392 1.R1040 Contig ID 5'-most EST ncj700984231.hl

Seq. No. 16203

Contig ID 43395 1.R1040

5'-most EST LIB3109-035-Q1-K4-F1

Method BLASTX q2443757 NCBI GI BLAST score 352 E value 3.0e-33 Match length 94

% identity 68

NCBI Description (AF020434) cyclophilin [Arabidopsis thaliana]

16204 Seq. No.

43399 1.R1040 Contig ID 5'-most EST g5510270 Method BLASTX NCBI GI g3834316 BLAST score 507 E value 4.0e-51 Match length 164 % identity

NCBI Description (AC005679) Similar to qb X16648 pathogenesis related

protein from Hordeum vulgare. EST gb Z18206 comes from

this gene. [Arabidopsis thaliana]

Seq. No. 16205

Contig ID 43399 2.R1040

5'-most EST LIB3093-009-Q1-K1-E3

Method BLASTX NCBI GI q1346809 BLAST score 376 4.0e-36 E value Match length 146

2688



Seq. No. 16206

Contig ID 43399 3.R1040 5'-most EST uaw700666458.h1

Method BLASTX
NCBI GI g1346809
BLAST score 155
E value 8.0e-22
Match length 112
% identity 54

NCBI Description PATHOGEN-RELATED PROTEIN >gi\_499074\_emb\_CAA34641\_ (X16648)

pathogenesis related protein [Hordeum vulgare]

Seq. No. 16207

Contig ID 43400\_1.R1040 5'-most EST ekl700968134.h1

Method BLASTX
NCBI GI g2244952
BLAST score 728
E value 7.0e-77
Match length 186
% identity 76

NCBI Description (Z97340) strong similarity to ZK688.3 protein -

Caenorhabditis elegans [Arabidopsis thaliana]

Seq. No. 16208

Contig ID 43415 1.R1040

5'-most EST LIB3092-044-Q1-K1-F12

Method BLASTX
NCBI GI g2244878
BLAST score 408
E value 8.0e-40
Match length 123
% identity 72

NCBI Description (Z97338) hypothetical protein [Arabidopsis thaliana]

Seq. No. 16209

Contig ID 43416\_1.R1040 5'-most EST zpv700759646.h1

Seq. No. 16210

Contig ID 43423 1.R1040 5'-most EST LIB3092-044-Q1-K1-C4

Method BLASTX
NCBI GI g2598575
BLAST score 807
E value 1.0e-92
Match length 237
% identity 73

NCBI Description (Y15293) MtN21 [Medicago truncatula]

Seq. No. 16211

Contig ID 43425 1.R1040

5'-most EST LIB3092-044-Q1-K1-C6



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16212
Seq. No.
                   43432 1,R1040
Contig ID
5'-most EST
                   smc70\overline{0}747462.h1
                  16213
Seq. No.
Contig ID
                   43437 1.R1040
                  LIB3092-044-Q1-K1-A5
5'-most EST
Seq. No.
                   16214
Contig ID
                   43449 1.R1040
5'-most EST
                  LIB3138-124-Q1-N1-F6
Method
                   BLASTX
NCBI GI
                   q1082340
BLAST score
                   414
E value
                   6.0e-40
Match length
                   222
% identity
                   43
                  DNA-binding protein R kappa B - human
NCBI Description
                   >gi 695579 emb CAA56846 (X80878) R kappa B [Homo sapiens]
Seq. No.
                   16215
Contig ID
                   43449 2.R1040
5'-most EST
                   jC-gmf102220099f08d1
Seq. No.
                   16216
Contig ID
                   43453 1.R1040
5'-most EST
                   uC-gmrominsoy222c01b1
Method
                   BLASTN
                   g21895
NCBI GI
BLAST score
                   72
                   4.0e-32
E value
                   91
Match length
% identity
                   100
NCBI Description T.aestivum (clone pTAU2.3) U2 snRNA
Seq. No.
                   16217
                   43467 1.R1040
Contig ID
                   vwf70\overline{0}679835.h1
5'-most EST
                   BLASTN
Method
NCBI GI
                   g4220638
BLAST score
                   48
E value
                   1.0e-17
Match length
                   386
% identity
                   83
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MIF21, complete sequence [Arabidopsis thaliana]
```

Contig ID 43469\_1.R1040

5'-most EST LIB3093-013-Q1-K1-F4

Seq. No. 16219

Contig ID 43479 1.R1040 5'-most EST awf700839495.h1

Seq. No. 16220



Contig ID 43503\_1.R1040

5'-most EST jC-gmle01810047b07d1

Seq. No. 16221

Contig ID 43503\_2.R1040 5'-most EST yza700763942.h1

Seq. No. 16222

Contig ID 43517\_1.R1040 5'-most EST pxt700943995.h1

Method BLASTN
NCBI GI g4210834
BLAST score 192
E value 1.0e-103
Match length 379
% identity 88

NCBI Description Pisum sativum mRNA for ketol-acid reductoisomerase

Seq. No. 16223

Contig ID 43526\_1.R1040 5'-most EST dpv701100243.h1

Method BLASTX
NCBI GI g4038036
BLAST score 360
E value 7.0e-34
Match length 293
% identity 39

NCBI Description (AC005936) unknown protein [Arabidopsis thaliana]

Seq. No. 16224

Contig ID 43527 1.R1040 5'-most EST q4260136 Method BLASTX g3395436 NCBI GI BLAST score 296 1.0e-26 E value Match length 71 72 % identity

NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]

Seq. No. 16225

Contig ID 43528\_1.R1040 5'-most EST epx701104533.h1

Method BLASTX
NCBI GI 94056456
BLAST score 328
E value 2.0e-30
Match length 74
% identity 85

NCBI Description (AC005990) Strong similarity to gb\_U20808 auxin-induced

protein from Vigna radiata and a member of the zinc-binding dehydrogenase family PF\_00107. ESTs gb\_T43674, gb\_H77006 and gb AA395179 come from this gene. [Arabidopsis thaliana]

Seq. No. 16226

Contig ID 43528\_2.R1040

5'-most EST jC-gmle01810025d06a1



Contig ID 43530 1.R1040

5'-most EST LIB3106-068-P1-K1-A11

Method BLASTX
NCBI GI g1421730
BLAST score 2129
E value 0.0e+00
Match length 505
% identity 78

NCBI Description (U43082) RF2 [Zea mays]

Seq. No. 16228

Contig ID 43531\_1.R1040 5'-most EST leu701155490.h1

Method BLASTX
NCBI GI g1652327
BLAST score 316
E value 1.0e-28
Match length 198
% identity 39

NCBI Description (D90904) hypothetical protein [Synechocystis sp.]

Seq. No. 16229

Contig ID 43534\_1.R1040 5'-most EST txt700735452.h1

Method BLASTX
NCBI GI g3121837
BLAST score 1840
E value 0.0e+00
Match length 418
% identity 82

NCBI Description PHOSPHATIDATE CYTIDYLYLTRANSFERASE (CDP-DIGLYCERIDE

SYNTHETASE) (CDP-DIGLYCERIDE PYROPHOSPHORYLASE)

(CDP-DIACYLGLYCEROL SYNTHASE) (CDS) (CTP:PHOSPHATIDATE

CYTIDYLYLTRANSFERASE) (CDP-DAG SYNTHASE)

>gi\_2182104\_emb\_CAA63004\_ (X91909) CDP-diacylglycerol

synthetase [Solanum tuberosum]

Seq. No. 16230

Contig ID 43534\_2.R1040 5'-most EST fua701039367.h1

Method BLASTX
NCBI GI g3121837
BLAST score 384
E value 6.0e-37
Match length 97
% identity 78

NCBI Description PHOSPHATIDATE CYTIDYLYLTRANSFERASE (CDP-DIGLYCERIDE

SYNTHETASE) (CDP-DIGLYCERIDE PYROPHOSPHORYLASE)

(CDP-DIACYLGLYCEROL SYNTHASE) (CDS) (CTP:PHOSPHATIDATE

CYTIDYLYLTRANSFERASE) (CDP-DAG SYNTHASE)

>gi\_2182104\_emb\_CAA63004\_ (X91909) CDP-diacylglycerol

synthetase [Solanum tuberosum]

Seq. No. 16231

Contig ID 43544 1.R1040



```
5'-most EST
                  LIB3092-042-Q1-K1-E1
                  16232
Seq. No.
                  43554 1.R1040
Contig ID
5'-most EST
                  LIB3106-042-Q1-K1-E5
                  BLASTX
Method
NCBI GI
                  q2828292
BLAST score
                  401
E value
                  7.0e-39
Match length
                  115
% identity
                  70
NCBI Description
                  (AL021687) neoxanthin cleavage enzyme-like protein
                  [Arabidopsis thaliana]
                  16233
Seq. No.
                  43556 1.R1040
Contig ID
5'-most EST
                  LIB3092-042-Q1-K1-F3
Method
                  BLASTX
NCBI GI
                  g2129752
BLAST score
                  333
                  7.0e-31
E value
Match length
                  111
% identity
                  58
NCBI Description thioredoxin - Arabidopsis thaliana >gi 992964 emb CAA84612
                  (Z35475) thioredoxin [Arabidopsis thaliana]
Seq. No.
                  16234
Contig ID
                  43559 1.R1040
5'-most EST
                  jC-gmro02910063h03a1
Seq. No.
                  16235
Contig ID
                  43570 1.R1040
5'-most EST
                  LIB3107-028-Q1-K1-B11
Method
                  BLASTX
NCBI GI
                  q4415931
BLAST score
                  468
E value
                  1.0e-46
Match length
                  140
% identity
                  63
NCBI Description
                  (AC006418) unknown protein [Arabidopsis thaliana]
                  >gi_4559393_gb_AAD23053.1_AC006526_18 (AC006526) unknown
                  protein [Arabidopsis thaliana]
Seq. No.
                  16236
Contig ID
                  43576 1.R1040
5'-most EST
                  awf700838109.h1
Method
                  BLASTX
NCBI GI
                  g2062175
BLAST score
                  253
E value
                  8.0e-22
Match length
                  91
% identity
```

Contig ID 43586 1.R1040

5'-most EST LIB3092-042-Q1-K1-A8

NCBI Description (AC001645) hypothetical protein [Arabidopsis thaliana]



Method BLASTX
NCBI GI g1483232
BLAST score 596
E value 1.0e-61
Match length 147
% identity 80

NCBI Description (X99655) MADS5 protein [Betula pendula]

Seq. No. 16238

Contig ID 43586\_2.R1040 5'-most EST nsy700645658.h1

Method BLASTN
NCBI GI g1483231
BLAST score 134
E value 5.0e-69
Match length 294
% identity 86

NCBI Description B.pendula mRNA for MADS box protein, MADS5

Seq. No. 16239

Contig ID 43586\_3.R1040 5'-most EST leu701146334.h1

Method BLASTN
NCBI GI g2618603
BLAST score 60
E value 3.0e-25
Match length 96
% identity 91

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MSL3, complete sequence [Arabidopsis thaliana]

Seq. No. 16240

Contig ID 43586\_4.R1040

5'-most EST uC-gmflminsoy011d04b1

Method BLASTN
NCBI GI g1004364
BLAST score 64
E value 1.0e-27
Match length 124
% identity 88

NCBI Description Arabidopsis thaliana agamous-like 8 (AGL8) mRNA, complete

cds

Seq. No. 16241

Contig ID 43595\_1.R1040

5'-most EST LIB3106-109-Q1-K1-G1

Method BLASTX
NCBI GI g2191172
BLAST score 176
E value 2.0e-12
Match length 43
% identity 70

NCBI Description (AF007270) contains similarity to GATA-type zinc fingers

(PS:PS00344) [Arabidopsis thaliana]

Seq. No. 16242

Contig ID 43595\_2.R1040



5'-most EST xpa700797389.hl

Seq. No. 16243

Contig ID 43595\_3.R1040 5'-most EST zzp700835346.h1

Method BLASTX
NCBI GI g4538944
BLAST score 169
E value 6.0e-12
Match length 40
% identity 70

NCBI Description (AL049483) putative transcription factor [Arabidopsis

thaliana]

Seq. No. 16244

Contig ID 43599\_1.R1040 5'-most EST rlr700897812.h1

Method BLASTX
NCBI GI g3258570
BLAST score 828
E value 1.0e-88
Match length 237
% identity 69

NCBI Description (U89959) Unknown protein [Arabidopsis thaliana]

Seq. No. 16245

Contig ID 43606\_1.R1040 5'-most EST wrg700790637.h2

Method BLASTX
NCBI GI g2827992
BLAST score 713
E value 3.0e-75
Match length 254
% identity 53

NCBI Description (AF034743) UDP-glucuronosyltransferase [Pisum sativum]

Seq. No. 16246

Contig ID 43621\_1.R1040

5'-most EST LIB3092-041-Q1-K1-D1

Seq. No. 16247

Contig ID 43625\_1.R1040

5'-most EST jC-gmf102220057f08a1

Seq. No. 16248

Contig ID 43632 1.R1040

5'-most EST LIB3092-040-Q1-K1-G5

Method BLASTX
NCBI GI g2435514
BLAST score 341
E value 4.0e-32
Match length 136
% identity 53

NCBI Description (AF024504) Similar to serine/threonine protein kinase;

coded for by A. thaliana cDNA T20930; coded for by A.

thaliana cDNA T43472 [Arabidopsis thaliana]



```
Seq. No. 16249
Contig ID 43642_1.R1040
```

5'-most EST LIB3092-041-01-K1-A10

Seq. No. 16250

Contig ID 43645\_1.R1040

5'-most EST uC-gmflminsoy055g09b1

Method BLASTX
NCBI GI g2911044
BLAST score 363
E value 4.0e-41
Match length 219
% identity 48

NCBI Description (AL021961) putative protein [Arabidopsis thaliana]

Seq. No. 16251

Contig ID 43648\_1.R1040

5'-most EST jC-gmf102220106e08a1

Method BLASTX
NCBI GI g2736186
BLAST score 1595
E value 1.0e-178
Match length 394
% identity 78

NCBI Description (AF024623) galactose kinase [Arabidopsis thaliana]

Seq. No.

Contig ID 43648\_2.R1040

5'-most EST LIB3092-040-Q1-K1-D1

16252

Method BLASTX
NCBI GI g2736186
BLAST score 775
E value 2.0e-82
Match length 201
% identity 75

NCBI Description (AF024623) galactose kinase [Arabidopsis thaliana]

Seq. No. 16253

Contig ID 43648 3.R1040

5'-most EST jC-gmle01810064d01d1

Method BLASTX
NCBI GI g2736186
BLAST score 180
E value 3.0e-13
Match length 53
% identity 68

NCBI Description (AF024623) galactose kinase [Arabidopsis thaliana]

Seq. No. 16254

Contig ID 43653\_1.R1040

5'-most EST LIB3092-040-Q1-K1-D8

Seq. No. 16255

Contig ID 43655 1.R1040 5'-most EST g4307423 Method BLASTX NCBI GI g4371280



BLAST score 437 E value 4.0e-43 Match length 104 % identity 83

NCBI Description (AC006260) hypothetical protein [Arabidopsis thaliana]

Seq. No. Contig ID

16256 43658 1.R1040

5'-most EST

LIB3092-040-Q1-K1-F10

Seq. No.

16257

Contig ID 5'-most EST

43658\_3.R1040 jex700907142.h1

Seq. No.

16258

Contig ID

43658\_4.R1040

5'-most EST

jC-gmf102220061f06d1

Method NCBI GI BLAST score BLASTN g2654107 49

BLAST score E value Match length

2.0e-18 125

% identity NCBI Description 85 Pisum sativum cytosine-5 DNA methyltransferase mRNA,

complete cds

Seq. No.

16259

Contig ID

43660 1.R1040

5'-most EST

uC-gmflminsoy001e02b1

Method NCBI GI BLAST score BLASTX g3687389 973

E value Match length 1.0e-105 228

% identity

86

NCBI Description

(Y16124) putative cullin protein [Lycopersicon esculentum]

Seq. No.

16260

Contig ID

43672 1.R1040

5'-most EST

LIB3092-040-Q1-K1-B2

Method NCBI GI BLAST score BLASTX g1345132 607

BLAST score E value Match length

4.0e-79 210

75

% identity NCBI Description

(U47029) ERECTA [Arabidopsis thaliana]

>gi\_1389566\_dbj\_BAA11869 (D83257) receptor protein kinase
[Arabidopsis thaliana] >gi\_3075386 (AC004484) receptor

protein kinase, ERECTA [Arabidopsis thaliana]

Seq. No.

16261

Contig ID 5'-most EST 43673\_1.R1040 gsv701046385.h1

Method NCBI GI BLASTX g3046693

BLAST score

465

BLAST score

Match length

E value

444

143

5.0e-44



```
2.0e-46
E value
Match length
                   95
                   87
% identity
NCBI Description
                  (AL022140) receptor like protein (fragment) [Arabidopsis
                  thaliana]
Seq. No.
                   16262
Contig ID
                   43673 2.R1040
5'-most EST
                  leu701150581.h1
Seq. No.
                  16263
                  43679 1.R1040
Contig ID
                  LIB3092-039-Q1-K1-G12
5'-most EST
                  BLASTN
Method
NCBI GI
                  g21004
BLAST score
                  276
E value
                  1.0e-154
Match length
                  360
                   94
% identity
NCBI Description French Bean mRNA for plastid-located glutamine synthetase
                   (EC 6.3.1.2)
                  16264
Seq. No.
Contig ID
                  43683 1.R1040
5'-most EST
                  LIB3092-039-Q1-K1-G6
Method
                  BLASTX
NCBI GI
                  g4309972
BLAST score
                  152
E value
                  2.0e-09
Match length
                  84
% identity
                   46
                 (AC002983) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  16265
Seq. No.
                   43683 2.R1040
Contig ID
5'-most EST
                  kl1701213422.h1
Seq. No.
                  16266
Contig ID
                   43686 1.R1040
5'-most EST
                   zhf700954648.h1
Method
                  BLASTX
NCBI GI
                  g2244905
BLAST score
                   312
E value
                  1.0e-28
Match length
                  129
                   47
% identity
NCBI Description
                  (Z97339) indole-3-acetate beta-glucosyltransferase
                   [Arabidopsis thaliana]
Seq. No.
                  16267
                   43689 1.R1040
Contig ID
5'-most EST
                  fde700875593.h1
                  BLASTX
Method
NCBI GI
                  g3386617
```

% identity NCBI Description (AC004665) putative cell division protein (ftsY) [Arabidopsis thaliana] 16268 Seq. No. 43691 1.R1040 Contig ID uC-gmrominsoy173f09b1 5'-most EST BLASTX Method NCBI GI g4580517 342 BLAST score E value 3.0e-32 Match length 86 % identity 76 NCBI Description (AF036302) scarecrow-like 5 [Arabidopsis thaliana] 16269 Seq. No. 43702 1.R1040 Contig ID 5'-most EST leu701156379.h1 Method BLASTX q4490315 NCBI GI BLAST score 354 E value 5.0e-33 Match length 97 66 % identity NCBI Description (AL035678) hypothetical protein [Arabidopsis thaliana] Seq. No. 16270 Contig ID 43708\_1.R1040 5'-most EST txt700735026.h1 Method BLASTX g4455316 NCBI GI BLAST score 206 E value 5.0e-16 136 Match length NCBI Description (AL035528) putative protein [Arabidopsis thaliana]

% identity

Seq. No. 16271

43714 1.R1040 Contig ID 5'-most EST pcp700990952.h1

16272 Seq. No.

Contig ID 43722 1.R1040

LIB3092-039-Q1-K1-D2 5'-most EST

Method BLASTX NCBI GI g3445204 BLAST score 418 E value 4.0e-41 Match length 116 % identity

NCBI Description (AC004786) putative GTP-binding protein [Arabidopsis

thaliana]

Seq. No. 16273

43730 1.R1040 Contig ID

5'-most EST uC-gmrominsoy217h04b1

Method BLASTX



NCBI GI g4467125
BLAST score 818
E value 1.0e-87
Match length 225
% identity 68

NCBI Description (AL035538) putative protein [Arabidopsis thaliana]

Seq. No. 16274

Contig ID 43733 1.R1040 5'-most EST nsy700645521.hl

Seq. No. 16275

Contig ID 43746\_1.R1040 5'-most EST kl1701210470.h1

Seq. No. 16276

Contig ID 43752\_1.R1040 5'-most EST uC-gmropic007g11b1

Method BLASTX
NCBI GI g3688186
BLAST score 537
E value 6.0e-55
Match length 143
% identity 71

NCBI Description (AL031804) putative protein [Arabidopsis thaliana]

Seq. No. 16277

Contig ID 43758 1.R1040

5'-most EST LIB3092-035-Q1-K1-H9

Seq. No. 16278

Contig ID 43762 1.R1040

5'-most EST LIB3092-038-Q1-K1-B7

Method BLASTX
NCBI GI g3128192
BLAST score 324
E value 4.0e-38
Match length 106
% identity 75

NCBI Description (AC004521) axi 1-like protein [Arabidopsis thaliana]

Seq. No. 16279

Contig ID 43762\_2.R1040 5'-most EST ssr700557514.h1

Seq. No. 16280

Contig ID 43778\_1.R1040 5'-most EST uC-gmropic107g02b1

Seq. No. 16281

Contig ID 43795\_1.R1040

5'-most EST uC-gmrominsoy230d05b1

Method BLASTX
NCBI GI g4519936
BLAST score 144
E value 1.0e-08
Match length 105



% identity 24

NCBI Description (AB019186) RPR1 [Oryza sativa]

Seq. No. 16282

Contig ID 43801\_1.R1040 5'-most EST fC-gmro7000749034a1

Method BLASTX
NCBI GI g2853078
BLAST score 223
E value 7.0e-18
Match length 142
% identity 40

NCBI Description (AL021768) TMV resistance protein N-like [Arabidopsis

thaliana]

Seq. No. 16283

Contig ID 43812 1.R1040

5'-most EST LIB3109-011-Q1-K1-B1

Method BLASTX
NCBI GI g2252863
BLAST score 840
E value 8.0e-98
Match length 350
% identity 54

NCBI Description (AF013294) similar to nucleolin protein [Arabidopsis

thaliana]

Seq. No. 16284

Contig ID 43812 2.R1040

5'-most EST ASG3244V4R-02-Q1-E1-G3

Method BLASTN
NCBI GI g2290120
BLAST score 35
E value 5.0e-10
Match length 55
% identity 91

NCBI Description HIV-1 strain M02 from USA, envelope glycoprotein (env)

gene, partial cds

Seq. No. 16285

Contig ID 43812 3.R1040

5'-most EST jC-gmro02910046b01d1

Seq. No. 16286

Contig ID 43821\_1.R1040 5'-most EST uC-gmropic055g12b1

Method BLASTX
NCBI GI g836954
BLAST score 495
E value 8.0e-50
Match length 192
% identity 53

NCBI Description (U20948) receptor protein kinase [Ipomoea trifida]

Seq. No. 16287

Contig ID 43826\_1.R1040

5'-most EST LIB30 $\overline{9}2$ -037-Q1-K1-E4



Contig ID 43838 1.R1040

5'-most EST LIB3107-017-Q1-K1-E9

Method BLASTX
NCBI GI g114176
BLAST score 1205
E value 1.0e-132
Match length 331
% identity 72

NCBI Description 3-PHOSPHOSHIKIMATE 1-CARBOXYVINYLTRANSFERASE PRECURSOR (5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE SYNTHASE) (EPSP

SYNTHASE) >gi 66620 pir XUPJVS 3-phosphoshikimate

1-carboxyvinyltransferase (EC 2.5.1.19) precursor - garden

petunia >gi 169191 (M21084)

5-enolpyruvylshikimate-3-phosphate synthase precursor

[Petunia hybrida]

Seq. No. 16289

Contig ID 43844\_1.R1040 5'-most EST fde700875202.h1

Method BLASTX
NCBI GI g4417279
BLAST score 395
E value 4.0e-38
Match length 153
% identity 55

NCBI Description (AC007019) hypothetical protein [Arabidopsis thaliana]

Seq. No. 16290

Contig ID 43857 1.R1040

5'-most EST LIB3092-036-Q1-K1-H5

Seq. No. 16291

Contig ID 43861 1.R1040

5'-most EST LIB3092-037-Q1-K1-A1

Seq. No. 16292

Contig ID 43873 1.R1040

5'-most EST LIB31 $\overline{3}$ 8-022-Q1-N1-E3

Seq. No. 16293

Contig ID 43901\_1.R1040 5'-most EST trc700565937.h1

Seq. No. 16294

Contig ID 43901 2.R1040

5'-most EST LIB3092-036-Q1-K1-A11

Seq. No. 16295

Contig ID 43902 1.R1040

5'-most EST LIB30 $\overline{9}2$ -036-Q1-K1-A12

Seq. No. 16296

Contig ID 43905 1.R1040

5'-most EST jC-gmst02400052h12a1

Method BLASTX



NCBI GI q4531444 BLAST score 209 2.0e-16 E value 56 Match length 77 % identity

(AC006224) putative protein kinase [Arabidopsis thaliana] NCBI Description

16297 Seq. No.

43905 2.R1040 Contig ID kmv700740350.h1 5'-most EST

Method BLASTX NCBI GI q4531444 BLAST score 1592 E value 1.0e-178 Match length 371 % identity 80

(AC006224) putative protein kinase [Arabidopsis thaliana] NCBI Description

Seq. No.

16298 43905\_3.R1040 Contig ID

5'-most EST uC-gmrominsoy099b10b1

Method BLASTX NCBI GI g4531444 BLAST score 296 E value 8.0e-27 Match length 85 65 % identity

NCBI Description (AC006224) putative protein kinase [Arabidopsis thaliana]

Seq. No. 16299

43912 1.R1040 Contig ID 5'-most EST eep700869175.h1

Seq. No. 16300

43918 1.R1040 Contig ID 5'-most EST asn701135937.h1

Seq. No. 16301

43919 1.R1040 Contig ID

uC-gmflminsoy046b09b1 5'-most EST

Method BLASTN NCBI GI g3176075 BLAST score 387 0.0e+00E value Match length 1071 % identity 85

NCBI Description Medicago sativa mRNA for protein phosphatase 1, delta

subunit

16302 Seq. No.

Contig ID 43944\_1.R1040

LIB3106-092-Q1-K1-C12 5'-most EST

Method BLASTX NCBI GI q1518860 BLAST score 312 E value 4.0e-28 258 Match length

```
% identity
NCBI Description
                  (U66249) CASP [Mus musculus]
                  16303
Seq. No.
Contig ID
                  43945 1.R1040
5'-most EST
                  LIB3107-026-Q1-K1-E9
Seq. No.
                  16304
Contig ID
                  43954 1.R1040
5'-most EST
                  zzp700832904.h1
Method
                  BLASTX
                  g3894387
NCBI GI
BLAST score
                  1002
                  1.0e-108
E value
Match length
                  657
% identity
                  12
NCBI Description (AF053995) Hcr2-0B [Lycopersicon esculentum]
Seq. No.
                  16305
                  43959 1.R1040
Contig ID
5'-most EST
                  g5058142
                  BLASTX
Method
NCBI GI
                  q4455312
BLAST score
                  478
                  9.0e-48
E value
Match length
                  135
% identity
                   67
NCBI Description (AL035528) DnaJ-like protein [Arabidopsis thaliana]
Seq. No.
                  16306
                   43959 2.R1040
Contig ID
5'-most EST
                  LIB3106-051-Q1-K1-A9
Method
                  BLASTX
NCBI GI
                  g4455312
                  398
BLAST score
E value
                  1.0e-38
Match length
                  106
                   67
% identity
NCBI Description (AL035528) DnaJ-like protein [Arabidopsis thaliana]
Seq. No.
                  16307
Contig ID
                   43963 1.R1040
5'-most EST
                   jC-qmf102220056f07a1
Method
                   BLASTX
```

NCBI GI q2213882 BLAST score 2085

0.0e+00E value 530 Match length % identity 76

NCBI Description (AF004165) 2-isopropylmalate synthase [Lycopersicon

pennellii]

16308 Seq. No.

Contig ID 43966 1.R1040 5'-most EST ssr700553914.hl

Seq. No. 16309



Contig ID 43966\_2.R1040 5'-most EST uC-gmronoir023h12b1 Seq. No. 16310 Contig ID 43970 1.R1040

5'-most EST LIB3092-035-Q1-K1-C11
Method BLASTX
NCBI GI g4335754
BLAST score 535
E value 8.0e-55

E value 8.0e
Match length 140
% identity 72

NCBI Description (AC006284) putative acid phophatase (contains metallo-phosphoesterase motif, prosite: QDOC50185)

[Arabidopsis thaliana]

Seq. No. 16311

Contig ID 43977 1.R1040

5'-most EST LIB3107-031-Q1-K1-A9

Seq. No. 16312

Contig ID 43977\_2.R1040 5'-most EST leu701148694.h1

Seq. No. 16313

Contig ID 44001 1.R1040

5'-most EST LIB3092-034-Q1-K1-G12

Seq. No. 16314

Contig ID 44006 1.R1040

5'-most EST jC-gmle01810043e01a1

Seq. No. 16315

Contig ID 44007\_1.R1040

5'-most EST LIB3092-034-Q1-K1-G9

Seq. No. 16316

Contig ID 44016\_1.R1040 5'-most EST jex700908960.h1

Method BLASTX
NCBI GI g4455360
BLAST score 236
E value 3.0e-27
Match length 154
% identity 5

NCBI Description (AL035524) putative protein [Arabidopsis thaliana]

Seq. No. 16317

Contig ID 44018\_1.R1040 5'-most EST rlr700899192.h1

Seq. No. 16318

Contig ID 44020 1.R1040

5'-most EST LIB3092-034-Q1-K1-E1

Seq. No. 16319

Contig ID 44024\_1.R1040

2705



```
qsv701051235.hl
5'-most EST
                  16320
Seq. No.
                  44045 1.R1040
Contig ID
                  ssr700555341.hl
5'-most EST
                  BLASTX
Method
                  g2252840
NCBI GI
                  486
BLAST score
                  9.0e-49
E value
                  153
Match length
                  56
% identity
                  (AF013293) contains regions of similarity to Haemophilus
NCBI Description
                  influenzae permease (SP:P38767) [Arabidopsis thaliana]
Seq. No.
                  16321
                  44047_1.R1040
Contig ID
                  q5605970
5'-most EST
                  16322
Seq. No.
                  44047 2.R1040
Contig ID
                  trc700562865.hl
5'-most EST
                  16323
Seq. No.
                   44064 1.R1040
Contig ID
                  LIB3092-034-Q1-K1-B12
5'-most EST
                   16324
Seq. No.
                   44067 1.R1040
Contig ID
5'-most EST
                   LIB3092-033-Q1-K1-E8
                   16325
Seq. No.
                   44068 1.R1040
Contig ID
                   LIB3092-033-Q1-K1-F4
5'-most EST
Method
                   BLASTX
                   q3540206
NCBI GI
BLAST score
                   228
                   7.0e-19
E value
                   97
Match length
                   31
% identity
NCBI Description (AC004260) Hypothetical protein [Arabidopsis thaliana]
                   16326
Seq. No.
Contig ID
                   44070 1.R1040
                   LIB3092-033-Q1-K1-F8
5'-most EST
                   16327
Seq. No.
                   44076 1.R1040
Contig ID
                   LIB3092-033-Q1-K1-G3
 5'-most EST
                   BLASTX
Method
                   q2500649
NCBI GI
                   263
 BLAST score
                   8.0e-23
 E value
                   173
Match length
```

(RNA-3'-PHOSPHATE CYCLASE) (RNA CYCLASE)

NCBI Description PROBABLE RNA 3'-TERMINAL PHOSPHATE CYCLASE

36

% identity



Contig ID 44078 1.R1040

5'-most EST LIB3092-033-Q1-K1-G7

Seq. No. 16329

Contig ID 44078\_2.R1040 5'-most EST uC-gmropic066h01b1

Seq. No. 16330

Contig ID 44085\_1.R1040 5'-most EST pmv700890905.h1

Seq. No. 16331

Contig ID 44088 1.R1040

5'-most EST LIB3092-033-Q1-K1-D4

Seq. No. 16332

Contig ID 44090\_1.R1040 5'-most EST txt700735094.h1

Seq. No. 16333

Contig ID 44106\_1.R1040

5'-most EST uC-gmrominsoy044g10b1

Method BLASTX
NCBI GI g2262107
BLAST score 780
E value 4.0e-83
Match length 180

Match length 180 % identity 81

NCBI Description (AC002343) Ser/Thr protein kinase isolog [Arabidopsis

thaliana]

16334

Seq. No.

Contig ID 44106\_2.R1040

5'-most EST LIB3138-024-Q1-N1-E4

Method BLASTX
NCBI GI g2262107
BLAST score 233
E value 2.0e-19

Match length 60 % identity 77

NCBI Description (AC002343) Ser/Thr protein kinase isolog [Arabidopsis

thaliana]

Seq. No.

16335

Contig ID 44108\_1.R1040

5'-most EST LIB3092-033-Q1-K1-C10

Seq. No.

16336

Contig ID 44108\_2.R1040 5'-most EST ssr700554446.h1

Seq. No.

16337

Contig ID 5'-most EST

44118\_1.R1040 vzy700754257.h1

Method BLASTN NCBI GI g3600062



BLAST score 118 E value 1.0e-59 Match length 322 % identity 86

NCBI Description Arabidopsis thaliana BAC T25C13

Seq. No. 16338

Contig ID 44120\_1.R1040 5'-most EST awf700843191.h1 Method BLASTX

NCBI GI g4544451
BLAST score 325
E value 3.0e-55
Match length 160
% identity 67

NCBI Description (AC006592) unknown protein [Arabidopsis thaliana]

Seq. No. 16339

Contig ID 44122 1.R1040

5'-most EST LIB3092-032-Q1-K1-H6

Method BLASTX
NCBI GI g2739368
BLAST score 223
E value 3.0e-18
Match length 54
% identity 78

NCBI Description (AC002505) cyclin-like protein [Arabidopsis thaliana]

Seq. No. 16340

Contig ID 44128\_1.R1040

5'-most EST LIB3092-033-Q1-K1-A11

Method BLASTX
NCBI GI g3776559
BLAST score 466
E value 2.0e-46
Match length 147
% identity 62

NCBI Description (AC005388) Strong similarity to gene F14J9.26 gi 3482933

cdc2 protein kinase homolog from A. thaliana BAC

gb\_AC003970. ESTs gb\_Z35332 and gb\_F19907 come from this

gene. [Arabidopsis thaliana]

Seq. No. 16341

Contig ID 44130\_1.R1040 5'-most EST zlv700807511.h1

Seq. No. 16342

Contig ID 44132\_1.R1040 5'-most EST uC-gmropic018d02b1

Seq. No. 16343

Contig ID 44142 1.R1040

5'-most EST LIB3092-032-Q1-K1-G10

Seq. No. 16344

Contig ID 44147\_1.R1040

5'-most EST LIB3092-032-Q1-K1-G6

BLAST score

Match length

% identity

E value

289 1.0e-162

337

96



16345 Seq. No. 44150 1.R1040 Contig ID  $jC-gm\overline{l}e01810093f06a1$ 5'-most EST BLASTX Method q4415924 NCBI GI 388 BLAST score 2.0e-37 E value 131 Match length 56 % identity (AC006282) putative glucosyl transferase [Arabidopsis NCBI Description thaliana] 16346 Seq. No. 44169 1.R1040 Contig ID LIB3092-032-Q1-K1-B2 5'-most EST BLASTX Method q4415923 NCBI GI 296 BLAST score 1.0e-26 E value 144 Match length 49 % identity (AC006282) putative glucosyl transferase [Arabidopsis NCBI Description thaliana] 16347 Seq. No. 44187 1.R1040 Contig ID LIB3167-077-P1-K2-A12 5'-most EST BLASTX Method g631955 NCBI GI 305 BLAST score 1.0e-27 E value 141 Match length 45 % identity chlorophyll a/b binding protein type II (LHCI) - Lolium NCBI Description temulentum L 16348 Seq. No. 44192\_1.R1040 Contig ID uC-gmronoir060h04b1 5'-most EST BLASTX Method q4481810 NCBI GI 293 BLAST score 5.0e-26 E value 274 Match length 29 % identity (AL035632) BACN32G11.d [Drosophila melanogaster] NCBI Description 16349 Seq. No. 44199 1.R1040 Contig ID LIB3092-032-Q1-K1-A4 5'-most EST Method BLASTN g2055227 NCBI GI

2709



NCBI Description Glycine max mRNA for SRC1, complete cds

Seq. No. 16350

Contig ID 44210 1.R1040

5'-most EST LIB3138-014-Q1-N2-B4

Seq. No. 16351

Contig ID 44220 1.R1040

5'-most EST LIB3092-012-Q1-K1-D11

Method BLASTX
NCBI GI g2827558
BLAST score 290
E value 9.0e-26
Match length 89
% identity 64

NCBI Description (AL021635) putative DNA binding protein [Arabidopsis

thaliana]

Seq. No. 16352

Contig ID 44224\_1.R1040

5'-most EST LIB3138-100-Q1-N1-B7

Method BLASTX
NCBI GI g4263703
BLAST score 970
E value 1.0e-105
Match length 231

% identity 78

NCBI Description (AC006223) hypothetical protein [Arabidopsis thaliana]

Seq. No. 16353

Contig ID 44230\_1.R1040 5'-most EST hyd700726102.h1

Seq. No. 16354

Contig ID 44240\_1.R1040

5'-most EST LIB3092-030-Q1-K1-G3

Seq. No. 16355

Contig ID 44252 1.R1040 5'-most EST zpv700759579.h1

Method BLASTX
NCBI GI g4388717
BLAST score 347
E value 2.0e-57
Match length 329
% identity 41

NCBI Description (AC006413) putative nuclear phosphoprotein (contains

multiple TPR repeats prosite:QDOC50005) [Arabidopsis

thaliana]

Seq. No. 16356

Contig ID 44265\_1.R1040 5'-most EST trc700564406.h1

Method BLASTX
NCBI GI 94455186
BLAST score 276
E value 4.0e-24

```
Match length
                  146
% identity
                   48
NCBI Description (AL035521) putative protein [Arabidopsis thaliana]
Seq. No.
                  16357
Contig ID
                  44279 1.R1040
5'-most EST
                  pmv700888832.h1
Method
                  BLASTX
NCBI GI
                  g1653702
BLAST score
                  486
E value
                  1.0e-48
Match length
                  138
% identity
                  68
NCBI Description
                  (D90915) dihydrolipoamide acetyltransferase component (E2)
                  of pyruvate dehydrogenase complex [Synechocystis sp.]
                  16358
Seq. No.
                  44281 2.R1040
Contig ID
5'-most EST
                  bth700844559.h1
                  16359
Seq. No.
Contig ID
                  44282 1.R1040
5'-most EST
                  gsv701050704.h1
Method
                  BLASTX
NCBI GI
                  q586858
BLAST score
                  244
E value
                  2.0e-20
Match length
                  88
% identity
                  51
NCBI Description
                  >gi 2127020_pir__S66042 hypothetical protein - Bacillus
```

HYPOTHETICAL 21.4 KD PROTEIN IN DACA-SERS INTERGENIC REGION

subtilis >gi\_467402\_dbj\_BAA05248\_ (D26185) unknown [Bacillus subtilis] >gi 2632279 emb CAB11788 (Z99104) similar to hypothetical proteins [Bacillus subtilis]

Seq. No. 16360

Contig ID 44302 1.R1040

5'-most EST LIB3092-029-Q1-K1-B12

Method BLASTX NCBI GI g3775989 BLAST score 181 E value 3.0e-13 47 Match length 74 % identity

NCBI Description (AJ010458) RNA helicase [Arabidopsis thaliana]

Seq. No. 16361

Contig ID 44307 1.R1040

5'-most EST LIB3092-029-Q1-K1-B8

Method BLASTN NCBI GI q535443 BLAST score 38 E value 1.0e-11 38 Match length 100 % identity

NCBI Description Pisum sativum Alaska calmodulin mRNA, complete cds

Match length

% identity

134

81



```
16362
Seq. No.
                  44315 1.R1040
Contig ID
                  epx701107356.h1
5'-most EST
Seq. No.
                  16363
                  44324 1.R1040
Contig ID
                  uC-qmrominsoy198h09b1
5'-most EST
                  BLASTX
Method
                  q3445212
NCBI GI
BLAST score
                  913
                  9.0e-99
E value
                  253
Match length
                  73
% identity
                  (AC004786) putative chloroplast envelope Ca2+-ATPase
NCBI Description
                   [Arabidopsis thaliana]
                  16364
Seq. No.
                  44326 1.R1040
Contig ID
                  pmv700894906.h1
5'-most EST
Seq. No.
                  16365
                   44341 1.R1040
Contig ID
                  LIB3092-028-Q1-K1-E8
5'-most EST
                  BLASTX
Method
                   g1813489
NCBI GI
BLAST score
                   147
                   3.0e-09
E value
Match length
                   79
% identity
                   44
NCBI Description (U64312) amidase [Bacillus firmus]
                   16366
Seq. No.
                   44343 1.R1040
Contig ID
                   jC-gmle01810037c11a2
5'-most EST
                   16367
Seq. No.
                   44346 1.R1040
Contig ID
                   LIB3092-027-Q1-K1-H10
5'-most EST
                   BLASTN
Method
                   g2687432
NCBI GI
                   34
BLAST score
                   2.0e-09
E value
                   38
Match length
                   97
% identity
NCBI Description Plumbago auriculata large subunit 26S ribosomal RNA gene,
                   partial sequence
                   16368
Seq. No.
Contig ID
                   44353 1.R1040
                   vzy700752351.h1
5'-most EST
Method
                   BLASTX
                   q4455302
NCBI GI
                   476
BLAST score
                   1.0e-58
E value
```

NCBI Description (AL035528) putative protein [Arabidopsis thaliana]



```
16369
Seq. No.
                  44361_1.R1040
Contig ID
                  ssr700555015.hl
5'-most EST
Method
                  BLASTN
                  q3869075
NCBI GI
BLAST score
                  54
                  2.0e-21
E value
Match length
                  148
                  88
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MXK3, complete sequence [Arabidopsis thaliana]
                  16370
Seq. No.
                  44368 1.R1040
Contig ID
                  jC-gmst02400016a09d1
5'-most EST
                  BLASTX
Method
                  q4454043
NCBI GI
BLAST score
                  462
                  4.0e-46
E value
Match length
                  134
% identity
                  70
                  (AL035394) putative receptor kinase [Arabidopsis thaliana]
NCBI Description
                  16371
Seq. No.
                   44381 1.R1040
Contig ID
                  sat701003320.h1
5'-most EST
                  16372
Seq. No.
                   44381 2.R1040
Contig ID
                  LIB3170-054-Q1-J1-D6
5'-most EST
                   16373
Seq. No.
                   44382 1.R1040
Contig ID
                   LIB3092-022-Q1-K1-H9
5'-most EST
                   16374
Seq. No.
                   44382 2.R1040
Contig ID
                   wvk700682053.h1
5'-most EST
                   16375
Seq. No.
                   44386 1.R1040
Contig ID
                   jC-gmro02800041d06a1
5'-most EST
                   BLASTX
Method
                   q4467125
NCBI GI
                   1151
BLAST score
                   1.0e-126
E value
                   300
Match length
 % identity
                   72
NCBI Description (AL035538) putative protein [Arabidopsis thaliana]
```

Contig ID 44389\_1.R1040 5'-most EST leu701151303.h1

Method BLASTX
NCBI GI g4337040
BLAST score 1190



1.0e-131 E value 360 Match length 66 % identity

(AF124159) molybdopterin synthase sulphurylase [Arabidopsis NCBI Description thaliana] >gi\_4337042 gb\_AAD18051 (AF124160) molybdopterin

synthase sulphurylase [Arabidopsis thaliana]

16377 Seq. No.

44389 2.R1040 Contig ID zhf700953230.h1 5'-most EST

BLASTX Method g4337046 NCBI GI 229 BLAST score 6.0e-19 E value Match length 90 59 % identity

(AF124162) molybdopterin synthase sulphurylase [Nicotiana NCBI Description

plumbaginifolia]

16378 Seq. No.

44393\_1.R1040 Contig ID zsg701124432.h1 5'-most EST

BLASTX Method q4490316 NCBI GI BLAST score 456 3.0e-45 E value 196 Match length 46 % identity

(AL035678) nucellin-like protein [Arabidopsis thaliana] NCBI Description

16379 Seq. No.

44393 2.R1040 Contig ID zsq701118166.hl 5'-most EST

BLASTX Method q4490316 NCBI GI BLAST score 236 E value 1.0e-19 Match length 77

% identity

(AL035678) nucellin-like protein [Arabidopsis thaliana] NCBI Description

Seq. No. 16380

44393 4.R1040 Contig ID gsv701051353.h1 5'-most EST

Method BLASTX g4490316 NCBI GI BLAST score 188 E value 8.0e-23 111 Match length % identity 53

(AL035678) nucellin-like protein [Arabidopsis thaliana] NCBI Description

Seq. No.

44398 1.R1040 Contig ID

jC-gmle01810034b09a2 5'-most EST

16381

BLASTX Method g3024871 NCBI GI



BLAST score 1.0e-117 E value 542 Match length % identity 44

HYPOTHETICAL 77.3 KD PROTEIN SLL0005 NCBI Description

>gi\_1001579\_dbj\_BAA10206\_ (D64000) ABC1-like [Synechocystis

sp.]

16382 Seq. No.

44399\_1.R1040 Contig ID

LIB3092-022-Q1-K1-F9 5'-most EST

16383 Seq. No.

44402 1.R1040 Contig ID

uC-gmrominsoy093g03b1 5'-most EST

BLASTX Method g3335060 NCBI GI 2139 BLAST score 0.0e + 00E value 496 Match length 83 % identity

(AF025842) plasma membrane-type calcium ATPase [Arabidopsis NCBI Description

thaliana] >gi\_4468989\_emb\_CAB38303\_ (AL035605) plasma membrane-type calcium ATPase (ACA2) [Arabidopsis thaliana]

16384 Seq. No.

44402 2.R1040 Contig ID wvk700684033.hl 5'-most EST

BLASTX Method q509810 NCBI GI 349 BLAST score 2.0e-34 E value 151 Match length 74 % identity

NCBI Description (L08468) envelope Ca2+-ATPase [Arabidopsis thaliana]

16385 Seq. No.

44417 1.R1040 Contig ID fua701040864.hl 5'-most EST

Method BLASTX q3335366 NCBI GI 649 BLAST score 1.0e-67 E value 201 Match length % identity 63

NCBI Description (AC003028) unknown protein [Arabidopsis thaliana]

16386 Seq. No.

44417 2.R1040 Contig ID

5'-most EST LIB3106-105-Q1-K1-F10

Method BLASTX q3335366 NCBI GI 548 BLAST score 7.0e-56 E value 174 Match length 63 % identity

NCBI Description (AC003028) unknown protein [Arabidopsis thaliana]



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16387
Seq. No.
                  44418 1.R1040
Contig ID
                  jC-gmle01810084h12a1
5'-most EST
                  16388
Seq. No.
                  44418 3.R1040
Contig ID
                  LIB3109-018-Q1-K1-H6
5'-most EST
Seq. No.
                  16389
                  44422 1.R1040
Contig ID
                  leu701153828.h1
5'-most EST
                  BLASTX
Method
                  g3935175
NCBI GI
BLAST score
                  370
                  2.0e-35
E value
                  136
Match length
                  62
% identity
                  (AC004557) F17L21.18 [Arabidopsis thaliana]
NCBI Description
                  16390
Seq. No.
                  44444 1.R1040
Contig ID
                  LIB3092-021-Q1-K1-G3
5'-most EST
                  16391
Seq. No.
                   44446 2.R1040
Contig ID
                   kl1701215038.hl
5'-most EST
                   16392
Seq. No.
                   44449 1.R1040
Contig ID
                   fua701039910.h1
5'-most EST
                   BLASTX
Method
                   g2623310
NCBI GI
                   184
BLAST score
                   2.0e-13
E value
                   58
Match length
                   62
% identity
                   (AC002409) unknown protein [Arabidopsis thaliana]
NCBI Description
                   >qi 3402721 (AC004261) unknown protein [Arabidopsis
                   thaliana]
                   16393
Seq. No.
                   44452 1.R1040
Contig ID
                   fde700870881.hl
5'-most EST
Method
                   BLASTX
                   g2252871
NCBI GI
BLAST score
                   325
                   8.0e-30
E value
                   159
Match length
 % identity
                   47
NCBI Description (AF013294) No definition line found [Arabidopsis thaliana]
```

 Seq. No.
 16394

 Contig ID
 44470\_1.R1040

 5'-most EST
 rca700996419.h1

Method BLASTX NCBI GI g4056506



```
BLAST score 743
E value 1.0e-78
Match length 331
% identity 46
```

NCBI Description (AC005896) nodulin-like protein [Arabidopsis thaliana]

Seq. No. 16395

Contig ID 44472\_1.R1040 5'-most EST fua701041572.h1

Seq. No. 16396

Contig ID 44472\_2.R1040 5'-most EST eep700869311.h1

Seq. No. 16397

Contig ID 44514\_1.R1040 5'-most EST wvk700684993.h1

Seq. No. 16398

Contig ID 44528 1.R1040

5'-most EST jC-gmf102220054d06a1

Method BLASTX
NCBI GI g3164222
BLAST score 293
E value 3.0e-26
Match length 118
% identity 53

NCBI Description (AB008518) RMA1 [Arabidopsis thaliana] >gi\_4206205

(AF071527) RMA1 RING zinc finger protein [Arabidopsis

thaliana]

Seq. No. 16399

Contig ID 44530\_1.R1040 5'-most EST pmv700890535.h1

Method BLASTX
NCBI GI g3831441
BLAST score 165
E value 5.0e-11
Match length 47
% identity 79

NCBI Description (AC005819) hypothetical protein [Arabidopsis thaliana]

Seq. No. 16400

Contig ID 44555\_1.R1Q40 5'-most EST epx701106481.h1

Method BLASTX
NCBI GI g2190259
BLAST score 420
E value 1.0e-48
Match length 135
% identity 72

NCBI Description (D86385) A-type cyclin [Catharanthus roseus]

Seq. No. 16401

Contig ID 44572 1.R1040 5'-most EST sat701009956.h2

Method BLASTX



g2493133 NCBI GI 424 BLAST score 2.0e-41E value 166 Match length 52 % identity VACUOLAR ATP SYNTHASE SUBUNIT D (V-ATPASE D SUBUNIT) NCBI Description >gi\_2183244 (AF002134) Vma8p [Candida albicans]

16402 Seq. No.

44573 1.R1040 Contig ID

LIB3092-019-Q1-K1-H12 5'-most EST

16403 Seq. No.

Contig ID 44590 1.R1040

uC-gmrominsoy201b05b1 5'-most EST

16404 Seq. No.

44597 1.R1040 Contig ID wvk700681606.hl 5'-most EST

16405 Seq. No.

44613 1.R1040 Contig ID

LIB3139-089-P1-N1-E3 5'-most EST

BLASTN Method NCBI GI q2264309 63 BLAST score 1.0e-26 E value 179 Match length 84

% identity NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MJJ3, complete sequence [Arabidopsis thaliana]

16406 Seq. No.

44624 1.R1040 Contig ID  $smw70\overline{0}646248.h1$ 5'-most EST

16407 Seq. No.

44666 1.R1040 Contig ID uC-gmropic113d03b1 5'-most EST

Method BLASTX q100225 NCBI GI 534 BLAST score 6.0e-54 E value 236 Match length % identity 48

heat shock transcription factor 8 - tomato NCBI Description

>gi\_19260\_emb\_CAA47868\_ (X67599) heat stress transcription factor 8 [Lycopersicon esculentum]

Seq. No. 16408

44666 2.R1040 Contig ID has700548142.h1 5'-most EST

BLASTX Method g729775 NCBI GI 236 BLAST score 2.0e-35 E value 144 Match length



16409

% identity HEAT SHOCK FACTOR PROTEIN HSF8 (HEAT SHOCK TRANSCRIPTION NCBI Description FACTOR 8) (HSTF 8) (HEAT STRESS TRANSCRIPTION FACTOR) >gi\_100264\_pir\_\_S25481 heat shock transcription factor 8 - Peruvian tomato >gi\_19492\_emb\_CAA47869\_ (X67600) heat shock transcription factor 8 [Lycopersicon peruvianum]

44682 1.R1040 Contig ID txt700733359.h1 5'-most EST BLASTX Method g3097312 NCBI GI 177 BLAST score 2.0e-12 E value

94 Match length 36 % identity

Seq. No.

(AB009024) capping enzyme 1B [Homo sapiens] NCBI Description

16410 Seq. No.

44691 1.R1040 Contig ID

uC-gmrominsoy106b11b1 5'-most EST

BLASTX Method g2435511 NCBI GI BLAST score 463 E value 4.0e-46 Match length 102 78 % identity

(AF024504) contains similarity to prolyl 4-hydroxylase NCBI Description

alpha subunit [Arabidopsis thaliana]

16411 Seq. No.

44697 1.R1040 Contig ID q5677986 5'-most EST Method BLASTX g2494151 NCBI GI BLAST score 173 E value 6.0e-1263 Match length 56 % identity

DNAJ PROTEIN >gi 2119734 pir \_\_JC4739 chaperonin dnaJ -NCBI Description

Bacillus stearothermophilus >gi 1568475 emb CAA62240

(X90709) dnaJ [Bacillus stearothermophilus]

16412 Seq. No.

44697 2.R1040 Contig ID ssr700560683.hl 5'-most EST

Seq. No. 16413

44719 1.R1040 Contig ID zzp700831117.h1 5'-most EST

BLASTX Method q3335375 NCBI GI 762 BLAST score 2.0e-81 E value 156 Match length 90 % identity

NCBI Description (AC003028) putative amidase [Arabidopsis thaliana]



Contig ID 44721\_1.R1040

5'-most EST LIB3139-054-P1-N1-C9

Method BLASTX
NCBI GI 93850588
BLAST score 946
E value 1.0e-102
Match length 218
% identity 79

NCBI Description (AC005278) Contains similarity to gb\_AB011110 KIAA0538

protein from Homo sapiens brain and to phospholipid-binding domain C2 PF\_00168. ESTs gb\_AA585988 and gb\_T04384 come

from this gene. [Arabidopsis thaliana]

Seq. No. 16415

Contig ID 44721\_2.R1040 5'-most EST wrg700786731.h2

Method BLASTX
NCBI GI g3850588
BLAST score 388
E value 1.0e-37
Match length 121
% identity 60

NCBI Description (AC005278) Contains similarity to gb\_AB011110 KIAA0538

protein from Homo sapiens brain and to phospholipid-binding domain C2 PF\_00168. ESTs gb\_AA585988 and gb\_T04384 come

from this gene. [Arabidopsis thaliana]

Seq. No. 16416

Contig ID 44724\_1.R1040

5'-most EST LIB3092-017-Q1-K1-F5

Seq. No. 16417

Contig ID 44738\_1.R1040

5'-most EST LIB3092-017-Q1-K1-F2

Seq. No. 16418

Contig ID 44742 1.R1040 5'-most EST seb700653164.h1

Method BLASTX
NCBI GI g1076414
BLAST score 880
E value 1.0e-94
Match length 348
% identity 53

NCBI Description subtilisin-like proteinase (EC 3.4.21.-) - Arabidopsis thaliana (fragment) >gi\_757534 emb\_CAA59963\_ (X85974)

subtilisin-like protease [Arabidopsis thaliana]

Seq. No. 16419

Contig ID 44754\_1.R1040 5'-most EST bth700849132.h1

Method BLASTX
NCBI GI g3522931
BLAST score 701
E value 4.0e-74



Match length 159
% identity 82
NCBI Description (AC002535) putative Na+/Ca2+ exchanger [Arabidopsis thaliana]

Seq. No. 16420
Contig ID 44760\_1.R1040
5'-most EST LIB3092-017-Q1-K1-B9

Method BLASTX
NCBI GI g1931639
BLAST score 197
E value 4.0e-15
Match length 96
% identity 39

NCBI Description (U95973) lysophospholipase isolog [Arabidopsis thaliana]

Seq. No. 16421

Contig ID 44764\_1.R1040 5'-most EST uC-gmropic039h03b1

Seq. No. 16422

Contig ID 44772 1.R1040

5'-most EST jC-gmle01810011e04a1

Method BLASTX
NCBI GI g3337366
BLAST score 356
E value 2.0e-33
Match length 224
% identity 22

NCBI Description (AC004481) unknown protein [Arabidopsis thaliana]

Seq. No. 16423

Contig ID 44777\_1.R1040

5'-most EST LIB3092-016-Q1-K1-H5

Seq. No. 16424

Contig ID 44777\_2.R1040 5'-most EST epx701109503.h1

Seq. No. 16425

Contig ID 44782\_2.R1040

5'-most EST LIB3092-017-Q1-K1-A2

Seq. No. 16426

Contig ID 44807 1.R1040

5'-most EST jC-gmro02910015b12a1

Method BLASTX
NCBI GI g4406809
BLAST score 199
E value 8.0e-15
Match length 133
% identity 44

NCBI Description (AC006201) unknown protein [Arabidopsis thaliana]

Seq. No. 16427

Contig ID 44808\_1.R1040 5'-most EST zhf700962690.h1



Contig ID 44809 1.R1040

5'-most EST LIB3092-016-Q1-K1-E11

Seq. No. 16429

Contig ID 44811 1.R1040

5'-most EST uC-gmrominsoy206f02b1

Method BLASTX
NCBI GI g3033381
BLAST score 793
E value 1.0e-84
Match length 177
% identity 84

NCBI Description (AC004238) putative UDP-galactose-4-epimerase [Arabidopsis

1

thaliana]

Seq. No. 16430

Contig ID 44816 1.R1040

5'-most EST jC-gmro02910040d09a1

Method BLASTX
NCBI GI g3668089
BLAST score 204
E value 5.0e-16
Match length 71
% identity 66

NCBI Description (AC004667) unknown protein [Arabidopsis thaliana]

Seq. No. 16431

Contig ID 44816\_2.R1040 5'-most EST seb700653870.h1

Seq. No. 16432

Contig ID 44831\_1.R1040

5'-most EST LIB3170-076-Q1-J1-G10

Seq. No. 16433

Contig ID 44834 1.R1040

5'-most EST uC-gmrominsoy185e03b1

Method BLASTX
NCBI GI g1170504
BLAST score 183
E value 2.0e-13
Match length 68
% identity 53

NCBI Description EUKARYOTIC INITIATION FACTOR (ISO) 4F SUBUNIT P82

(IEIF-(ISO)4F P82)  $>gi_452440$  (M95747) initiation factor

(iso)4f p82 subunit [Triticum aestivum]

Seq. No. 16434

Contig ID 44838\_1.R1040

5'-most EST LIB3092-016-Q1-K1-A6

Method BLASTX
NCBI GI g2980767
BLAST score 248
E value 4.0e-21
Match length 96



% identity (AL022198) putative protein [Arabidopsis thaliana] NCBI Description

16435 Seq. No.

44854 1.R1040 Contig ID

LIB3092-015-Q1-K1-H12 5'-most EST

85

Method BLASTN q4220630 NCBI GI BLAST score 66 1.0e-28 E value Match length 170

% identity Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: NCBI Description

K2K18, complete sequence [Arabidopsis thaliana]

16436 Seq. No.

44856 1.R1040 Contig ID 5'-most EST sat701012455.h1

Method BLASTX NCBI GI g2252836 BLAST score 629 E value 3.0e-65 Match length 272 % identity 49

(AF013293) contains weak similarity to S. cerevisiae BOB1 NCBI Description

protein (PIR:S45444) [Arabidopsis thaliana]

16437 Seq. No.

Contig ID 44884 1.R1040

jC-qmf102220127g04d1 5'-most EST

BLASTX Method NCBI GI q1305531 BLAST score 162 E value 5.0e-11 Match length 55 % identity 51

(U55219) defective chloroplasts and leaves; required for NCBI Description

chloroplast development and palisade cell differentiation in leaves [Lycopersicon esculentum] >gi\_1323698 (U55278)

DCL [Solanum lycopersicum]

16438 Seq. No.

44890 1.R1040 Contig ID

uC-gmrominsoy041g02b1 5'-most EST

BLASTX Method NCBI GI g4262174 823 BLAST score 3.0e-88 E value Match length 188 78 % identity

(AC005508) 9058 [Arabidopsis thaliana] NCBI Description

Seq. No.

44890 3.R1040 Contig ID

5'-most EST uC-gmropic008e01b1

16439

Seq. No. 16440



Contig ID 44890\_4.R1040 5'-most EST pmv700892424.h1

Method BLASTX
NCBI GI g4262174
BLAST score 241
E value 2.0e-20
Match length 56
% identity 80

NCBI Description (AC005508) 9058 [Arabidopsis thaliana]

Seq. No. 16441

Contig ID 44892 1.R1040

5'-most EST jC-gmst02400072e05a1

Method BLASTX
NCBI GI g4218122
BLAST score 447
E value 5.0e-44
Match length 343
% identity 40

NCBI Description (AL035353) putative protein [Arabidopsis thaliana]

Seq. No. 16442

Contig ID 44893 1.R1040

5'-most EST jC-gmle01810089e09d1

Seq. No. 16443

Contig ID 44894\_1.R1040 5'-most EST kl1701212508.h1

Method BLASTX
NCBI GI g339878
BLAST score 516
E value 6.0e-52
Match length 156
% identity 63

NCBI Description (M55169) tripeptidyl peptidase II [Homo sapiens]

Seq. No. 16444

Contig ID 44894\_2.R1040 5'-most EST eep700866865.h1

Method BLASTX
NCBI GI g2499872
BLAST score 468
E value 8.0e-47
Match length 161
% identity 58

NCBI Description TRIPEPTIDYL-PEPTIDASE II (TPP II) (TRIPEPTIDYL

AMINOPEPTIDASE) >gi 2137836 pir I48855

tripeptidyl-peptidase II (EC 3.4.14.10) - mouse

>gi\_575955\_emb\_CAA57103\_ (X81323) tripeptidyl-peptidase ii

[Mus musculus]

Seq. No. 16445

Contig ID 44913 1.R1040

5'-most EST LIB3092-015-Q1-K1-D10

Seq. No. 16446

Contig ID 44922 1.R1040



```
LIB3092-014-Q1-K1-H9
5'-most EST
                  16447
Seq. No.
                  44943 1.R1040
Contig ID
                  dpv701102324.h1
5'-most EST
                  BLASTX
Method
                  q4160302
NCBI GI
                  625
BLAST score
                  7.0e-65
E value
                  242
Match length
                  54
% identity
                  (AJ011894) cyclin D3.2 protein [Nicotiana tabacum]
NCBI Description
                  16448
Seq. No.
                  44948 1.R1040
Contig ID
                  pmv700891056.h1
5'-most EST
                  BLASTX
Method
                  g2271477
NCBI GI
                  351
BLAST score
                  3.0e-33
E value
Match length
                  75
                   91
% identity
                  (AF009631) AP47/50p [Arabidopsis thaliana]
NCBI Description
                   16449
Seq. No.
                   44964 1.R1040
Contig ID
                   uC-gmflminsoy035g06b1
5'-most EST
                   BLASTN
Method
                   g3821780
NCBI GI
                   33
BLAST score
                   1.0e-08
E value
                   33
Match length
                   58
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                   16450
Seq. No.
                   44979 1.R1040
Contig ID
                   LIB3092-014-Q1-K1-B1
5'-most EST
                   16451
Seq. No.
                   44988 1.R1040
Contig ID
                   ssr700560158.hl
5'-most EST
Method
                   BLASTX
                   q4572671
NCBI GI
BLAST score
                   1250
                   1.0e-138
E value
                   313
Match length
                   79
% identity
                   (AC006954) putative cyclic nucleotide regulated ion channel
NCBI Description
                   [Arabidopsis thaliana]
                   16452
Seq. No.
                   44990 1.R1040
Contig ID
```

jC-gmle01810058e12a1 5'-most EST

16453 Seq. No.

44992 1.R1040 Contig ID

BLAST score

Match length % identity

E value

186 1.0e-13

58



```
LIB3092-013-Q1-K1-G2
5'-most EST
                  BLASTX
Method
                  g2494116
NCBI GI
                  764
BLAST score
                  2.0e-81
E value
                  165
Match length
% identity
                  (AC002376) Similar to Synechocystis hypothetical protein
NCBI Description
                   (gb_D90915). [Arabidopsis thaliana]
                  16454
Seq. No.
                  44996 1.R1040
Contig ID
                  fde700873341.h1
5'-most EST
                  BLASTX
Method
                  g3183421
NCBI GI
                  205
BLAST score
                  7.0e-16
E value
                  130
Match length
                   38
% identity
                  HYPOTHETICAL PROTEIN MJ1541 >gi_2129138_pir__D64492
NCBI Description
                  N-ethylammeline chlorohydrolase homolog - Methanococcus
                   jannaschii >gi_1592173 (U67595) N-ethylammeline
                   chlorohydrolase (trzA) [Methanococcus jannaschii]
                   16455
Seq. No.
                   45004 1.R1040
Contig ID
                   LIB3092-013-Q1-K1-H3
5'-most EST
                   16456
Seq. No.
                   45004 2.R1040
Contig ID
                   zzp700832894.h1
5'-most EST
                   16457
Seq. No.
                   45006 1.R1040
Contig ID
                   xpa700793178.hl
5'-most EST
                   16458
Seq. No.
                   45007 1.R1040
Contig ID
                   wvk700682072.hl
5'-most EST
Method
                   BLASTX
                   a2494280
NCBI GI
                   248
BLAST score
                   5.0e-21
E value
                   84
Match length
% identity
                   58
                  ELONGATION FACTOR TS (EF-TS) >gi 1653231 dbj BAA18146
NCBI Description
                   (D90912) elongation factor TS [Synechocystis sp.]
                   16459
Seq. No.
                   45007 2.R1040
Contig ID
                   taw700656251.hl
5'-most EST
                   BLASTX
Method
                   q2494280
NCBI GI
```



NCBI Description ELONGATION FACTOR TS (EF-TS) >gi 1653231 dbj BAA18146

(D90912) elongation factor TS [Synechocystis sp.]

Seq. No. 16460

Contig ID 45015 1.R1040

5'-most EST jC-gmro02910011f12a1

Seq. No. 16461

Contig ID 45030\_1.R1040

5'-most EST jC-gmle01810020e10a1

Method BLASTX
NCBI GI g2191152
BLAST score 325
E value 8.0e-30
Match length 187
% identity 43

NCBI Description (AF007269) A\_IG002N01.31 gene product [Arabidopsis

thaliana]

Seq. No. 16462

Contig ID 45035\_1.R1040

5'-most EST LIB3092-013-Q1-K1-C9

Seq. No. 16463

Contig ID 45035\_2.R1040

5'-most EST uC-gmrominsoy244g12b1

Seq. No. 16464

Contig ID 45045\_1.R1040 5'-most EST kl1701205124.h1

Method BLASTX
NCBI GI g4510424
BLAST score 205
E value 4.0e-23
Match length 87
% identity 74

NCBI Description (AC006929) putative carboxypeptidase [Arabidopsis thaliana]

Seq. No. 16465

Contig ID 45045\_2.R1040 5'-most EST asn701137770.h1

Seq. No.

16466

Contig ID 45055\_1.R1040 5'-most EST bth700845078.h1

Method BLASTX
NCBI GI g927575
BLAST score 735
E value 5.0e-78
Match length 188
% identity 71

NCBI Description (U12926) alpha galactosidase [Glycine max]

Seq. No.

16467

Contig ID 5'-most EST 45063\_1.R1040 pxt700945283.h1

Method BLASTX



```
g3269295
NCBI GI
                   217
BLAST score
                   2.0e-17
E value
                   61
Match length
                   64
% identity
NCBI Description (AL030978) putative protein [Arabidopsis thaliana]
                   16468
Seq. No.
                   45070 1.R1040
Contig ID
                   leu70\overline{1}146967.h1
5'-most EST
                   16469
Seq. No.
                   45079 1.R1040
Contig ID
5'-most EST
                   LIB3092-012-Q1-K1-D6
                   BLASTX
Method
```

g2245124 NCBI GI 220 BLAST score 8.0e-18 E value 82 Match length 57 % identity

NCBI Description (Z97343) protein kinase [Arabidopsis thaliana]

16470 Seq. No. 45079 2.R1040 Contig ID

LIB3139-003-P1-N1-B12 5'-most EST

Seq. No. 16471

45113 1.R1040 Contig ID

LIB3092-011-Q1-K1-H3 5'-most EST

BLASTX Method g4191780 NCBI GI BLAST score 262 2.0e-22 E value Match length 95 49 % identity

(AC005917) putative cytokinin oxidase [Arabidopsis NCBI Description

thaliana]

16472 Seq. No.

Contig ID 45132 1.R1040

LIB3092-011-Q1-K1-F7 5'-most EST

16473 Seq. No.

45142 1.R1040 Contig ID

LIB3092-011-Q1-K1-C6 5'-most EST

16474 Seq. No.

45156 1.R1040 Contig ID

LIB3093-042-Q1-K1-D6 5'-most EST

16475 Seq. No.

45172 1.R1040 Contig ID

jC-gmf102220063b02a1 5'-most EST

BLASTX Method g2501572 NCBI GI BLAST score 154 6.0e-11 E value



```
Match length
                  71
                  56
% identity
NCBI Description LATE EMBRYOGENESIS ABUNDANT PROTEIN EMB8 >gi 1350545
                  (L47118) EMB8 gene product [Picea glauca]
                  16476
Seq. No.
                  45174 1.R1040
Contig ID
                  pcp700994186.hl
5'-most EST
Method
                  BLASTX
                  g3738324
NCBI GI
                  609
BLAST score
                  6.0e-63
E value
                  240
Match length
                  47
% identity
                  (AC005170) GMP synthase-like protein [Arabidopsis thaliana]
NCBI Description
                  16477
Seq. No.
                  45174 2.R1040
Contig ID
                  LIB3139-102-P1-N1-F3
5'-most EST
Method
                  BLASTX
                  g3738324
NCBI GI
                  291
BLAST score
                  5.0e-26
E value
                  101
Match length
                  51
% identity
                  (AC005170) GMP synthase-like protein [Arabidopsis thaliana]
NCBI Description
                  16478
Seq. No.
                  45186 1.R1040
Contiq ID
5'-most EST
                  uC-gmropic035e08b1
                  BLASTX
Method
                  g3075398
NCBI GI
BLAST score
                  420
E value
                  5.0e-41
                  134
Match length
% identity
                  59
NCBI Description (AC004484) unknown protein [Arabidopsis thaliana]
                  16479
Seq. No.
                  45186 2.R1040
Contig ID
5'-most EST
                  zzp700835476.h1
                  BLASTX
Method
NCBI GI
                  g3688186
BLAST score
                  151
                  9.0e-10
E value
                  56
Match length
                   55
% identity
                  (AL031804) putative protein [Arabidopsis thaliana]
NCBI Description
```

Contig ID 45186\_3.R1040

5'-most EST jC-gmro02910005e12a1

Seq. No. 16481

Contig ID 45194\_1.R1040 5'-most EST kll701207379.h1

Method BLASTX



```
g2341039
NCBI GI
BLAST score
                  372
                  2.0e-35
E value
                  146
Match length
                  52
% identity
                   (AC000104) Similar to Nicotiana lesion-inducing ORF
NCBI Description
                   (gb U66269). [Arabidopsis thaliana]
                  16482
Seq. No.
                  45194 2.R1040
Contig ID
5'-most EST
                  uaw700661795.hl
Method
                  BLASTX
NCBI GI
                  q2341039
BLAST score
                   269
                  1.0e-23
E value
Match length
                   81
                   65
% identity
                   (AC000104) Similar to Nicotiana lesion-inducing ORF
NCBI Description
                   (gb U66269). [Arabidopsis thaliana]
                   16483
Seq. No.
                   45199 1.R1040
Contig ID
5'-most EST
                  bth700844887.h1
Seq. No.
                   16484
                   45204 1.R1040
Contig ID
                   wvk700685732.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g1084374
BLAST score
                   306
E value
                   6.0e-28
Match length
                   126
                   55
% identity
                   histone-lysine N-methyltransferase (EC 2.1.1.43) large
NCBI Description
                   chain N-methyltransferase - garden pea >gi_508551 (L34291)
                   ribulose-1,5 bisphosphate carboxylase large subunit
                   N-methyltransferase [Pisum sativum]
Seq. No.
                   16485
                   45223 1.R1040
Contig ID
                   zzp700834659.h1
5'-most EST
                   BLASTX
Method
```

g500734 NCBI GI 744 BLAST score 2.0e-78 E value 398 Match length

34 % identity (U10414) similar to ATP-binding transport protein family NCBI Description (ABC transporters) [Caenorhabditis elegans]

16486 Seq. No. 45228 1.R1040 Contig ID

LIB3092-008-Q1-K1-H6 5'-most EST

BLASTX Method g3482917 NCBI GI BLAST score 348 E value 1.0e-32



```
171
Match length
                  51
% identity
                  (AC003970) Similar to Glucose-6-phosphate dehydrogenases,
NCBI Description
                  gi 2276344, gi_2829880, gi_2352919 and others. [Arabidopsis
                  thaliana]
                  16487
Seq. No.
                  45228 2.R1040
Contig ID
                  kmv70\overline{0}740931.h1
5'-most EST
                  16488
Seq. No.
                  45248 1.R1040
Contig ID
                  uC-gmrominsoy226b12b1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g3894393
BLAST score
                  316
                  1.0e-28
E value
                  233
Match length
                  5
% identity
                  (AF053998) Hcr2-5D [Lycopersicon esculentum]
NCBI Description
                  16489
Seq. No.
                  45251 1.R1040
Contig ID
                  LIB3092-008-Q1-K1-F9
5'-most EST
                  BLASTX
Method
                   g2842757
NCBI GI
                   250
BLAST score
                   3.0e-21
E value
                   149
Match length
                   43
% identity
                  LIGHT-INDUCIBLE PROTEIN CPRF-2 >gi_1806261_emb_CAA41453_
NCBI Description
                   (X58577) DNA-binding protein; bZIP type [Petroselinum
                   crispum]
                   16490
Seq. No.
                   45256 1.R1040
Contig ID
5'-most EST
                   LIB3092-008-Q1-K1-G3
                  BLASTX
Method
                   q2708752
NCBI GI
BLAST score
                   427
                   8.0e-42
E value
                   146
Match length
% identity
                  (AC003952) putative histidine kinase [Arabidopsis thaliana]
NCBI Description
                   16491
Seq. No.
                   45292 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy299c02b1
Method
                   BLASTX
```

Method BLASTX
NCBI GI g3414809
BLAST score 192
E value 4.0e-14
Match length 148
% identity 4

NCBI Description (AF061529) rjs [Mus musculus]

Seq. No. 16492



```
Contig ID 45295_1.R1040
5'-most EST bth700848529.h1
Method BLASTX
NCBI GI q4063751
```

NCBI GI g406375 BLAST score 208 E value 2.0e-16 Match length 124 % identity 31

NCBI Description (AC005851) putative white protein [Arabidopsis thaliana]

>gi\_4510409\_gb\_AAD21495.1\_ (AC006929) putative white

protein [Arabidopsis thaliana]

Seq. No. 16493

Contig ID 45298\_1.R1040

5'-most EST uC-gmflminsoy065h10b1

Seq. No. 16494

Contig ID 45311\_1.R1040 5'-most EST sat701009254.h1

Method BLASTX
NCBI GI g1922242
BLAST score 194
E value 1.0e-14
Match length 71
% identity 52

NCBI Description (Y10084) hypothetical protein [Arabidopsis thaliana]

Seq. No. 16495

Contig ID 45314\_1.R1040

5'-most EST LIB3092-007-Q1-K1-G12

Method BLASTX
NCBI GI g1353114
BLAST score 165
E value 2.0e-11
Match length 101
% identity 18

NCBI Description HYPOTHETICAL 84.7 KD PROTEIN ZK1098.1 IN CHROMOSOME III

>gi\_3881493\_emb\_CAA80142\_ (Z22176) similar to WW/rsp5/WWP

domain containing proteins (2 domains); cDNA EST

EMBL:D68819 comes from this gene; cDNA EST EMBL:D76048 comes from this gene; cDNA EST yk205d6.3 comes from this

gene; cDNA EST yk205d6.5 comes fro

Seq. No. 16496

Contig ID 45315\_1.R1040

5'-most EST LIB3092-007-Q1-K1-G2

Method BLASTX
NCBI GI g3608138
BLAST score 193
E value 1.0e-14
Match length 71
% identity 54

NCBI Description (AC005314) hypothetical protein [Arabidopsis thaliana]

Seq. No. 16497

Contig ID 45325\_1.R1040

5'-most EST LIB3138-034-Q1-N1-A10

```
Seq. No.
                  16498
                  45325 2.R1040
Contig ID
                  kmv700739194.h1
5'-most EST
                  BLASTX
Method
                  g3935168
NCBI GI
BLAST score
                  779
                  1.0e-82
E value
                  275
Match length
                  59
% identity
NCBI Description
                  (AC004557) F17L21.11 [Arabidopsis thaliana]
Seq. No.
                  16499
                  45325 3.R1040
Contig ID
5'-most EST
                  jC-gmf102220073h01d1
                  16500
Seq. No.
Contig ID
                   45330 1.R1040
5'-most EST
                  LIB3092-007-Q1-K1-E4
Seq. No.
                  16501
                   45334_1.R1040
Contig ID
5'-most EST
                  epx701109535.hl
                  BLASTX
Method
                  q1350548
NCBI GI
                   279
BLAST score
                   8.0e-25
E value
                  89
Match length
% identity
                   60
NCBI Description
                  (L47609) heat shock-like protein [Picea glauca]
Seq. No.
                   16502
Contig ID
                   45337 1.R1040
5'-most EST
                  pmv700891902.h1
Seq. No.
                   16503
                   45347 1.R1040
Contig ID
                   leu701144496.h1
5'-most EST
Seq. No.
                   16504
                   45349 1.R1040
Contig ID
                   LIB3092-007-Q1-K1-C2
5'-most EST
                   BLASTX
Method
                   g3746069
NCBI GI
BLAST score
                   155
                   5.0e-10
E value
Match length
                   92
                   36
% identity
                   (AC005311) putative reverse transcriptase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   16505
```

Contig ID

45354 1.R1040

5'-most EST

LIB3092-007-Q1-K1-D6

Seq. No.

16506

Contig ID

45362 1.R1040



```
LIB3092-007-Q1-K1-A12
5'-most EST
                  16507
Seq. No.
                  45366 1.R1040
Contig ID
                  LIB3106-022-Q1-K1-B6
5'-most EST
                  BLASTX
Method
                  g3549667
NCBI GI
                  629
BLAST score
                  1.0e-80
E value
                  267
Match length
                  60
% identity
                 (AL031394) Arabidopsis dynamin-like protein ADL2
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  16508
                  45373 1.R1040
Contig ID
                  LIB3092-007-Q1-K1-B4
5'-most EST
                  16509
Seq. No.
                  45405 1.R1040
Contig ID
                  zsg701124607.hl
5'-most EST
                  16510
Seq. No.
                  45405 2.R1040
Contig ID
5'-most EST
                  uC-gmflminsoy024c05b1
Seq. No.
                  16511
                  45427 1.R1040
Contig ID
5'-most EST
                  uC-gmropic031f08b1
                  BLASTN
Method
                  q2062691
NCBI GI
                  34
BLAST score
                  2.0e-09
E value
Match length
                  34
                  62
% identity
NCBI Description Human sodium phosphate transporter (NPT4) mRNA, complete
                  cds
Seq. No.
                  16512
                   45429 1.R1040
Contig ID
                  LIB3092-005-Q1-K1-G7
5'-most EST
Method
                  BLASTX
                   g4467359
NCBI GI
BLAST score
                   346
                   1.0e-32
E value
Match length
                   158
% identity
                   50
                  (AJ002685) Phosphatidylinositol 4-kinase [Arabidopsis
NCBI Description
                   thaliana]
```

Contig ID 45434\_1.R1040 5'-most EST zsg701129787.h1

Seq. No. 16514

Contig ID 45435\_1.R1040 5'-most EST eep700864532.h1



```
BLASTX
Method
                  g3876231
NCBI GI
                  225
BLAST score
                  3.0e-18
E value
Match length
                  93
                  47
% identity
                  (Z50044) cDNA EST yk400h8.3 comes from this gene; cDNA EST
NCBI Description
                  yk400h8.5 comes from this gene [Caenorhabditis elegans]
                  16515
Seq. No.
                  45435 2.R1040
Contig ID
                  q5509646
5'-most EST
                  BLASTX
Method
                  g3283893
NCBI GI
BLAST score
                  156
                   2.0e-10
E value
Match length
                   56
                   59
% identity
                  (AF070626) unknown [Homo sapiens]
NCBI Description
Seq. No.
                   16516
                   45448 1.R1040
Contig ID
                   uC-gmronoir010a01b1
5'-most EST
                   16517
Seq. No.
                   45462 1.R1040
Contig ID
                   LIB3092-005-Q1-K1-D4
5'-most EST
                   BLASTX
Method
                   g3127137
NCBI GI
                   232
BLAST score
                   3.0e-19
E value
                   136
Match length
                   38
% identity
                   (AF061021) actin [Spirogyra sp. SVCK-253]
NCBI Description
                   16518
Seq. No.
                   45463 1.R1040
Contig ID
                   LIB3092-005-Q1-K1-A1
5'-most EST
                   16519
Seq. No.
                   45468 1.R1040
Contig ID
                   LIB3138-048-Q1-N1-G4
 5'-most EST
                   BLASTX
Method
                   q2654868
NCBI GI
BLAST score
                   441
                   2.0e-55
E value
                   150
Match length
                   79
 % identity
                   (AF015301) RbohAp108 [Arabidopsis thaliana]
 NCBI Description
                   16520
 Seq. No.
                   45474 1.R1040
 Contig ID
                   LIB3092-005-Q1-K1-C4
 5'-most EST
                   BLASTX
 Method
                   g1762144
 NCBI GI
```

2735

172

3.0e-12

BLAST score

E value



```
105
Match length
                  40
% identity
                  (U48435) putative cytochrome P450 [Solanum chacoense]
NCBI Description
                  16521
Seq. No.
                  45476 1.R1040
Contig ID
                  LIB3092-005-Q1-K1-C8
5'-most EST
                  BLASTX
Method
                   g2618704
NCBI GI
                   878
BLAST score
                   3.0e-95
E value
                   250
Match length
                   70
% identity
                  (AC002510) putative thioredoxin reductase [Arabidopsis
NCBI Description
                   thaliana]
                   16522
Seq. No.
                   45483 1.R1040
Contig ID
                   LIB3092-004-Q1-K1-G8
5'-most EST
                   BLASTX
Method
                   g4559351
NCBI GI
                   146
BLAST score
                   4.0e-09
E value
                   86
Match length
                   43
% identity
                   (AC006585) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   16523
Seq. No.
                   45503 1.R1040
Contig ID
                   has700548108.h1
5'-most EST
                   BLASTX
Method
                   g3193292
NCBI GI
                   1226
BLAST score
                   1.0e-135
E value
Match length
                   287
                   85
% identity
                   (AF069298) similar to ATPases associated with various
NCBI Description
                   cellular activites (Pfam: AAA.hmm, score: 230.91)
                   [Arabidopsis thaliana]
Seq. No.
                   16524
                   45508 1.R1040
Contig ID
                   LIB3092-004-Q1-K1-F5
5'-most EST
Seq. No.
                   16525
                   45514 1.R1040
Contig ID
                   LIB3092-004-Q1-K1-B12
5'-most EST
```

Contig ID 45523 1.R1040

5'-most EST LIB3092-004-Q1-K1-D8

Method BLASTN
NCBI GI g2511532
BLAST score 118
E value 2.0e-59
Match length 278
% identity 86





```
NCBI Description Eleusine indica alpha-tubulin 2 (TUA2) mRNA, complete cds
```

Contig ID 45535\_1.R1040

5'-most EST LIB3092-004-Q1-K1-B8

Method BLASTX
NCBI GI g3063694
BLAST score 236
E value 1.0e-19
Match length 86
% identity 62

NCBI Description (AL022537) putative protein [Arabidopsis thaliana]

Seq. No. 16528

Contig ID 45545\_1.R1040 5'-most EST leu701148747.h1

Method BLASTN
NCBI GI g2827075
BLAST score 468
E value 0.0e+00
Match length 756
% identity 90

NCBI Description Medicago sativa chloroplast malate dehydrogenase precursor

(plmdh) mRNA, nuclear gene encoding chloroplast protein,

complete cds

Seq. No. 16529

Contig ID 45545\_2.R1040 5'-most EST hrw701061102.h1

Method BLASTN
NCBI GI g2827075
BLAST score 85
E value 5.0e-40
Match length 220
% identity 85

% identity 85
NCBI Description Medicago sativa chloroplast malate dehydrogenase precursor

(plmdh) mRNA, nuclear gene encoding chloroplast protein,

complete cds

Seq. No. 16530

Contig ID 45545\_3.R1040 5'-most EST fde700873423.h1

Method BLASTN
NCBI GI g169090
BLAST score 67
E value 4.0e-29
Match length 123
% identity 89

NCBI Description Pea glyceraldehyde-3-phosphate dehydrogenase (GapC1) mRNA,

complete cds

Seq. No. 16531

Contig ID 45545\_4.R1040 5'-most EST wrg700789619.h2

Seq. No. 16532

Contig ID 45548 1.R1040



```
LIB3092-003-Q1-K1-F9
5'-most EST
Method
                  BLASTX
                  g2781348
NCBI GI
                  489
BLAST score
                  2.0e-85
E value
                  328
Match length
                  55
% identity
                  (AC003113) F2401.4 [Arabidopsis thaliana]
NCBI Description
                  16533
Seq. No.
                  45550 1.R1040
Contig ID
                  jC-gmf102220090e05a1
5'-most EST
                  BLASTX
Method
                  g445113
NCBI GI
BLAST score
                  568
                  2.0e-58
E value
                  157
Match length
                  66
% identity
NCBI Description acid phosphatase 1 [Lycopersicon esculentum]
                  16534
Seq. No.
                  45550 2.R1040
Contig ID
                  g4313842
5'-most EST
                  BLASTX
Method
                   g130718
NCBI GI
BLAST score
                   224
                   3.0e-35
E value
                   102
Match length
% identity
                   75
                  ACID PHOSPHATASE PRECURSOR 1 >gi_170370 (M83211) acid
NCBI Description
                   phosphatase type 1 [Lycopersicon esculentum] >gi_170372
                   (M67474) acid phosphatase type 5 [Lycopersicon esculentum]
                   >gi_445121_prf__1908427A acid phosphatase 1 [Lycopersicon
                   esculentum]
                   16535
Seq. No.
                   45550 3.R1040
Contig ID
                   LIB3092-003-Q1-K1-G12
5'-most EST
                   16536
Seq. No.
Contig ID
                   45573 1.R1040
                   LIB3092-003-Q1-K1-B6
5'-most EST
                   BLASTX
Method
                   q4567263
NCBI GI
BLAST score
                   492
                   1.0e-49
E value
                   150
Match length
% identity
                   (AC006841) putative cell division inhibitor [Arabidopsis
NCBI Description
                   thaliana]
```

45579 1.R1040 Contig ID

LIB3107-064-Q1-K1-C10 5'-most EST

16538 Seq. No.

45579\_2.R1040 Contig ID



```
rca700996308.h1
5'-most EST
                  16539
Seq. No.
                  45585 1.R1040
Contig ID
5'-most EST
                  LIB3092-003-Q1-K1-A9
                  BLASTX
Method
NCBI GI
                  q1617274
                  1056
BLAST score
                  1.0e-115
E value
Match length
                  242
                  80
% identity
NCBI Description (Z72152) AMP-binding protein [Brassica napus]
                  16540
Seq. No.
Contig ID
                  45588 1.R1040
                  LIB3092-003-Q1-K1-B11
5'-most EST
                   16541
Seq. No.
                   45597 1.R1040
Contig ID
                  LIB3092-002-Q1-K1-F2
5'-most EST
                   16542
Seq. No.
                   45611 1.R1040
Contig ID
5'-most EST
                   epx701106873.h1
                   BLASTX
Method
                   g2191152
NCBI GI
                   614
BLAST score
                   8.0e-64
E value
Match length
                   235
% identity
                   57
                   (AF007269) A IG002N01.31 gene product [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   16543
                   45611 2.R1040
Contig ID
5'-most EST
                   LIB3106-076-Q1-K1-D11
Method
                   BLASTX
                   g2191152
NCBI GI
BLAST score
                   146
                   3.0e-10
E value
Match length
                   88
% identity
                   30
                   (AF007269) A IG002N01.31 gene product [Arabidopsis
NCBI Description
                   thaliana]
                   16544
Seq. No.
                   45621 1.R1040
Contig ID
                   LIB3092-002-Q1-K1-D9
5'-most EST
                   BLASTX
Method
                   g3319884
NCBI GI
                   442
BLAST score
                   1.0e-43
E value
                   221
Match length
                   33
% identity
                   (AJ224306) PRT1 [Arabidopsis thaliana]
NCBI Description
```

thaliana]

>gi 3319886\_emb\_CAA11892\_ (AJ224307) PRT1 [Arabidopsis



```
16545
Seq. No.
Contig ID
                   45632 1.R1040
                   \mathtt{sat70\overline{1}004111.h1}
5'-most EST
                   BLASTX
Method
                   g3297815
NCBI GI
                   392
BLAST score
                   3.0e-38
E value
                   104
Match length
                   72
% identity
NCBI Description (AL031032) putative protein [Arabidopsis thaliana]
                   16546
Seq. No.
                   45639 1.R1040
Contig ID
                   kl1701205228.h1
5'-most EST
                   BLASTX
Method
                   g4580513
NCBI GI
                   492
BLAST score
                   3.0e-85
E value
                   225
Match length
% identity
                   73
                   (AF036300) scarecrow-like 1 [Arabidopsis thaliana]
NCBI Description
                   16547
Seq. No.
                   45648 1.R1040
Contig ID
                   uC-gmropic019d09b1
5'-most EST
                   BLASTX
Method
                   g2062169
NCBI GI
                   920
BLAST score
                   2.0e-99
E value
                   334
Match length
                   36
% identity
                   (AC001645) ABC transporter (PDR5-like) isolog [Arabidopsis
NCBI Description
                   thaliana]
                   16548
Seq. No.
                   45662 1.R1040
Contig ID
5'-most EST
                   zzp700835310.h1
Seq. No.
                   16549
                   45663 1.R1040
Contig ID
5'-most EST
                   LIB3092-001-Q1-K1-E4
                   16550
Seq. No.
                   45675 1.R1040
Contig ID
                   g5342416
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3947690
BLAST score
                   676
E value
                   3.0e-77
                   397
Match length
                    43
% identity
```

(AJ131245) Sec24B protein [Homo sapiens] NCBI Description 16551 Seq. No.

45695 1.R1040 Contig ID 5'-most EST LIB3092-001-Q1-K1-A2



```
BLASTX
Method
NCBI GI
                  g1652704
                  193
BLAST score
                  5.0e-15
E value
                  88
Match length
                  47
% identity
NCBI Description (D90907) hypothetical protein [Synechocystis sp.]
                  16552
Seq. No.
                  45705_1.R1040
Contig ID
5'-most EST
                  uC-gmropic033h04b1
Method
                  BLASTX
                  g3668086
NCBI GI
                   333
BLAST score
E value
                   6.0e - 31
                   95
Match length
                   67
% identity
NCBI Description (AC004667) unknown protein [Arabidopsis thaliana]
                   16553
Seq. No.
                   45705 2.R1040
Contig ID
                   gsv701050456.hl
5'-most EST
                   BLASTX
Method
                   q3668086
NCBI GI
                   223
BLAST score
E value
                   4.0e-18
                   59
Match length
                   71
% identity
NCBI Description (AC004667) unknown protein [Arabidopsis thaliana]
                   16554
Seq. No.
                   45716 1.R1040
Contig ID
5'-most EST
                   LIB3092-013-Q1-K1-A4
Seq. No.
                   16555
                   45723 1.R1040
Contig ID
                   LIB3092-029-Q1-K1-H3
5'-most EST
Method
                   BLASTN
NCBI GI
                   q532289
BLAST score
                   48
                   6.0e-18
E value
Match length
                   92
% identity
                   88
                  Soybean mRNA for late nodulin, complete cds
NCBI Description
                   16556
Seq. No.
                   45724 1.R1040
Contig ID
5'-most EST
                   LIB3092-033-Q1-K1-G9
                   16557
Seq. No.
                   45734 1.R1040
Contig ID
                   LIB3092-053-Q1-K1-E1
5'-most EST
```

45738 1.R1040 Contig ID 5'-most EST zsg701125417.hl



```
16559
Seq. No.
                  45739 1.R1040
Contig ID
5'-most EST
                  nsy700645550.hl
Seq. No.
                  16560
                  45781 1.R1040
Contig ID
                  LIB3092-016-Q1-K1-H4
5'-most EST
                  BLASTX
Method
                  g3242708
NCBI GI
BLAST score
                  1114
                  1.0e-122
E value
Match length
                  321
% identity
                  68
                  (AC003040) putative serine/threonine protein kinase
NCBI Description
                  [Arabidopsis thaliana]
                  16561
Seq. No.
                  45781_2.R1040
Contig ID
                  uC-qmrominsoy319d04b1
5'-most EST
                  BLASTX
Method
                  g3242708
NCBI GI
                  538
BLAST score
                  1.0e-54
E value
                  180
Match length
                   64
% identity
                   (AC003040) putative serine/threonine protein kinase
NCBI Description
                   [Arabidopsis thaliana]
                  16562
Seq. No.
                   45792 1.R1040
Contig ID
                  dpv701097902.h1
5'-most EST
                  BLASTN
Method
                   g3985957
NCBI GI
                   41
BLAST score
                   3.0e-13
E value
                   163
Match length
                   86
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MYN8, complete sequence [Arabidopsis thaliana]
                   16563
Seq. No.
Contig ID
                   45793 1.R1040
                   LIB3092-019-Q1-K1-F7
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4468817
                   588
BLAST score
                   5.0e-61
E value
                   147
Match length
% identity
                  (AL035601) putative protein [Arabidopsis thaliana]
```

NCBI Description

16564 Seq. No.

45797 1.R1040 Contig ID

LIB3092-022-Q1-K1-G7 5'-most EST

16565 Seq. No.

45811 1.R1040 Contig ID



```
LIB3092-033-Q1-K1-G5
5'-most EST
                  BLASTX
Method
                  g4490341
NCBI GI
BLAST score
                  373
                  3.0e-37
E value
                  193
Match length
% identity
NCBI Description (AL035656) putative protein [Arabidopsis thaliana]
                  16566
Seq. No.
                  45820 1.R1040
Contig ID
                  uC-gmflminsoy079e08b1
5'-most EST
Seq. No.
                  16567
Contig ID
                  45823 1.R1040
                  jC-gmst02400051g03a1
5'-most EST
                  BLASTX
Method
                  g3047114
NCBI GI
                  445
BLAST score
                  5.0e-44
E value
                  139
Match length
                   64
% identity
NCBI Description (AF058919) No definition line found [Arabidopsis thaliana]
                   16568
Seq. No.
                   45836 1.R1040
Contig ID
                  LIB3092-046-Q1-K1-C7
5'-most EST
                   16569
Seq. No.
                   45837 1.R1040
Contig ID
                   jC-gmro02910013b12d1
5'-most EST
                   16570
Seq. No.
                   45841 1.R1040
Contig ID
                   rca700996979.h1
5'-most EST
                   BLASTX
Method
                   g4220472
NCBI GI
BLAST score
                   658
                   5.0e-69
E value
                   142
Match length
% identity
                   91
                  (AC006069) similar to yeast cccl protein [Arabidopsis
NCBI Description
                   thaliana]
                   16571
Seq. No.
                   45844 1.R1040
Contig ID
                   LIB3170-020-Q1-K1-A10
5'-most EST
Seq. No.
                   16572
                   45847 1.R1040
 Contig ID
                   LIB3093-045-Q1-K1-E5
 5'-most EST
```

16573

Contig ID

45881 1.R1040

 $jC-gm\overline{f}102220086a11a1$ 5'-most EST

BLASTX Method g3135257 NCBI GI



BLAST score 246 E value 2.0e-20 Match length 295 % identity 31

NCBI Description (AC003058) unknown protein [Arabidopsis thaliana]

Seq. No. 16574

Contig ID 45895\_1.R1040 5'-most EST taw700655641.h1

Seq. No. 16575

Contig ID 45896\_1.R1040 5'-most EST taw700660537.h1

Method BLASTX
NCBI GI g119640
BLAST score 124
E value 4.0e-15
Match length 72
% identity 61

% identity 61 NCBI Description 1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE HOMOLOG (PROTEIN

E8) >gi\_82109\_pir\_\_S01642 ripening protein E8 - tomato >gi\_19199\_emb\_CAA31789\_ (X13437) E8 protein [Lycopersicon

esculentum]

Seq. No. 16576

Contig ID 45898\_1.R1040 5'-most EST ssr700555352.h1

Seq. No. 16577

Contig ID 45906\_1.R1040 5'-most EST ncj700978775.h1

Seq. No.

Contig ID 45917\_1.R1040

5'-most EST LIB3093-058-Q1-K1-E8

16578

Method BLASTX
NCBI GI g2262115
BLAST score 150
E value 5.0e-27
Match length 169
% identity 44

NCBI Description (AC002343) cellulose synthase isolog [Arabidopsis thaliana]

Seq. No. 16579

Contig ID 45919 1.R1040 5'-most EST zhf700962291.h1

Method BLASTX
NCBI GI g1519680
BLAST score 143
E value 1.0e-08
Match length 128
% identity 31

NCBI Description (U67953) contains similarity to C3HC4-class zinc finger

(PS:PS00518) [Caenorhabditis elegans]

Seq. No. 16580

Contig ID 45939\_1.R1040



```
uC-gmronoir060h08b1
5'-most EST
                  16581
Seq. No.
                  45950 1.R1040
Contig ID
                  gsv701053117.h1
5'-most EST
                  BLASTX
Method
                  q4240207
NCBI GI
                  202
BLAST score
                  2.0e-15
E value
                  145
Match length
                  37
% identity
                  (AB020666) KIAA0859 protein [Homo sapiens]
NCBI Description
                  16582
Seq. No.
                   45960 1.R1040
Contig ID
                  dpv701097635.h1
5'-most EST
                   16583
Seq. No.
                   45974 1.R1040
Contiq ID
                  LIB3093-057-Q1-K1-F3
5'-most EST
                  BLASTX
Method
                   g2462732
NCBI GI
                   210
BLAST score
                   2.0e-16
E value
                   56
Match length
                   68
% identity
                  (AC002292) Hypothetical Protein [Arabidopsis thaliana]
NCBI Description
                   16584
Seq. No.
                   45976 1.R1040
Contig ID
                   kmv700742036.h1
5'-most EST
                   BLASTX
Method
                   g2213590
NCBI GI
BLAST score
                   444
                   8.0e-44
E value
                   232
Match length
                   41
% identity
                  (AC000348) T7N9.10 [Arabidopsis thaliana]
NCBI Description
                   16585
Seq. No.
                   45977 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220050d07a1
Seq. No.
                   16586
                   46021 1.R1040
Contig ID
                   uC-gmropic019h01b1
 5'-most EST
                   16587
 Seq. No.
                   46022 1.R1040
 Contig ID
                   jC-gmle01810078b12d1
 5'-most EST
                   BLASTX
 Method
                   g1705930
 NCBI GI
                   465
 BLAST score
                   4.0e-46
 E value
                   133
 Match length
                   70
 % identity
 NCBI Description ATP-DEPENDENT CLP PROTEASE PROTEOLYTIC SUBUNIT 1
```



(ENDOPEPTIDASE CLP 1) >gi\_1001349\_dbj\_BAA10836\_ (D64006) ATP-dependent protease ClpP [Synechocystis sp.]

Seq. No. 16588

Contig ID 46027 1.R1040

5'-most EST jC-gmfl02220069g10a1

Seq. No. 16589

Contig ID 46032 1.R1040 5'-most EST vzy700750617.h1

Method BLASTX
NCBI GI g320585
BLAST score 911
E value 2.0e-98
Match length 217
% identity 74

NCBI Description polygalacturonase (EC 3.2.1.15) 1 beta chain precursor -

tomato >gi\_170480 (M98466) polygalacturonase isoenzyme 1 beta subunit [Lycopersicon esculentum] >gi\_1762586 (U63374) polygalacturonase isoenzyme 1 beta subunit [Lycopersicon

esculentum]

Seq. No. 16590

Contig ID 46043\_1.R1040 5'-most EST vwf700675417.h1

Seq. No. 16591

Contig ID 46043 2.R1040

5'-most EST uC-gmflminsoy016f07b1

Seq. No. 16592

Contig ID 46045\_1.R1040 5'-most EST epx701103981.h1

Method BLASTX
NCBI GI g3212859
BLAST score 184
E value 1.0e-21
Match length 87

% identity 62

NCBI Description (AC004005) hypothetical protein [Arabidopsis thaliana]

Seq. No. 16593

Contig ID 46059 1.R1040

5'-most EST LIB3093-056-Q1-K1-E6

Seq. No. 16594

Contig ID 46067\_1.R1040 5'-most EST 2DC-02-Q1-B1-B5

Method BLASTX
NCBI GI g3608142
BLAST score 177
E value 8.0e-13
Match length 118
% identity 38

NCBI Description (AC005314) putative hin1 [Arabidopsis thaliana]

Seq. No. 16595



```
46070 1.R1040
Contig ID
                  fua701042374.hl
5'-most EST
                  16596
Seq. No.
                  46070 2.R1040
Contig ID
                  jC-gmst02400011f09a1
5'-most EST
                  16597
Seq. No.
                  46070 4.R1040
Contig ID
                  jex700903573.hl
5'-most EST
                  16598
Seq. No.
                  46074 1.R1040
Contig ID
5'-most EST
                  LIB3093-056-Q1-K1-C4
                  BLASTX
Method
                   g4539333
NCBI GI
BLAST score
                   318
                   2.0e-29
E value
                   111
Match length
                   56
% identity
                  (AL035539) putative amino acid transport protein
NCBI Description
                   [Arabidopsis thaliana]
                   16599
Seq. No.
                   46078 1.R1040
Contig ID
                   pmv700889181.hl
5'-most EST
                   BLASTX
Method
                   q3763916
NCBI GI
BLAST score
                   686
                   4.0e-72
E value
                   260
Match length
                   53
% identity
                   (AC004450) unknown protein [Arabidopsis thaliana]
NCBI Description
                   >qi 4531439 gb AAD22124.1 AC006224_6 (AC006224) unknown
                   protein [Arabidopsis thaliana]
                   16600
Seq. No.
                   46078 2.R1040
Contig ID
5'-most EST
                   txt700737563.h1
                   16601
Seq. No.
                   46078 5.R1040
Contig ID
5'-most EST
                   awf700838952.h1
Seq. No.
                   16602
                   46081 1.R1040
Contig ID
5'-most EST
                   hrw701062892.h1
Method
                   BLASTX
                   g1354510
NCBI GI
BLAST score
                   223
                   5.0e-18
E value
```

83 Match length % identity 60

(U55205) HAL2-like protein [Arabidopsis thaliana] NCBI Description

Seq. No.

46082 1.R1040

16603

Contig ID



```
5'-most EST
                  LIB3093-053-Q1-K1-H4
Seq. No.
                  16604
Contig ID
                  46096 1.R1040
5'-most EST
                  sat701002922.h1
                  16605
Seq. No.
Contig ID
                  46101 1.R1040
5'-most EST
                  kl1701208881.h1
Method
                  BLASTX
NCBI GI
                  q4558556
BLAST score
                  402
E value
                  6.0e-39
Match length
                  210
% identity
                  31
NCBI Description
                  (AC007138) predicted protein of unknown function
                  [Arabidopsis thaliana]
Seq. No.
                  16606
Contig ID
                  46102 1.R1040
5'-most EST
                  uC-gmflminsoy057b04b1
Method
                  BLASTX
                  g3355477
NCBI GI
BLAST score
                  1056
E value
                  1.0e-115
Match length
                  238
% identity
                  43
                  (AC004218) putative P-glycoprotein, pgp1 [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  16607
                   46108 1.R1040
Contig ID
5'-most EST
                  uaw700666147.hl
Seq. No.
                  16608
                   46113 1.R1040
Contig ID
5'-most EST
                  LIB31\overline{3}8-011-Q1-N2-F1
Method
                  BLASTX
NCBI GI
                  g172945
BLAST score
                  218
                  1.0e-17
E value
Match length
                  128
% identity
NCBI Description
                  (J03964) Phe-RNA synthetase [Saccharomyces cerevisiae]
Seq. No.
                  16609
                  46113 2.R1040
Contiq ID
5'-most EST
                  LIB3093-053-Q1-K1-E9
Method
                  BLASTX
```

Method BLASTX
NCBI GI g4104933
BLAST score 558
E value 3.0e-57
Match length 209
% identity 52

NCBI Description (AF042346) putative phenylalanyl-tRNA synthetase

beta-subunit; PheHB [Homo sapiens]



```
Seq. No.
                  46114 1.R1040
Contig ID
                  LIB3170-085-Q1-K1-B11
5'-most EST
                  16611
Seq. No.
                  46118 1.R1040
Contig ID
                  uC-qmflminsoy007h05b1
5'-most EST
                  BLASTX
Method
                  q3319682
NCBI GI
                  2093
BLAST score
                  0.0e + 00
E value
                  548
Match length
% identity
NCBI Description (Y17720) SPINDLY protein [Petunia x hybrida]
                   16612
Seq. No.
                   46124 1.R1040
Contig ID
                   LIB3093-053-Q1-K1-C5
5'-most EST
                   BLASTN
Method
                   g2055227
NCBI GI
                   35
BLAST score
E value
                   3.0e-10
                   155
Match length
                   88
% identity
NCBI Description Glycine max mRNA for SRC1, complete cds
Seq. No.
                   16613
                   46126 1.R1040
Contig ID
                   ncj700981719.hl
5'-most EST
Method
                   BLASTX
                   g3047104
NCBI GI
BLAST score
                   350
                   4.0e-33
E value
                   101
Match length
                   69
% identity
                  (AF058919) No definition line found [Arabidopsis thaliana]
NCBI Description
                   16614
Seq. No.
                   46129 1.R1040
Contig ID
                   LIB3093-053-Q1-K1-D10
5'-most EST
                   BLASTX
Method
                   g1016270
NCBI GI
                   432
BLAST score
                   1.0e-42
E value
                   130
Match length
                   67
 % identity
                   (U35123) p-glycoprotein [Urechis caupo]
 NCBI Description
                   16615
 Seq. No.
                   46131 1.R1040
 Contig ID
 5'-most EST
                   LIB3093-053-Q1-K1-D12
 Method
                   BLASTX
                   q4039155
 NCBI GI
                   455
 BLAST score
 E value
                   2.0e-45
 Match length
                   132
```

61

% identity



```
(AF104258) putative copper-inducible 35.6 kDa protein
NCBI Description
                  [Festuca rubra]
                  16616
Seq. No.
                  46134_1.R1040
Contig ID
                  uC-gmrominsoy040g10b1
5'-most EST
                  BLASTX
Method
                  q266410
NCBI GI
                  190
BLAST score
                  3.0e-14
E value
Match length
                  83
% identity
                   67
                  CDC2+/CDC28-RELATED PROTEIN KINASE R2 >gi_82507_pir__S13934
NCBI Description
                  protein kinase (EC 2.7.1.37) chain cdc2/cdc28 homolog -
                  rice >gi 20194_emb_CAA41172_ (X58194) cdc2+/CDC28-related
                  protein kinase [Oryza sativa]
                   16617
Seq. No.
                   46142 1.R1040
Contig ID
                   uC-gmropic091h08b1
5'-most EST
Method
                   BLASTX
                   g3297819
NCBI GI
                   1431
BLAST score
                   1.0e-159
E value
                   286
Match length
                   93
% identity
                   (AL031032) protein kinase - like protein [Arabidopsis
NCBI Description
                   thaliana]
                   16618
Seq. No.
                   46155 1.R1040
Contig ID
                   pxt700943439.hl
5'-most EST
                   16619
Seq. No.
                   46160 1.R1040
Contig ID
                   LIB3093-052-Q1-K1-H3
5'-most EST
                   16620
Seq. No.
                   46166 1.R1040
Contig ID
5'-most EST
                   uC-gmropic091a09b1
                   16621
Seq. No.
                   46166 2.R1040
Contig ID
                   gsv701055871.hl
5'-most EST
                   16622
Seq. No.
                   46174 1.R1040
Contig ID
                   jC-qmst02400073h03a1
 5'-most EST
Method
                   BLASTX
                   g1854581
NCBI GI
BLAST score
                   1019
                   1.0e-111
E value
                   296
Match length
                   65
 % identity
                   (L24120) peroxidase precursor [Linum usitatissimum]
NCBI Description
```

2750

16623

Seq. No.



```
46175 1.R1040
Contig ID
5'-most EST
                   rlr700899173.hl
                   16624
Seq. No.
                   46181 1.R1040
Contig ID
                   \verb"jC-gmf102220050h06a1"
5'-most EST
                   BLASTX
Method
                   g3885341
NCBI GI
                   1006
BLAST score
                   1.0e-109
E value
                   243
Match length
                   72
% identity
NCBI Description (AC005623) unknown protein [Arabidopsis thaliana]
Seq. No.
                   16625
                   46183 1.R1040
Contig ID
                   uC-gmflminsoy058d02b1
5'-most EST
                   BLASTX
Method
                   g3249109
NCBI GI
                   143
BLAST score
                   3.0e-17
E value
                   60
Match length
                   77
% identity
                   (AC003114) Contains similarity to pre-mRNA splicing factor
NCBI Description
                   (SF2), P33 subunit gb_M72709 from Homo sapiens. ESTs
                   gb_{142588} and gb_{R655\overline{1}4} come from this gene. [Arabidopsis
                   thaliana]
                   16626
Seq. No.
                   46187 1.R1040
Contig ID
                   zsg701124380.hl
5'-most EST
                   BLASTX
Method
                   q1644291
NCBI GI
BLAST score
                   310
                   2.0e-28
E value
Match length
                   126
% identity
                   (Z73295) receptor-like protein kinase [Catharanthus roseus]
NCBI Description
Seq. No.
                   16627
                   46191 1.R1040
Contig ID
5'-most EST
                   LIB3093-052-Q1-K1-G7
                   BLASTX
Method
NCBI GI
                   g4415926
BLAST score
                   363
                   4.0e-34
E value
Match length
                   153
                   46
% identity
```

(AC006282) unknown protein [Arabidopsis thaliana] NCBI Description

16628 Seq. No.

46196 1.R1040 Contig ID

LIB3093-052-Q1-K1-C4 5'-most EST

16629 Seq. No.

46196 2.R1040 Contig ID

5'-most EST jC-gmf102220098c03d1



```
16630
Seq. No.
                  46198 1.R1040
Contig ID
                  LIB3139-041-P1-N1-E5
5'-most EST
                  BLASTX
Method
                  g3063451
NCBI GI
BLAST score
                  377
                  3.0e-36
E value
                  142
Match length
                  54
% identity
NCBI Description (AC003981) F22013.13 [Arabidopsis thaliana]
                  16631
Seq. No.
                  46204 1.R1040
Contig ID
                  zzp700834872.hl
5'-most EST
                  16632
Seq. No.
                  46208 1.R1040
Contig ID
5'-most EST
                  k11701202363.h1
                  16633
Seq. No.
                  46210_1.R1040
Contig ID
                  kl1701210075.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g4538911
BLAST score
                  1266
                  1.0e-140
E value
                   330
Match length
                  72
% identity
                  (ALO49482) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   16634
Seq. No.
                   46214 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy043e11b1
                   BLASTX
Method
NCBI GI
                   q4510407
BLAST score
                   237
                   2.0e-19
E value
                   192
Match length
% identity
                   43
NCBI Description (AC006587) unknown protein [Arabidopsis thaliana]
                   16635
Seq. No.
                   46214 2.R1040
Contig ID
                   uC-gmflminsoy053e03b1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g4510407
BLAST score
                   189
                   8.0e-14
E value
                   199
Match length
                   44
% identity
                  (AC006587) unknown protein [Arabidopsis thaliana]
NCBI Description
```

Contig ID 46217\_1.R1040

5'-most EST LIB3093-052-Q1-K1-A12



Contig ID 46225 1.R1040 5'-most EST wvk700684405.h1

Seq. No. 16638

Contig ID 46235 1.R1040

5'-most EST LIB3093-051-Q1-K1-G12

Method BLASTX NCBI GI q4538939 BLAST score 278 2.0e-24 E value Match length 59 90 % identity

NCBI Description (AL049483) Col-O casein kinase I-like protein [Arabidopsis

thaliana]

16639

Seq. No.

Contig ID 46235 2.R1040 5'-most EST sat701002875.h1

Method BLASTX q4538939 NCBI GI BLAST score 278 E value 7.0e-25 Match length 60 % identity 88

NCBI Description (AL049483) Col-0 casein kinase I-like protein [Arabidopsis

thaliana]

Seq. No.

16640

Contig ID

46247 1.R1040

5'-most EST

jC-gmro02800029b10a1

Method BLASTX NCBI GI g3386618 BLAST score 151 1.0e-09 E value Match length 140 35

% identity

NCBI Description (AC004665) hypothetical protein [Arabidopsis thaliana]

Seq. No.

16641

Contig ID

46247 2.R1040

5'-most EST

LIB3093-051-Q1-K1-D12

Seq. No.

16642

Contig ID 5'-most EST 46247 3.R1040 sat701009105.hl

Seq. No.

16643

Contig ID 5'-most EST 46251 1.R1040 vzy700755033.hl

Method BLASTX g3738230 NCBI GI BLAST score 336 3.0e-31 E value Match length 115 % identity 59

NCBI Description (AB007790) DREB2A [Arabidopsis thaliana]



```
>gi_4126706_dbj_BAA36705_ (AB016570) DREB2A [Arabidopsis
                  thaliana]
                  16644
Seq. No.
                  46255_1.R1040
Contig ID
                  dpv701101580.h1
5'-most EST
                  BLASTX
Method
                  g4510375
NCBI GI
                   1278
BLAST score
                   1.0e-141
E value
                   660
Match length
                   51
% identity
                   (AC007017) putative homeotic protein BEL1 [Arabidopsis
NCBI Description
                   thaliana]
                   16645
Seq. No.
                   46255 2.R1040
Contig ID
                   uC-gmflminsoy079a01b1
5'-most EST
                   BLASTX
Method
                   q4510375
NCBI GI
                   178
BLAST score
                   1.0e-12
E value
                   170
Match length
                   35
% identity
                  (AC007017) putative homeotic protein BEL1 [Arabidopsis
NCBI Description
                   thaliana]
                   16646
Seq. No.
                   46255 3.R1040
Contig ID
                   eep70\overline{0}866011.h1
5'-most EST
                   16647
Seq. No.
                   46255 4.R1040
Contiq ID
                   g5753089
5'-most EST
                   BLASTX
Method
                   g4510375
NCBI GI
                   395
BLAST score
                   4.0e-38
E value
                   80
Match length
                   93
% identity
                    (AC007017) putative homeotic protein BEL1 [Arabidopsis
NCBI Description
                   thaliana]
                   16648
Seq. No.
                    46259 1.R1040
Contig ID
                   LIB3093-042-Q1-K1-F12
5'-most EST
                   BLASTX
Method
                    q81760
NCBI GI
BLAST score
                    190
                    3.0e-14
E value
Match length
                    103
                    41
 % identity
```

Contig ID 46283\_1.R1040

5'-most EST LIB3093-050-Q1-K1-H8

NCBI Description auxin-induced protein - soybean (fragment)



Method BLASTX
NCBI GI g2245378
BLAST score 195
E value 3.0e-15
Match length 101
% identity 46

NCBI Description (U83245) auxin response factor 1 [Arabidopsis thaliana]

Seq. No.

16650

Contig ID

46291\_1.R1040

5'-most EST

LIB3093-051-Q1-K1-A4

Seq. No.

16651

Contig ID

46298 1.R1040

5'-most EST

LIB3093-051-Q1-K1-B11

Method BLASTX
NCBI GI g2088651
BLAST score 416
E value 7.0e-54
Match length 184

% identity
NCBI Description

on (AF002109) hypersensitivity-related gene 201 isolog

[Arabidopsis thaliana]

Seq. No.

16652

66

Contig ID 5'-most EST

46306\_1.R1040 hyd700729794.h1

Seq. No.

16653

Contig ID

46309 1.R1040

5'-most EST

LIB3093-050-Q1-K1-F8

Method NCBI GI BLAST score BLASTX g1171642 473

E value
Match length

1.0e-47 117

% identity

74

NCBI Description

PROBABLE SERINE/THREONINE-PROTEIN KINASE NAK

>gi\_481206\_pir\_\_S38326 protein kinase - Arabidopsis
thaliana >gi\_166809 (L07248) protein kinase [Arabidopsis

thaliana]

Seq. No.

16654

Contig ID

46316 1.R1040

5'-most EST

LIB3093-050-Q1-K1-G9

Seq. No.

16655

Contig ID

46327 1.R1040

5'-most EST

LIB3093-050-Q1-K1-D11

Method BLASTX
NCBI GI g1086252
BLAST score 544
E value 2.0e-55
Match length 244

% identity NCBI Description 48
sucrose cleavage protein - Potato >gi\_707001\_bbs\_157931
(S74161) sucrolytic enzyme/ferredoxin homolog [Solanum



tuberosum=potatoes, cv. Cara, leaf, Peptide, 322 aa] [Solanum tuberosum]

Seq. No. 16656

Contig ID 46335\_1.R1040

5'-most EST LIB3093-050-Q1-K1-E12

Method BLASTX
NCBI GI 94263695
BLAST score 315
E value 8.0e-29
Match length 212
% identity 5

NCBI Description (AC006223) putative myosin II heavy chain [Arabidopsis

thaliana]

Seq. No. 16657

Contig ID 46336\_1.R1040 5'-most EST taw700657389.h1

Seq. No. 16658

Contig ID 46337\_1.R1040 5'-most EST uC-gmropic080e07b1

Method BLASTX
NCBI GI g3298544
BLAST score 284
E value 4.0e-25
Match length 69
% identity 68

NCBI Description (AC004681) unknown protein [Arabidopsis thaliana]

Seq. No. 16659

Contig ID 46340\_1.R1040

5'-most EST LIB3093-050-Q1-K1-A11

Method BLASTX
NCBI GI g4539330
BLAST score 871
E value 6.0e-94
Match length 215
% identity 77

NCBI Description (AL035679) putative receptor-like protein kinase (fragment)

[Arabidopsis thaliana]

Seq. No.

Contig ID 46344 1.R1040 5'-most EST sat701009536.h1

Seq. No.

16661

16660

Contig ID 46346\_1.R1040

5'-most EST g5677123
Method BLASTX
NCBI GI g4324597
BLAST score 889
E value 9.0e-96
Match length 265
% identity 65

NCBI Description (AF106324) sodium proton exchanger Nhx1 [Arabidopsis

thaliana]



```
Seq. No.
                  16662
Contig ID
                  46347 1.R1040
5'-most EST
                  zzp700835854.h1
Method
                  BLASTX
NCBI GI
                  g4538928
BLAST score
                  190
                  4.0e-14
E value
Match length
                  65
% identity
                  63
                  (AL049483) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  16663
Contig ID
                  46360 1.R1040
5'-most EST
                  LIB3093-049-Q1-K1-F9
Seq. No.
                  16664
Contig ID
                  46378 1.R1040
5'-most EST
                  LIB3093-049-Q1-K1-D6
Method
                  BLASTX
NCBI GI
                  g4455015
BLAST score
                  91
E value
                  1.0e-08
Match length
                  162
                  18
% identity
NCBI Description (AF113131) host cell factor homolog LCP [Homo sapiens]
Seq. No.
                  16665
                  46380 1.R1040
Contig ID
                  LIB3093-005-Q1-K1-F12
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3860325
BLAST score
                  655
                  1.0e-68
E value
Match length
                  142
% identity
                  80
NCBI Description (AJ012689) ribonuclease T2 [Cicer arietinum]
Seq. No.
                  16666
Contig ID
                  46383 1.R1040
5'-most EST
                  LIB3138-001-Q1-N1-D6
Method
                  BLASTX
NCBI GI
                  q1184316
BLAST score
                  152
                  9.0e-10
E value
                  66
Match length
                  41
% identity
NCBI Description (U45878) inhibitor of apoptosis protein 1 [Homo sapiens]
```

Contig ID 46388\_1.R1040

5'-most EST LIB3093-049-Q1-K1-F10

Method BLASTX
NCBI GI g2959767
BLAST score 432
E value 9.0e-43
Match length 127

2757



% identity 69

NCBI Description (AJ002584) AtMRP4 [Arabidopsis thaliana] >gi\_3738292 (AC005309) glutathione-conjugate transporter AtMRP4

[Arabidopsis thaliana]

Seq. No. 16668

Contig ID 46389 1.R1040

5'-most EST LIB3093-049-Q1-K1-F11

Seq. No. 16669

Contig ID 46393 1.R1040

5'-most EST LIB3109-048-Q1-K1-F7

Seq. No. 16670

Contig ID 46396\_1.R1040 5'-most EST epx701108164.h1

Seq. No. 16671

Contig ID 46402\_1.R1040 5'-most EST zsg701124868.h1

Seq. No. 16672

Contig ID 46406\_1.R1040 5'-most EST rlr700901382.h1

Method BLASTX
NCBI GI g1853970
BLAST score 1327
E value 1.0e-147
Match length 315
% identity 77

NCBI Description (D88122) CPRD46 protein [Vigna unguiculata]

Seq. No.

16673

Contig ID 46407\_1.R1040

5'-most EST LIB3093-049-Q1-K1-D10

Seq. No. 16674

Contig ID 46408 1.R1040

5'-most EST LIB3093-048-Q1-K1-G5

Method BLASTX
NCBI GI g2102696
BLAST score 186
E value 4.0e-14
Match length 100
% identity 41

NCBI Description (U72761) karyopherin beta 3 [Homo sapiens]

>gi 4504909 ref NP 002262.1 pKPNB3 karyopherin (importin)

beta

Seq. No. 16675

Contig ID 46415\_1.R1040 5'-most EST zhf700951782.h1

Method BLASTX
NCBI GI g2674203
BLAST score 288
E value 4.0e-26
Match length 90



99

58

[Arabidopsis thaliana]

Match length

NCBI Description

% identity

....

% identity (AF036328) CLP protease regulatory subunit CLPX NCBI Description [Arabidopsis thaliana] 16676 Seq. No. 46430 1.R1040 Contig ID LIB3093-048-Q1-K1-E6 5'-most EST BLASTX Method g2342683 NCBI GI 898 BLAST score 5.0e-97 E value 235 Match length 70 % identity NCBI Description (AC000106) Contains similarity to Bos beta-mannosidase (gb U46067). [Arabidopsis thaliana] 16677 Seq. No. 46435 1.R1040 Contig ID fC-gmst700653015f4 5'-most EST 16678 Seq. No. 46438 1.R1040 Contig ID LIB3093-048-Q1-K1-F7 5'-most EST BLASTX Method g2160185 NCBI GI 504 BLAST score 4.0e-51 E value 152 Match length 58 % identity NCBI Description (AC000132) Similar to S. pombe ISP4 (gb\_D83992). [Arabidopsis thaliana] 16679 Seq. No. 46439 1.R1040 Contig ID zhf700953968.h1 5'-most EST BLASTX Method q3738302 NCBI GI BLAST score 818 1.0e-87 E value 263 Match length % identity (AC005309) tubby-like protein [Arabidopsis thaliana] NCBI Description >gi 4249398 (AC006072) putative tubby protein [Arabidopsis thaliana] 16680 Seq. No. 46439 2.R1040 Contig ID LIB3107-017-Q1-K1-H5 5'-most EST Method BLASTX g2829918 NCBI GI 222 BLAST score 4.0e-24 E value

2759

(AC002291) similar to "tub" protein gp\_U82468\_2072162



```
16681
Seq. No.
                  46446 1.R1040
Contig ID
                  LIB3093-048-Q1-K1-D2
5'-most EST
                  BLASTX
Method
                  g3892709
NCBI GI
                  200
BLAST score
                  2.0e-15
E value
                  63
Match length
                  62
% identity
                  (AL033545) putative protein [Arabidopsis thaliana]
NCBI Description
                  16682
Seq. No.
                   46458_1.R1040
Contig ID
                  uC-qmrominsoy111b01b1
5'-most EST
                  BLASTX
Method
                   g4314370
NCBI GI
                   328
BLAST score
                   2.0e-34
E value
Match length
                   110
                   72
% identity
                  (AC006340) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   16683
Seq. No.
                   46458 2.R1040
Contig ID
5'-most EST
                   LIB3093-002-Q1-K1-F3
                   BLASTX
Method
                   g4314370
NCBI GI
                   305
BLAST score
                   7.0e-28
E value
Match length
                   122
                   55
% identity
                   (AC006340) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   16684
Seq. No.
                   46459 1.R1040
Contig ID
5'-most EST
                   LIB3093-047-Q1-K1-H9
Seq. No.
                   16685
                   46463 1.R1040
Contig ID
5'-most EST
                   bth700847557.h1
Seq. No.
                   16686
                   46468 1.R1040
Contig ID
                   LIB3093-048-Q1-K1-B3
5'-most EST
Method
                   BLASTX
                   g2760843
NCBI GI
BLAST score
                   263
                   6.0e-23
E value
Match length
                   115
                   48
 % identity
NCBI Description (AC003105) unknown protein [Arabidopsis thaliana]
                   16687
 Seq. No.
                   46470 1.R1040
 Contig ID
                   jC-gmle01810085f01a1
 5'-most EST
```

2760

BLASTX

g4204303

Method

NCBI GI



BLAST score E value 2.0e-56 Match length 112 % identity 87

NCBI Description (AC003027) lcl prt seq No definition line found

[Arabidopsis thaliana]

Seq. No. 16688

Contig ID 46470 2.R1040 5'-most EST uC-gmronoir052g03b1

Method BLASTX NCBI GI q3892045 BLAST score 274 E value 9.0e-26 Match length 71 % identity 85

(AC002330) putative zinc finger protein [Arabidopsis NCBI Description

thaliana]

Seq. No. 16689

46473 1.R1040 Contig ID 5'-most EST  $r1r70\overline{0}895887.h1$ 

Method BLASTX g3327150 NCBI GI BLAST score 252 E value 2.0e-21 Match length 187 % identity 33

NCBI Description (AB014568) KIAA0668 protein [Homo sapiens]

Seq. No.

16690 46491 1.R1040 Contig ID 5'-most EST g5058372

Method BLASTX NCBI GI g3176662 BLAST score 182 E value 2.0e-13 Match length 111 % identity 38

(ACO04393) Similar to mannosyl-oligosaccharide glucosidase NCBI Description

gb X87237 from Homo sapiens. [Arabidopsis thaliana]

Seq. No. 16691

Contig ID 46493 1.R1040

5'-most EST LIB3093-047-Q1-K1-C8

16692 Seq. No.

Contig ID 46495 1.R1040

5'-most EST LIB3093-047-Q1-K1-D12

16693 Seq. No.

46500 1.R1040 Contig ID

5'-most EST LIB3093-047-Q1-K1-D6

Method BLASTX g2498512 NCBI GI BLAST score 154 E value 8.0e-10



Match length 244 % identity 28 NCBI Description LDL

LDLC PROTEIN >gi\_1082264\_pir\_\_A53542 brefeldin A-sensitive Golgi protein LDLC - human >gi\_575654\_emb\_CAA84427\_

(Z34975) ldlCp [Homo sapiens]

Seq. No. 16694

Contig ID 46527\_1.R1040 5'-most EST wrg700787835.h2

Method BLASTX
NCBI GI g729775
BLAST score 680
E value 2.0e-71
Match length 199
% identity 69

NCBI Description HEAT SHOCK FACTOR PROTEIN HSF8 (HEAT SHOCK TRANSCRIPTION

FACTOR 8) (HSTF 8) (HEAT STRESS TRANSCRIPTION FACTOR)

>gi\_100264\_pir\_\_S25481 heat shock transcription factor 8 
Peruvian tomato >gi\_19492\_emb\_CAA47869\_ (X67600) heat shock

transcription factor 8 [Lycopersicon peruvianum]

Seq. No. 16695

Contig ID 46530\_1.R1040 5'-most EST ncj700984702.h1

Method BLASTX
NCBI GI g3033381
BLAST score 1448
E value 1.0e-161
Match length 334
% identity 83

NCBI Description (AC004238) putative UDP-galactose-4-epimerase [Arabidopsis

thaliana]

Seq. No. 16696

Contig ID 46531\_1.R1040

5'-most EST LIB3093-046-Q1-K1-H4

Method BLASTX
NCBI GI g1175557
BLAST score 177
E value 1.0e-12
Match length 93
% identity 41

NCBI Description HYPOTHETICAL PROTEIN HIll61 >gi\_1073773\_pir\_\_A64187 15 kDa protein (P15) homolog - Haemophilus influenzae (strain Rd

protein (P15) homolog - Haemophilus influenzae (strain kd KW20) >gi\_1574088 (U32796) conserved hypothetical protein

[Haemophilus influenzae Rd]

Seq. No. 16697

Contig ID 46535\_1.R1040 5'-most EST uaw700663586.h1

Method BLASTX
NCBI GI g4079639
BLAST score 430
E value 8.0e-42
Match length 279
% identity 37

NCBI Description (AJ131635) beta-galactosidase [psychrophilic bacterium TAE



. . . .

Seq. No. 16698

Contig ID 46538\_1.R1040

5'-most EST LIB3093-047-Q1-K1-A12

Method BLASTX
NCBI GI g2281631
BLAST score 323
E value 7.0e-30
Match length 139
% identity 56

NCBI Description (AF003096) AP2 domain containing protein RAP2.3

[Arabidopsis thaliana]

Seq. No. 16699

Contig ID 46540\_1.R1040 5'-most EST epx701107649.h1

Seq. No. 16700

Contig ID 46540\_2.R1040 5'-most EST g5509022

Seq. No. 16701

Contig ID 46549 1.R1040 5'-most EST hrw701058806.h1

Seq. No. 16702

Contig ID 46549 2.R1040 5'-most EST bth700844280.h1

Seq. No. 16703

Contig ID 46551\_1.R1040 5'-most EST uaw700661411.h1

Seq. No. 16704

Contig ID 46554\_1.R1040 5'-most EST zhf700956907.h1

Seq. No. 16705

Contig ID 46573\_1.R1040

5'-most EST LIB3139-003-P1-N1-E7

Seq. No. 16706

Contig ID 46584\_1.R1040

5'-most EST uC-qmronoir014d03b1

Method BLASTX
NCBI GI g3928862
BLAST score 362
E value 5.0e-34
Match length 304
% identity 33

NCBI Description (AF089710) disease resistance protein RPP8 [Arabidopsis

thaliana]

Seq. No. 16707

Contig ID 46598 1.R1040

5'-most EST jC-gmle01810001h05a1



Contig ID 46605\_1.R1040

5'-most EST LIB3093-045-Q1-K1-H5

Seq. No. 16709

Contig ID 46620\_1.R1040 5'-most EST gsv701047865.h1

Method BLASTX
NCBI GI g2459445
BLAST score 373
E value 2.0e-35
Match length 206
% identity 29

NCBI Description (AC002332) putative ribonucleoprotein [Arabidopsis

thaliana]

Seq. No. 16710

Contig ID 46620\_2.R1040

5'-most EST jC-gmf102220051f03a1

Method BLASTX
NCBI GI g2500574
BLAST score 385
E value 7.0e-37
Match length 223
% identity 22

NCBI Description NUCLEAR POLYADENYLATED RNA-BINDING PROTEIN NAB4

>gi\_2131274\_pir\_\_S66820 heterogeneous nuclear

ribonucleoprotein HRP1 - yeast (Saccharomyces cerevisiae) >gi\_1016290 (U35737) nuclear polyadenylated RNA-binding

protein [Saccharomyces cerevisiae]

>gi\_1420003\_emb\_CAA99142\_ (Z74865) ORF YOL123w [Saccharomyces cerevisiae] >gi\_1550721\_emb\_CAA64546\_ (X95258) RNA binding protein [Saccharomyces cerevisiae] >gi\_1657691 (U38535) Hrplp [Saccharomyces cerevisiae]

Seq. No. 16711

Contig ID 46620\_4.R1040

5'-most EST uC-gmronoir016h01b1

Method BLASTX
NCBI GI g2500574
BLAST score 161
E value 8.0e-11
Match length 62
% identity 25

NCBI Description NUCLEAR POLYADENYLATED RNA-BINDING PROTEIN NAB4

>gi\_2131274\_pir\_\_S66820 heterogeneous nuclear

ribonucleoprotein HRP1 - yeast (Saccharomyces cerevisiae) >gi\_1016290 (U35737) nuclear polyadenylated RNA-binding

protein [Saccharomyces cerevisiae]

>gi\_1420003\_emb\_CAA99142\_ (Z74865) ORF YOL123w
[Saccharomyces cerevisiae] >gi\_1550721\_emb\_CAA64546\_
(X95258) RNA binding protein [Saccharomyces cerevisiae]
>gi\_1657691 (U38535) Hrplp [Saccharomyces cerevisiae]

Seq. No. 16712

Contig ID 46634\_1.R1040



```
LIB3106-109-Q1-K1-F12
5'-most EST
                  16713
Seq. No.
                  46634 3.R1040
Contig ID
                  epx701105940.h1
5'-most EST
                  16714
Seq. No.
                  46636 1.R1040
Contig ID
                  LIB3093-045-Q1-K1-D4
5'-most EST
                  BLASTN
Method
                  g304040
NCBI GI
                  356
BLAST score
                  0.0e+00
E value
                  428
Match length
% identity
                  96
NCBI Description Alnus incana chloroplast 23S ribosomal RNA (23S rRNA) gene
                  16715
Seq. No.
                  46639 1.R1040
Contig ID
                  LIB3093-045-Q1-K1-D7
5'-most EST
                  16716
Seq. No.
                   46640 1.R1040
Contig ID
                  LIB3093-037-Q1-K1-H6
5'-most EST
                  BLASTX
Method
                   g3738296
NCBI GI
                   289
BLAST score
                   2.0e-25
E value
                   170
Match length
                   36
% identity
NCBI Description (AC005309) hypothetical protein [Arabidopsis thaliana]
                   16717
Seq. No.
                   46640 2.R1040
Contig ID
                   LIB3170-082-Q1-K1-G7
5'-most EST
                   16718
Seq. No.
                   46654 1.R1040
Contig ID
                   LIB3093-045-Q1-K1-B7
5'-most EST
                   BLASTX
Method
                   g3402713
NCBI GI
                   299
BLAST score
E value
                   8.0e-27
                   181
Match length
% identity
                   (AC004261) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   16719
Seq. No.
                   46661 1.R1040
Contig ID
                   LIB3093-006-Q1-K1-E10
 5'-most EST
Method
                   BLASTX
                   q1208497
NCBI GI
                   259
BLAST score
                   8.0e-22
E value
Match length
                   131
                   42
 % identity
```

NCBI Description (D38125) EREBP-4 [Nicotiana tabacum]

```
16720
Seq. No.
                  46661 2.R1040
Contig ID
                  jC-gmro02910038e06a1
5'-most EST
                  16721
Seq. No.
                  46661 3.R1040
Contig ID
                  gsf700698320.hl
5'-most EST
                  16722
Seq. No.
                  46670_1.R1040
Contig ID
                  uC-gmflminsoy078c06b1
5'-most EST
                  BLASTX
Method
                  g1730771
NCBI GI
BLAST score
                  412
                  2.0e-39
E value
                  521
Match length
                  16
% identity
                  HYPOTHETICAL 110.9 KD PROTEIN IN SPC98-TOM70 INTERGENIC
NCBI Description
                   REGION >gi_2132752_pir__S63064 probable membrane protein
                  YNL123w - yeast (Saccharomyces cerevisiae)
                   >gi_1183950_emb_CAA93384_ (Z69382) N1897 [Saccharomyces
                  cerevisiae] >gi_1302054_emb_CAA96004_ (Z71399) ORF YNL123w
                   [Saccharomyces cerevisiae]
                   16723
Seq. No.
                   46670 2.R1040
Contig ID
                  LIB3170-086-Q1-J1-A6
5'-most EST
                   16724
Seq. No.
                   46672 1.R1040
Contig ID
                   LIB3093-045-Q1-K1-A3
5'-most EST
                   16725
Seq. No.
                   46682 1.R1040
Contig ID
5'-most EST
                   leu701151991.hl
                   BLASTX
Method
NCBI GI
                   q459002
                   203
BLAST score
E value
                   1.0e-15
                   159
Match length
```

% identity 30 NCBI Description (U00036) R151.6 gene product [Caenorhabditis elegans]

 Seq. No.
 16726

 Contig ID
 46682\_2.R1040

 5'-most EST
 g4305349

 Method
 BLASTX

 NCBI GI
 g459002

 BLAST score
 241

 E value
 2.0e-20

Match length 136 % identity 36

NCBI Description (U00036) R151.6 gene product [Caenorhabditis elegans]

Seq. No. 16727

Contig ID 46685\_1.R1040

2766



5'-most EST jC-gmle01810042e04a1

Method BLASTX
NCBI GI g2465923
BLAST score 1378
E value 1.0e-153
Match length 527
% identity 54

NCBI Description (AF024648) receptor-like serine/threonine kinase

[Arabidopsis thaliana]

Seq. No. 16728

Contig ID 46685 2.R1040

5'-most EST jC-gmro02910013b09a1

Method BLASTX
NCBI GI g2465923
BLAST score 186
E value 3.0e-16
Match length 152
% identity 39

NCBI Description (AF024648) receptor-like serine/threonine kinase

[Arabidopsis thaliana]

Seq. No. 16729

Contig ID 46690\_1.R1040

5'-most EST uC-gmrominsoy215e06b1

Method BLASTX
NCBI GI g2244753
BLAST score 360
E value 3.0e-34
Match length 159
% identity 40

NCBI Description (Z97335) hypothetical protein [Arabidopsis thaliana]

Seq. No. 16730

Contig ID 46692 1.R1040

5'-most EST LIB3093-044-Q1-K1-F7

Seq. No. 16731

Contig ID 46705\_1.R1040 5'-most EST ssr700558363.h1

Method BLASTX
NCBI GI g1091678
BLAST score 271
E value 2.0e-23
Match length 240
% identity 28

NCBI Description activator-like transposable element [Pennisetum glaucum]

Seq. No. 16732

Contig ID 46734\_1.R1040 5'-most EST fC-gmfl700863687f1

Method BLASTX
NCBI GI g2245136
BLAST score 1783
E value 0.0e+00
Match length 528
% identity 62



```
(Z97344) trehalose-6-phosphate synthase homolog
NCBI Description
                   [Arabidopsis thaliana]
                   16733
Seq. No.
                   46737 1.R1040
Contig ID
                   sat701011525.hl
5'-most EST
                   16734
Seq. No.
                   46743 1.R1040
Contig ID
                   LIB3093-042-Q1-K1-H8
5'-most EST
                   16735
Seq. No.
                   46747 1.R1040
Contig ID
                   ncj700984996.hl
5'-most EST
                   BLASTX
Method
                   g128838
NCBI GI
                   1922
BLAST score
                   0.0e + 00
E value
                   393
Match length
                   91
% identity
                   NADH-PLASTOQUINONE OXIDOREDUCTASE 49 KD SUBUNIT,
NCBI Description
                   CHLOROPLAST (ORF 393) >gi_82215_pir_ A05216 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 393 - common
                   tobacco chloroplast >gi_1223674_emb_CAA77398_ (Z00044) NADH
                   dehydrogenase 49kD subunit [Nicotiana tabacum]
                   16736
Seq. No.
                   46753 1.R1040
Contig ID
                   \verb|jC-gm\overline{l}e01810088h09d1|
5'-most EST
                   BLASTN
Method
                   g9740
NCBI GI
                   60
BLAST score
                   5.0e-25
E value
                   116
Match length
                   88
% identity
NCBI Description Naegleria gruberi mRNA for alpha-tubulin (2)
                   16737
Seq. No.
                   46762 1.R1040
Contig ID
                   q5752\overline{5}33
 5'-most EST
                   BLASTX
Method
                   g2832643
NCBI GI
BLAST score
                   545
                    9.0e-56
E value
                   204
Match length
 % identity
                   (AL021710) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                    16738
 Seq. No.
                    46764 1.R1040
 Contig ID
                    gsv701055444.hl
 5'-most EST
                    BLASTX
 Method
```

Method BLASTX
NCBI GI g2864622
BLAST score 247
E value 2.0e-20
Match length 128



```
% identity
NCBI Description (AL021811) putative protein [Arabidopsis thaliana]
                  16739
Seq. No.
                  46764 3.R1040
Contig ID
                  k11701205692.h1
5'-most EST
                  16740
Seq. No.
                  46773 1.R1040
Contig ID
                  uC-qmflminsoy070a12b1
5'-most EST
                  BLASTX
Method
                   g3927830
NCBI GI
                   169
BLAST score
                   8.0e-12
E value
Match length
                   137
% identity
                   15
NCBI Description (AC005727) hypothetical protein [Arabidopsis thaliana]
                   16741
Seq. No.
                   46775 1.R1040
Contig ID
                   gsv701054180.h1
5'-most EST
                   BLASTX
Method
                   g2213610
NCBI GI
                   207
BLAST score
                   4.0e-16
E value
Match length
                   134
% identity
                   24
NCBI Description (AC000103) F21J9.4 [Arabidopsis thaliana]
                   16742
Seq. No.
                   46778 1.R1040
Contig ID
                   fC-gmse7000760534f1
5'-most EST
                   16743
Seq. No.
                   46782 1.R1040
Contig ID
                   LIB3093-042-Q1-K1-C4
 5'-most EST
                   BLASTX
Method
                   q2262176
NCBI GI
                   310
BLAST score
                   5.0e-28
E value
                   105
Match length
                   57
 % identity
                   (AC002329) putative RING zinc-finger protein [Arabidopsis
 NCBI Description
                   thaliana] >gi 3790573 (AF078824) RING-H2 finger protein
                   RHA3a [Arabidopsis thaliana]
                   16744
```

46786 1.R1040 Contig ID sat701002810.hl 5'-most EST

BLASTX Method g2262178 NCBI GI 231 BLAST score 5.0e-19 E value 134 Match length % identity 42

(AC002329) putative Mlo-like protein [Arabidopsis thaliana] NCBI Description



```
Seq. No.
Contig ID
                   46787 1.R1040
5'-most EST
                  LIB3093-042-Q1-K1-C9
Seq. No.
                  16746
                  46800 1.R1040
Contig ID
5'-most EST
                  seb700654291.hl
                  BLASTX
Method
NCBI GI
                  g4097522
BLAST score
                  851
E value
                  2.0e-91
Match length
                  228
% identity
                  (U63534) cinnamyl alcohol dehydrogenase [Fragaria x
NCBI Description
                  ananassa]
Seq. No.
                  16747
Contig ID
                  46800 2.R1040
5'-most EST
                  uC-gmflminsoy025a02b1
Method
                  BLASTX
NCBI GI
                  g4097522
                  970
BLAST score
                  1.0e-105
E value
Match length
                  270
% identity
                  67
NCBI Description
                  (U63534) cinnamyl alcohol dehydrogenase [Fragaria x
                  ananassa]
Seq. No.
                  16748
Contig ID
                   46803 1.R1040
5'-most EST
                  bth700844352.h1
Method
                  BLASTN
NCBI GI
                  g2465528
BLAST score
                  174
E value
                  1.0e-92
                  525
Match length
                  83
% identity
                  Medicago truncatula phosphate transporter (MtPT2) mRNA,
NCBI Description
                  complete cds
Seq. No.
                  16749
Contig ID
                  46805 1.R1040
5'-most EST
                  LIB3093-042-Q1-K1-B8
                  BLASTX
                  g2911042
                  614
```

Method NCBI GI BLAST score

6.0e-73 E value Match length 200 % identity 71

NCBI Description (AL021961) Phosphoglycerate dehydrogenase - like protein [Arabidopsis thaliana]

16750 Seq. No.

Contig ID 46808 1.R1040 5'-most EST bth700848961.h1

Seq. No. 16751



Contig ID 46808 2.R1040

5'-most EST uC-qmflminsoy055h03b1

Method BLASTX NCBI GI g461812 BLAST score 390 E value 1.0e-37 Match length 173 45 % identity

NCBI Description CYTOCHROME P450 72 (CYPLXXII) (PROBABLE

GERANIOL-10-HYDROXYLASE) (GE10H) >gi 167484 (L10081)

Cytochrome P-450 protein [Catharanthus roseus]

>gi\_445604\_prf\_\_1909351A cytochrome P450 [Catharanthus

roseus]

16752

Seq. No.

Contig ID 46810 1.R1040

5'-most EST jC-gmro02910040f03a1

Method BLASTX NCBI GI q4454051 BLAST score 856 7.0e-92 E value Match length 296 55 % identity

NCBI Description (AL035394) putative polygalacturonase [Arabidopsis

thaliana]

Seq. No. 16753

Contig ID 46815 1.R1040

5'-most EST LIB3093-041-Q1-K1-H9

Method BLASTX NCBI GI g3128176 BLAST score 359 E value 7.0e-34 Match length 122 % identity 52

NCBI Description (AC004521) unknown protein [Arabidopsis thaliana]

Seq. No. 16754

Contig ID 46816 1.R1040 5'-most EST taw700656122.h1

Seq. No. 16755

Contig ID 46820 1.R1040 5'-most EST kl1701210925.h1

Method BLASTX NCBI GI g2342724 BLAST score 306 E value 6.0e-28 Match length 92 % identity 64

NCBI Description (AC002341) unknown protein [Arabidopsis thaliana]

Seq. No. 16756

46820 2.R1040 Contig ID

5'-most EST LIB3093-042-Q1-K1-A2

Method BLASTX NCBI GI g2342724

```
180
BLAST score
                  3.0e-13
E value
                  55
Match length
                  65
% identity
                  (AC002341) unknown protein [Arabidopsis thaliana]
NCBI Description
                  16757
Seq. No.
                  46820 3.R1040
Contig ID
                  qsv701046634.hl
5'-most EST
                  BLASTX
Method
                  g2342724
NCBI GI
                  144
BLAST score
                  4.0e-15
E value
                  67
Match length
% identity
                   64
                  (AC002341) unknown protein [Arabidopsis thaliana]
NCBI Description
                   16758
Seq. No.
                   46836 1.R1040
Contig ID
                   uC-gmrominsoy229b08b1
5'-most EST
                   BLASTX
Method
                   g2764524
NCBI GI
                   417
BLAST score
                   7.0e-41
E value
                   136
Match length
% identity
                   64
                  (AJ000520) Rieske iron-sulfur protein Tic55 [Pisum sativum]
NCBI Description
                   16759
Seq. No.
                   46836 2.R1040
Contig ID
                   zhf700963263.hl
5'-most EST
                   BLASTX
Method
                   g2764524
NCBI GI
                   362
BLAST score
                   2.0e-34
E value
                   130
Match length
                   62
% identity
                   (AJ000520) Rieske iron-sulfur protein Tic55 [Pisum sativum]
NCBI Description
                   16760
Seq. No.
                   46839 1.R1040
Contig ID
                   uaw700666257.h1
5'-most EST
                   16761
 Seq. No.
                   46840 1.R1040
 Contig ID
                   rlr700900711.h1
 5'-most EST
                   16762
 Seq. No.
                   46845 1.R1040
 Contig ID
                   dpv701097156.h1
 5'-most EST
 Method
                   BLASTX
                   g3641837
 NCBI GI
                   1206
 BLAST score
 E value
                   1.0e-133
                   312
 Match length
 % identity
                   76
 NCBI Description (AL023094) Nonclathrin coat protein gamma - like protein
```



## [Arabidopsis thaliana]

 Seq. No.
 16763

 Contig ID
 46847\_1.R1040

 5'-most EST
 gsv701054651.h1

Seq. No. 16764

Contig ID 46848\_1.R1040

5'-most EST LIB3093-041-Q1-K1-E9

Seq. No. 16765

Contig ID 46851\_1.R1040 5'-most EST g4287043

Seq. No. 16766

Contig ID 46862\_1.R1040

5'-most EST LIB3093-041-Q1-K1-C7

Method BLASTX
NCBI GI g3402683
BLAST score 299
E value 2.0e-27
Match length 92
% identity 72

NCBI Description (AC004697) patatin-like protein [Arabidopsis thaliana]

Seq. No. 16767

Contig ID 46864\_1.R1040 5'-most EST vzy700756364.h1

Method BLASTX
NCBI GI 94455180
BLAST score 1527
E value 1.0e-172
Match length 433
% identity 71

NCBI Description (AL035521) putative protein [Arabidopsis thaliana]

Seq. No. 16768

Contig ID 46868\_1.R1040

5'-most EST LIB3093-041-Q1-K1-D2

Method BLASTX
NCBI GI g3036797
BLAST score 462
E value 7.0e-46
Match length 191
% identity 53

NCBI Description (AL022373) hypothetical protein [Arabidopsis thaliana] >gi\_3805859\_emb\_CAA21479\_ (AL031986) hypothetical protein

[Arabidopsis thaliana]

Seq. No. 16769

Contig ID 46870\_1.R1040

5'-most EST LIB3093-041-Q1-K1-D4

Seq. No. 16770

Contig ID 46872\_1.R1040 5'-most EST g5509162



Contig ID 46884\_1.R1040

5'-most EST LIB3093-041-Q1-K1-B6

Method BLASTX
NCBI GI g2462911
BLAST score 1183
E value 1.0e-130
Match length 284
% identity 76

NCBI Description (Z83832) UDP-glucose:sterol glucosyltransferase [Avena

sativa]

Seq. No.

16772

Contig ID

46887 1.R1040

5'-most EST

LIB3093-041-Q1-K1-A11

Method BLASTX
NCBI GI g3281853
BLAST score 412
E value 6.0e-40
Match length 176
% identity 60

NCBI Description (AL031004) putative protein [Arabidopsis thaliana]

Seq. No. 16773

Contig ID 46894 1.R1040 5'-most EST kmv700743941.h1

Method BLASTN
NCBI GI g1619324
BLAST score 235
E value 1.0e-129
Match length 395
% identity 90

NCBI Description P.sativum mRNA for ADP-glucose pyrophosphorylase

Seq. No.

16774

Contig ID 46901\_1.R1040

5'-most EST LIB3093-041-Q1-K1-A1

Seq. No. 16775

Contig ID 46902 1.R1040 5'-most EST trc700563106.h1

Method BLASTX
NCBI GI g3548803
BLAST score 737
E value 2.0e-87
Match length 200
% identity 84

NCBI Description (AC005313) putative DNA-binding protein [Arabidopsis thaliana] >gi\_4335770 gb\_AAD17447\_ (AC006284) putative

SMUBP-2 [mouse] DNA-binding protein [Arabidopsis thaliana]

Seq. No. 16776

Contig ID 46905\_1.R1040 5'-most EST uaw700664786.h1

Method BLASTX NCBI GI g3142303 BLAST score 1508



E value 1.0e-168
Match length 331
% identity 89

NCBI Description

(AC002411) Strong similarity to MRP-like ABC transporter gb\_U92650 from A. thaliana and canalicular multi-drug resistance protein gb\_L49379 from Rattus norvegicus.
[Arabidopsis thaliana]

Seq. No. 16777

Contig ID 46911\_1.R1040 5'-most EST eep700866569.h1

Seq. No. 16778

Contig ID 46911\_2.R1040

5'-most EST LIB3093-040-Q1-K1-G1

Method BLASTX
NCBI GI g2244797
BLAST score 249
E value 3.0e-21
Match length 80
% identity 62

NCBI Description (Z97336) hypothetical protein [Arabidopsis thaliana]

Seq. No. 16779

Contig ID 46914\_1.R1040

5'-most EST LIB3093-040-Q1-K1-G12

Seq. No. 16780

Contig ID 46917\_1.R1040 5'-most EST fC-gmle700870679d1

Seq. No. 16781

Contig ID 46918\_1.R1040

5'-most EST LIB3093-040-Q1-K1-G6

Seq. No. 16782

Contig ID 46923\_1.R1040 5'-most EST trc700561718.h1

Method BLASTX
NCBI GI g2673918
BLAST score 229
E value 7.0e-19
Match length 65
% identity 69

NCBI Description (AC002561) unknwon protein [Arabidopsis thaliana]

Seq. No. 16783

Contig ID 46927\_1.R1040

5'-most EST LIB3107-078-Q1-K1-F7

Method BLASTX
NCBI GI g2981439
BLAST score 346
E value 1.0e-32
Match length 120
% identity 64

NCBI Description (AF051853) t-SNARE SED5 [Arabidopsis thaliana]



Contig ID 46936\_1.R1040

5'-most EST LIB3093-040-Q1-K1-F12

Seq. No. 16785

Contig ID 46956\_1.R1040 5'-most EST fC-gmse700839738f1

Method BLASTX
NCBI GI g4371291
BLAST score 191
E value 2.0e-14
Match length 109
% identity 46

NCBI Description (AC006260) hypothetical protein [Arabidopsis thaliana]

Seq. No. 16786

Contig ID 46958\_1.R1040 5'-most EST ssr700560804.h1

Method BLASTX
NCBI GI g3426039
BLAST score 725
E value 7.0e-77
Match length 199
% identity 66

NCBI Description (AC005168) unknown protein [Arabidopsis thaliana]

Seq. No. 16787

Contig ID 46962\_1.R1040 5'-most EST vzy700756385.h1

Seq. No. 16788

Contig ID 46965 1.R1040

5'-most EST LIB3093-040-Q1-K1-C11

Seq. No. 16789

Contig ID 46974\_1.R1040

5'-most EST LIB3093-027-Q1-K1-D12

Method BLASTX
NCBI GI g2499553
BLAST score 750
E value 1.0e-79
Match length 185
% identity 76

NCBI Description CRYPTOCHROME 1 APOPROTEIN (BLUE LIGHT PHOTORECEPTOR)

>gi\_629524\_pir\_\_S39058 probable deoxyribodipyrimidine

photo-lyase (EC 4.1.99.3) - Arabidopsis thaliana

>gi\_442529\_bbs\_139743 (S66907) flavin-type blue-light photoreceptor, HY4=DNA photolyase/tropomyosin A homolog [Arabidopsis thaliana, ecotype Columbia, Peptide, 681 aa]

[Arabidopsis thaliana]

Seq. No. 16790

Contig ID 46974 2.R1040

5'-most EST jC-qmfl02220079e01a1

Method BLASTX
NCBI GI g2499553
BLAST score 149



E value 1.0e-09
Match length 52
% identity 50

NCBI Description CRYPTOCHROME 1 APOPROTEIN (BLUE LIGHT PHOTORECEPTOR)

>gi\_629524\_pir\_\_S39058 probable deoxyribodipyrimidine photo-lyase (EC 4.1.99.3) - Arabidopsis thaliana

>gi\_442529\_bbs\_139743 (S66907) flavin-type blue-light photoreceptor, HY4=DNA photolyase/tropomyosin A homolog [Arabidopsis thaliana, ecotype Columbia, Peptide, 681 aa]

[Arabidopsis thaliana]

Seq. No. 16791

Contig ID 46974 3.R1040

5'-most EST LIB3093-036-Q1-K1-C1

Seq. No. 16792

Contig ID 46981 1.R1040

5'-most EST LIB3093-040-Q1-K1-A5

Method BLASTX
NCBI GI g1885381
BLAST score 168
E value 1.0e-11
Match length 77
% identity 53

NCBI Description (U77665) RNaseP protein P30 [Homo sapiens]

Seq. No. 16793

Contig ID 46985\_1.R1040 5'-most EST ekl700968210.h1

Method BLASTX
NCBI GI g3047082
BLAST score 209
E value 2.0e-16
Match length 93
% identity 55

NCBI Description (AF058914) similar to Vigna radiata pectinacetylesterase

precursor (GB:X99348) [Arabidopsis thaliana]

Seq. No. 16794

Contig ID 46989\_1.R1040 5'-most EST pxt700944981.h1

Method BLASTX
NCBI GI g4115382
BLAST score 158
E value 1.0e-10
Match length 45
% identity 62

NCBI Description (AC005967) hypothetical protein [Arabidopsis thaliana]

Seq. No. 16795

Contig ID 46989 2.R1040 5'-most EST hrw701057036.h2

Seq. No. 16796

Contig ID 47000 1.R1040

5'-most EST LIB3107-033-Q1-K1-E7

% identity

37

```
Seq. No.
                   16797
Contig ID
                   47012 1.R1040
5'-most EST
                   fua701038933.h1
Method
                   BLASTX
NCBI GI
                   g1752734
BLAST score
                   1012
E value
                   1.0e-110
                   297
Match length
% identity
                   66
NCBI Description
                   (D78510) beta-glucan-elicitor receptor [Glycine max]
Seq. No.
                   16798
Contig ID
                   47021 1.R1040
5'-most EST
                   LIB3167-049-P1-K1-B9
Seq. No.
                   16799
Contig ID
                   47026 1.R1040
5'-most EST
                   LIB3093-039-Q1-K1-C11
Seq. No.
                   16800
Contig ID
                   47034 1.R1040
5'-most EST
                   q4303205
Method
                   BLASTX
NCBI GI
                   g4091008
BLAST score
                   671
E value
                   2.0e-70
Match length
                   168
                   77
% identity
NCBI Description
                  (AF040700) methionyl-tRNA synthetase [Oryza sativa]
Seq. No.
                   16801
Contig ID
                   47037 1.R1040
5'-most EST
                   g4289796
Method
                   BLASTX
NCBI GI
                   g2708314
BLAST score
                   351
E value
                   6.0e-33
Match length
                   116
% identity
                   32
NCBI Description
                   (AF027727) protein disulfide isomerase RB60 [Chlamydomonas
                   reinhardtii] >gi_4104541 (AF036939) protein disulfide
                   isomerase [Chlamydomonas reinhardtii]
Seq. No.
                   16802
Contig ID
                   47045 1.R1040
5'-most EST
                   zhf700952864.h1
Seq. No.
                   16803
Contig ID
                   47051 1.R1040
5'-most EST
                  uC-gmrominsoy055d02b1
Method
                  BLASTX
NCBI GI
                  q3873913
BLAST score
                  177
E value
                  7.0e-13
Match length
                  111
```

2778

NCBI Description (Z71258) similar to Flavin-binding monooxygenase-like



## [Caenorhabditis elegans]

```
Seq. No.
                   16804
                   47055 1.R1040
Contig ID
5'-most EST
                  ncj700976794.h1
Seq. No.
                   16805
Contig ID
                   47059 1.R1040
5'-most EST
                  gsv701046537.h1
Seq. No.
                  16806
Contig ID
                   47062 1.R1040
5'-most EST
                  g5509232
```

Seq. No. 16807

Contig ID 47066\_2.R1040 5'-most EST zhf700960323.h1

 Seq. No.
 16808

 Contig ID
 47068

 5'-most EST
 LIB30

47068\_1.R1040 LIB3093-038-Q1-K1-H8

Method BLASTX
NCBI GI g3128172
BLAST score 530
E value 5.0e-54
Match length 185
% identity 53

NCBI Description (AC004521) hypothetical protein [Arabidopsis thaliana]

 Seq. No.
 16809

 Contig ID
 47077 1.R1040

 5'-most EST
 LIB3106-040-Q1-K1-G2

 Method
 BLASTX

 NCBI GI
 g729274

 BLAST score
 394

BLAST score 394
E value 4.0e-38
Match length 98
% identity 76
NCBI Description 40 KD PR

NCBI Description 40 KD PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE)
(ROTAMASE) (CYCLOPHILIN-40) (CYP-40) (CYCLOPHILIN-RELATED

PROTEIN) >gi\_422797\_pir\_\_A45981 peptidylprolyl isomerase

(EC 5.2.1.8) CyP-40 - human >gi\_348910 (L11667)

cyclophilin-40 [Homo sapiens] >gi\_1769812\_dbj\_BAA09923\_

(D63861) cyclophilin 40 [Homo sapiens]

Seq. No. 16810

Contig ID 47078 1.R1040

5'-most EST LIB3093-038-Q1-K1-F4 Method BLASTX

NCBI GI g2213581
BLAST score 163
E value 3.0e-11
Match length 48
% identity 60

NCBI Description (AC000348) T7N9.1 [Arabidopsis thaliana]

Seq. No. 16811



Contig ID 47080 1.R1040

5'-most EST LIB3138-054-Q1-N1-C10

Method BLASTX
NCBI GI g4558564
BLAST score 353
E value 2.0e-33
Match length 125
% identity 57

NCBI Description (AC007138) predicted protein of unknown function

[Arabidopsis thaliana]

Seq. No. 16812

Contig ID 47081\_1.R1040

5'-most EST LIB3093-038-Q1-K1-F6

Method BLASTX
NCBI GI g1644291
BLAST score 349
E value 1.0e-32
Match length 163
% identity 44

NCBI Description (Z73295) receptor-like protein kinase [Catharanthus roseus]

Seq. No. 16813

Contig ID 47082 1.R1040

5'-most EST LIB3093-038-Q1-K1-F8

Method BLASTX
NCBI GI g4191785
BLAST score 215
E value 2.0e-17
Match length 80
% identity 51

NCBI Description (AC005917) putative hydrolase [Arabidopsis thaliana]

Seq. No. 16814

Contig ID 47087 1.R1040 5'-most EST fde700873577.h1

Seq. No. 16815

Contig ID 47096 1.R1040 5'-most EST ssr700559844.h1

Method BLASTX
NCBI GI g2462732
BLAST score 518
E value 8.0e-53
Match length 146
% identity 65

NCBI Description (AC002292) Hypothetical Protein [Arabidopsis thaliana]

Seq. No. 16816

Contig ID 47098\_1.R1040

5'-most EST LIB30 $\overline{9}$ 3-038-Q1-K1-E2

Seq. No. 16817

Contig ID 47099\_1.R1040 5'-most EST taw700656057.h1

Seq. No. 16818

Method

NCBI GI

BLAST score E value



```
47099 2.R1040
Contig ID
                  LIB3107-022-Q1-K1-F8
5'-most EST
                  16819
Seq. No.
                  47104 1.R1040
Contig ID
                  LIB3093-038-Q1-K1-E8
5'-most EST
                  BLASTX
Method
                  g2765091
NCBI GI
BLAST score
                  265
                  4.0e-36
E value
                  148
Match length
                  53
% identity
NCBI Description (Y10982) putative cytochrome P450 [Glycine max]
Seq. No.
                  16820
                  47105 1.R1040
Contig ID
                  uC-gmropic030a11b1
5'-most EST
                  BLASTX
Method
                  g3941480
NCBI GI
BLAST score
                  226
                  2.0e-18
E value
                  102
Match length
                  73
% identity
                  (AF062894) putative transcription factor [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  16821
                  47105 2.R1040
Contig ID
                  jC-gmle01810056g05a1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3941480
                   546
BLAST score
                   2.0e-55
E value
Match length
                   308
% identity
                  (AF062894) putative transcription factor [Arabidopsis
NCBI Description
                   thaliana]
                   16822
Seq. No.
                   47105 3.R1040
Contig ID
                   LIB3138-090-P1-N1-F11
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3941480
BLAST score
                   366
E value
                   1.0e-49
Match length
                   104
                   89
% identity
                   (AF062894) putative transcription factor [Arabidopsis
NCBI Description
                   thaliana]
                   16823
Seq. No.
                   47105 4.R1040
Contig ID
                   jC-gmro02910019d05a1
5'-most EST
                   BLASTX
```

2781

g3941480

6.0e-51

502

Match length

% identity

55



```
121
Match length
% identity
                  (AF062894) putative transcription factor [Arabidopsis
NCBI Description
                  thaliana]
                  16824
Seq. No.
                  47108 1.R1040
Contig ID
                  LIB3139-028-P1-N1-F5
5'-most EST
                  BLASTX
Method
                  g4186184
NCBI GI
                  245
BLAST score
                  2.0e-20
E value
                  113
Match length
                   48
% identity
NCBI Description (AF111168) unknown [Homo sapiens]
                  16825
Seq. No.
                   47110 1.R1040
Contig ID
                  LIB3139-022-P1-N1-G4
5'-most EST
                  BLASTX
Method
                   g3928085
NCBI GI
                   984
BLAST score
                   1.0e-107
E value
                   274
Match length
                   70
% identity
                  (AC005770) unknown protein [Arabidopsis thaliana]
NCBI Description
                   16826
Seq. No.
                   47121 1.R1040
Contig ID
                   jex700905546.hl
5'-most EST
                   BLASTX
Method
                   g3914386
NCBI GI
                   262
BLAST score
                   2.0e-22
E value
                   145
Match length
                   37
% identity
NCBI Description ALLERGEN MF1 >gi 3445490 dbj BAA32435 (AB011804) MF1
                   [Malassezia furfur]
                   16827
Seq. No.
                   47125 1.R1040
Contig ID
                   LIB3093-038-Q1-K1-C11
5'-most EST
                   16828
Seq. No.
Contig ID
                   47129 1.R1040
                   LIB3093-038-Q1-K1-A9
5'-most EST
                   16829
Seq. No.
Contig ID
                   47138 1.R1040
                   epx701109741.hl
 5'-most EST
Method
                   BLASTX
                   g4249411
NCBI GI
                   234
BLAST score
                   7.0e-24
 E value
                   101
```

NCBI Description (AC006072) unknown protein [Arabidopsis thaliana]

```
16830
Seq. No.
                  47139 1.R1040
Contig ID
                  ejt700606140.h2
5'-most EST
                  BLASTX
Method
                  q2465923
NCBI GI
                  184
BLAST score
                  1.0e-13
E value
                   94
Match length
                   18
% identity
                   (AF024648) receptor-like serine/threonine kinase
NCBI Description
                   [Arabidopsis thaliana]
                   16831
Seq. No.
                   47141 1.R1040
Contig ID
                   uxk70\overline{0}667672.h1
5'-most EST
                   BLASTX
Method
                   q3549667
NCBI GI
                   443
BLAST score
                   1.0e-43
E value
                   168
Match length
                   55
% identity
                   (AL031394) Arabidopsis dynamin-like protein ADL2
NCBI Description
                   [Arabidopsis thaliana]
                   16832
Seq. No.
                   47144 1.R1040
Contig ID
                   pcp700993778.h1
5'-most EST
                   BLASTX
Method
                   g2352492
NCBI GI
                   717
BLAST score
                   2.0e-85
E value
                   292
Match length
                   31
% identity
                   (AF005047) transport inhibitor response 1 [Arabidopsis
NCBI Description
                   thaliana] >gi 2352494 (AF005048) transport inhibitor
                   response 1 [Arabidopsis thaliana]
                   16833
Seq. No.
                   47148 1.R1040
Contig ID
                   LIB3093-037-Q1-K1-H5
5'-most EST
                   16834
Seq. No.
                    47167 1.R1040
Contig ID
                    kl1701203311.h1
 5'-most EST
                   BLASTX
Method
                    q4049342
NCBI GI
                    206
BLAST score
                    7.0e-16
 E value
                    107
Match length
```

% identity 14

(AL034567) adenylate translocator (brittle-1)-like protein NCBI Description

[Arabidopsis thaliana]

Seq. No. Contig ID 16835 47189 1.R1040

uC-gmropic029g08b1 5'-most EST



```
Seq. No.
                  16836
                   47199 1.R1040
Contig ID
                  uC-qmflminsoy049d04b1
5'-most EST
Method
                  BLASTX
NCBI GI
                   q3255941
BLAST score
                   661
E value
                   3.0e-69
Match length
                   153
% identity
                   80
                  (AJ007332) PP1A protein [Catharanthus roseus]
NCBI Description
                   16837
Seq. No.
                   47204 1.R1040
Contig ID
5'-most EST
                  LIB3093-037-Q1-K1-D6
Method
                  BLASTX
                  g2245000
NCBI GI
BLAST score
                  181
E value
                   4.0e-13
Match length
                  70
                   54
% identity
                  (Z97341) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   16838
                   47209 1.R1040
Contig ID
5'-most EST
                   cks700764879.h1
Seq. No.
                   16839
                   47210 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400046a03a1
                   BLASTN
Method
NCBI GI
                   g4519192
BLAST score
                   56
                   2.0e-22
E value
                   116
Match length
% identity
                   87
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MBK21, complete sequence
Seq. No.
                   16840
Contig ID
                   47210 2.R1040
5'-most EST
                   zsq701123775.hl
Method
                   BLASTX
                   g1397319
NCBI GI
BLAST score
                   247
                   5.0e-21
E value
Match length
                   136
% identity
                   48
NCBI Description
                  (U61953) No definition line found [Caenorhabditis elegans]
Seq. No.
                   16841
                   47210 3.R1040
Contig ID
```

5'-most EST LIB30 $\overline{9}$ 3-037-Q1-K1-A9

Seq. No. 16842

Contig ID 47210\_5.R1040 5'-most EST pmv700891138.h1



```
Seq. No. 16843
```

Contig ID 47212\_1.R1040

5'-most EST LIB3093-037-Q1-K1-B10

Seq. No. 16844

Contig ID 47217\_1.R1040 5'-most EST sat701008123.h1

Method BLASTX
NCBI GI g282882
BLAST score 185
E value 1.0e-27
Match length 147
% identity 48

NCBI Description receptor-like protein kinase precursor - Arabidopsis

thaliana >gi 166848 (M84659) receptor-like protein kinase

[Arabidopsis thaliana]

Seq. No. 16845

Contig ID 47219 1.R1040

Match length 113 % identity 33

NCBI Description (AC000103) F21J9.21 [Arabidopsis thaliana]

Seq. No. 16846

Contig ID 47223 1.R1040 5'-most EST 94306597 Method BLASTX NCBI GI 9731507 BLAST score 156 E value 7.0e-10

Match length 220 % identity 28

NCBI Description HYPOTHETICAL 48.8 KD PROTEIN IN SSU81-SCS2 INTERGENIC

REGION >gi\_1077700\_pir\_\_S50622 hypothetical protein YER119c

- yeast (Saccharomyces cerevisiae) >gi\_603358 (U18916)

Yer119cp [Saccharomyces cerevisiae]

Seq. No. 16847

Contig ID 47228\_1.R1040 5'-most EST zvj700605238.h2

Method BLASTX
NCBI GI 93790585
BLAST score 329
E value 3.0e-30
Match length 85
% identity 71

NCBI Description (AF079181) RING-H2 finger protein RHFla [Arabidopsis

thaliana]

Seq. No. 16848

Contig ID 47233 1.R1040



5'-most EST zvj700605145.h2

Seq. No. 16849

Contig ID 47235\_1.R1040

5'-most EST LIB3093-036-Q1-K1-H9

Method BLASTX
NCBI GI g3056594
BLAST score 215
E value 3.0e-17
Match length 109
% identity 39

NCBI Description (AC004255) T1F9.15 [Arabidopsis thaliana]

Seq. No. 16850

Contig ID 47252 1.R1040

5'-most EST LIB3093-036-Q1-K1-F8

Method BLASTX
NCBI GI g2160180
BLAST score 804
E value 7.0e-86
Match length 244
% identity 69

NCBI Description (AC000132) No definition line found [Arabidopsis thaliana]

Seq. No.

Contig ID 47253 1.R1040 5'-most EST epx701104410.h1

Seq. No. 16852

Contig ID 47254 1.R1040

5'-most EST LIB3093-036-Q1-K1-G10

16851

Seq. No. 16853

Contig ID 47254 2.R1040 5'-most EST fua701041796.h1

Seq. No. 16854

Contig ID 47254\_3.R1040 5'-most EST hyd700729240.h1

Seq. No. 16855

Contig ID 47254\_4.R1040 5'-most EST gsv701048505.h1

Seq. No. 16856

Contig ID 47254 5.R1040

5'-most EST LIB3107-054-Q1-K1-G6

Seq. No. 16857

Contig ID 47264 1.R1040

5'-most EST LIB3093-036-Q1-K1-H1

Seq. No. 16858

Contig ID 47267\_1.R1040 5'-most EST dpv701100741.h1

Method BLASTX NCBI GI g3386618



BLAST score E value 7.0e-11 113 Match length 37 % identity

(AC004665) hypothetical protein [Arabidopsis thaliana] NCBI Description

Seq. No.

16859

Contig ID

47284 1.R1040

5'-most EST

iC-qmf102220065f07a1

Method BLASTX NCBI GI g1168470 BLAST score 1207 E value 1.0e-133 Match length 421 % identity

PROTEIN KINASE APK1A >gi\_282877\_pir\_\_S28615 protein kinase, NCBI Description

tyrosine/serine/threonine-specific (EC 2.7.1.-) -Arabidopsis thaliana >gi 217829 dbj BAA02092 (D12522) protein tyrosine-serine-threonine kinase [Arabidopsis

thaliana]

Seq. No.

16860

47284\_2.R1040 Contig ID 5'-most EST g5666595 Method BLASTX q1168470 NCBI GI 505 BLAST score 6.0e-51E value Match length 127 75 % identity

PROTEIN KINASE APKIA >gi 282877 pir S28615 protein kinase, NCBI Description

tyrosine/serine/threonine-specific (EC 2.7.1.-) -Arabidopsis thaliana >gi 217829\_dbj BAA02092 (D12522) protein tyrosine-serine-threonine kinase [Arabidopsis

thaliana]

16861 Seq. No.

47284 3.R1040 Contig ID 5'-most EST g5607095 Method BLASTX NCBI GI g3461835 BLAST score 343 E value 6.0e-32 Match length 136 % identity

NCBI Description (AC005315) putative protein kinase [Arabidopsis thaliana]

>qi 3927840 (AC005727) putative protein kinase [Arabidopsis

thaliana]

16862 Seq. No.

Contig ID 47284 4.R1040 5'-most EST asn701140089.hl

Seq. No. 16863

47286 1.R1040 Contig ID 5'-most EST ncj700978216.h1



Seq. No. 16864 47297 1.R1040 Contig ID

5'-most EST LIB3093-036-Q1-K1-D1

Seq. No.

16865

Contig ID

47308 1.R1040

5'-most EST

uC-gmrominsoy028e07b1

Seq. No.

16866

Contig ID 5'-most EST 47319 1.R1040 vzy700753294.h1

Seq. No.

16867

Contig ID

47329 1.R1040

5'-most EST

LIB3093-035-Q1-K1-H7

Method NCBI GI BLASTX g4580523

BLAST score

451

E value Match length 1.0e-44 130

% identity

67

NCBI Description

(AF036305) scarecrow-like 8 [Arabidopsis thaliana]

Seq. No.

16868

Contig ID

47332 1.R1040

5'-most EST

uC-gmrominsoy080d01b1

Seq. No.

16869

Contig ID

47333 1.R1040

5'-most EST

LIB3138-081-P1-N1-C2

Method NCBI GI BLASTX g2245004

BLAST score

372

E value

1.0e-35

Match length

96 69

% identity NCBI Description

(Z97341) similarity to membrane transport protein

[Arabidopsis thaliana]

Seq. No.

16870

Contig ID

47333 2.R1040

5'-most EST

LIB3093-035-Q1-K1-E6

Method NCBI GI BLASTX

BLAST score

q2245004

180

E value Match length 4.0e-18

% identity

75 61

NCBI Description

(Z97341) similarity to membrane transport protein

[Arabidopsis thaliana]

Seq. No.

16871

Contig ID 5'-most EST 47333 3.R1040 leu701149957.h1

Method NCBI GI BLASTX

g2245004

BLAST score 256

2788



E value 3.0e-22 Match length 67 % identity 67

NCBI Description (Z97341) similarity to membrane transport protein

[Arabidopsis thaliana]

Seq. No. 16872

Contig ID 47336 1.R1040

5'-most EST LIB3106-035-Q1-K1-B11

Method BLASTX
NCBI GI g4510402
BLAST score 881
E value 1.0e-94
Match length 440
% identity 50

NCBI Description (AC006587) putative AP2 domain [Arabidopsis thaliana]

Seq. No. 16873

Contig ID 47336\_2.R1040 5'-most EST fC-gmse700672157h2

Seq. No. 16874

Contig ID 47336\_3.R1040 5'-most EST fC-gmse700672157a3

Method BLASTX
NCBI GI g4510402
BLAST score 432
E value 3.0e-42
Match length 231
% identity 44

NCBI Description (AC006587) putative AP2 domain [Arabidopsis thaliana]

Seq. No. 16875

Contig ID 47336\_4.R1040

5'-most EST LIB3093-035-Q1-K1-F1

Method BLASTX
NCBI GI g4510402
BLAST score 273
E value 5.0e-24
Match length 165
% identity 36

NCBI Description (AC006587) putative AP2 domain [Arabidopsis thaliana]

Seq. No. 16876

Contig ID 47336\_6.R1040 5'-most EST fua701039415.h1

Method BLASTX
NCBI GI g2281639
BLAST score 350
E value 2.0e-33
Match length 81
% identity 50

NCBI Description (AF003100) AP2 domain containing protein RAP2.7

[Arabidopsis thaliana]

Seq. No. 16877

Contig ID 47341 1.R1040



```
LIB3170-062-Q1-J1-G7
5'-most EST
Seq. No.
                  16878
                  47344 1.R1040
Contig ID
5'-most EST
                  LIB3093-035-Q1-K1-F7
Method
                  BLASTX
NCBI GI
                  q4510418
BLAST score
                  272
E value
                  9.0e-28
Match length
                  137
% identity
                  53
                  (AC006929) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  16879
Seq. No.
Contig ID
                  47361 1.R1040
5'-most EST
                  LIB3093-035-Q1-K1-E11
                  16880
Seq. No.
Contig ID
                  47365 1.R1040
5'-most EST
                  LIB3093-035-Q1-K1-C9
Seq. No.
                  16881
Contig ID
                  47371 1.R1040
5'-most EST
                  LIB3093-035-Q1-K1-B9
Seq. No.
                  16882
                  47372 1.R1040
Contig ID
5'-most EST
                  jC-gmf102220079g03a1
Seq. No.
                  16883
Contig ID
                  47379 1.R1040
5'-most EST
                  LIB3109-032-Q1-K1-B2
                  BLASTX
Method
NCBI GI
                  q2262105
BLAST score
                  471
E value
                  8.0e - 94
Match length
                  300
% identity
                  56
                  (AC002343) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  16884
                  47384 1.R1040
Contig ID
5'-most EST
                  gsv701049932.hl
Method
                  BLASTX
                  g2213600
NCBI GI
BLAST score
                  373
E value
                  2.0e-35
Match length
                  131
% identity
NCBI Description (AC000348) T7N9.20 [Arabidopsis thaliana]
```

Contig ID 47384 2.R1040 5'-most EST vzy700754923.h1

Method BLASTX
NCBI GI g2826842
BLAST score 2135



E value 0.0e+00 Match length 509 % identity 74

NCBI Description (AJ002236) loxc homologue [Lycopersicon pimpinellifolium]

Seq. No. 16886

Contig ID 47384 3.R1040 5'-most EST taw700659966.h1

Seq. No.

16887

Contig ID

47392 1.R1040

5'-most EST

LIB3093-035-Q1-K1-A3

Seq. No.

16888

Contig ID

47394 1.R1040

5'-most EST

LIB3093-035-Q1-K1-A6

Seq. No.

16889

Contig ID

47395 1.R1040

5'-most EST

LIB3093-022-Q1-K1-F1

Method NCBI GI BLASTX g629688

BLAST score E value 208 1.0e-17

Match length % identity

150 39

NCBI Description

dehydroquinase shikimate dehydrogenase - Common tobacco >gi\_535771 (L32794) dehydroquinate dehydratase/shikimate

dehydrogenase [Nicotiana tabacum]

Seq. No.

16890

Contig ID 5'-most EST 47400\_1.R1040 uC-gmropic040f12b1

Seq. No.

16891

Contig ID

47405\_1.R1040

5'-most EST

uC-gmflminsoy010b06b1

Method NCBI GI BLAST score BLASTX g1076331 328

E value

1.0e-51 273

Match length % identity

41

NCBI Description

histidine transport protein - Arabidopsis thaliana

>gi\_510238\_emb\_CAA54634\_ (X77503) oligopeptide transporter
1-1 [Arabidopsis thaliana] >gi\_744157\_prf\_\_2014244A His

transporter [Arabidopsis thaliana]

Seq. No.

16892

Contig ID

47406\_1.R1040

5'-most EST

LIB3093-034-Q1-K1-F5

Method NCBI GI BLAST score BLASTX g3080374 225

E value Match length % identity 2.0e-18 159

3



NCBI Description (AL022580) putative protein [Arabidopsis thaliana]

Seq. No. 16893

Contig ID 47410 1.R1040

5'-most EST jC-gmro02910066a01a1

Seq. No. 16894

Contig ID 47422\_1.R1040 5'-most EST epx701108172.h1

Method BLASTN
NCBI GI g2104678
BLAST score 295
E value 1.0e-165
Match length 556
% identity 88

NCBI Description V.faba mRNA for transcription factor containing HMG-box

Seq. No. 16895

Contig ID 47422 2.R1040

5'-most EST LIB31 $\overline{3}$ 8-018-Q1-N1-F7

Method BLASTN
NCBI GI g2104678
BLAST score 129
E value 4.0e-66
Match length 278
% identity 86

NCBI Description V.faba mRNA for transcription factor containing HMG-box

Seq. No. 16896

Contig ID 47441 1.R1040 5'-most EST asn701137327.h1

Method BLASTX
NCBI GI g3182950
BLAST score 528
E value 1.0e-53
Match length 212
% identity 45

NCBI Description CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 2 (CHD-2)

>gi\_2645431 (AF006514) CHD2 [Homo sapiens]

>gi\_4557449\_ref\_NP\_001262.1\_pCHD2\_ chromodomain helicase

DNA binding protein

Seq. No. 16897

Contig ID 47442\_1.R1040 5'-most EST ssr700556304.h1

Method BLASTX
NCBI GI g1653333
BLAST score 295
E value 3.0e-26
Match length 110
% identity 50

NCBI Description (D90912) ferredoxin [Synechocystis sp.]

Seq. No. 16898

Contig ID 47442 2.R1040

5'-most EST LIB3093-008-Q1-K1-C7

Method BLASTX

```
q1653333
NCBI GI
                  246
BLAST score
                  6.0e-21
E value
                  91
Match length
                  51
% identity
NCBI Description (D90912) ferredoxin [Synechocystis sp.]
                  16899
```

47450 1.R1040 Contig ID LIB3093-034-Q1-K1-C1 5'-most EST BLASTX Method g4309700 NCBI GI 362 BLAST score 1.0e-34 E value

122 Match length 56 % identity

Seq. No.

NCBI Description (AC006266) hypothetical protein [Arabidopsis thaliana]

16900 Seq. No.

47458 1.R1040 Contig ID

LIB3093-027-Q1-K1-G1 5'-most EST

16901 Seq. No.

47460 1.R1040 Contig ID

 $LIB30\overline{9}3-033-Q1-K1-H6$ 5'-most EST

16902 Seq. No.

47467 1.R1040 Contig ID

LIB3093-034-Q1-K1-A2 5'-most EST

BLASTX Method q4539459 NCBI GI 479 BLAST score 7.0e-48E value Match length 133 % identity 68

(AL049500) putative protein [Arabidopsis thaliana] NCBI Description

16903 Seq. No.

47469 1.R1040 Contig ID 5'-most EST kl1701211518.hl

BLASTX Method g3152587 NCBI GI BLAST score 768 8.0e-82 E value Match length 241 47 % identity

(AC002986) Similar to CREB-binding protein homolog NCBI Description

gb\_U88570 from D. melanogaster and contains similarity to callus-associated protein gb U01961 from Nicotiana tabacum. EST gb\_W43427 comes from this gene. [Arabidopsis thaliana]

16904 Seq. No.

47472 1.R1040 Contig ID

uC-gmflminsoy021b04b1 5'-most EST

16905 Seq. No.

47487 1.R1040 Contig ID



```
LIB3139-103-P1-N1-A10
5'-most EST
                  BLASTX
Method
                  g2505870
NCBI GI
BLAST score
                  527
                   4.0e-89
E value
                  241
Match length
                  72
% identity
NCBI Description (Y12227) hypothetical protein [Arabidopsis thaliana]
                  16906
Seq. No.
                   47495 1.R1040
Contig ID
                  LIB3093-033-Q1-K1-E6
5'-most EST
                  BLASTX
Method
                   g4115534
NCBI GI
                   256
BLAST score
E value
                   2.0e-28
Match length
                   170
                   37
% identity
                  (AB012114) UDP-glycose:flavonoid glycosyltransferase [Vigna
NCBI Description
                   mungo]
                   16907
Seq. No.
                   47503 1.R1040
Contig ID
                   LIB30\overline{9}3-033-Q1-K1-F2
5'-most EST
                   BLASTX
Method
                   g3402684
NCBI GI
                   214
BLAST score
                   3.0e-17
E value
Match length
                   124
                   44
% identity
NCBI Description (AC004697) hypothetical protein [Arabidopsis thaliana]
                   16908
Seq. No.
                   47504 1.R1040
Contig ID
                   LIB3093-033-Q1-K1-F3
5'-most EST
                   16909
Seq. No.
                   47505 1.R1040
Contig ID
                   fua701038537.h1
5'-most EST
                   16910
Seq. No.
                   47507 1.R1040
Contig ID
                   xpa70\overline{0}793506.h1
5'-most EST
                   16911
Seq. No.
                   47516 1.R1040
Contig ID
                   LIB3139-040-P1-N1-B9
5'-most EST
Seq. No.
                   16912
                   47516 2.R1040
Contig ID
5'-most EST
                   pmv700895225.h1
                   16913
Seq. No.
                   47524 1.R1040
Contig ID
                   LIB3106-108-Q1-K1-D12
5'-most EST
```

2794

BLASTX

g3096944

Method

NCBI GI



BLAST score 307 E value 8.0e-28 Match length 112 % identity 56

NCBI Description (AL023094) putative protein [Arabidopsis thaliana]

Seq. No. 16914

Contig ID 47524 2.R1040

5'-most EST jC-gmst02400076a12a1

Method BLASTX
NCBI GI g3096944
BLAST score 291
E value 2.0e-26
Match length 83
% identity 67

NCBI Description (AL023094) putative protein [Arabidopsis thaliana]

Seq. No. 16915

Contig ID 47527\_1.R1040 5'-most EST ncj700980777.h1

Method BLASTX
NCBI GI g2864613
BLAST score 306
E value 6.0e-28
Match length 112
% identity 54

NCBI Description (AL021811) S-receptor kinase -like protein [Arabidopsis

thaliana] >gi\_4049333\_emb\_CAA22558\_ (AL034567) S-receptor

kinase-like protein [Arabidopsis thaliana]

Seq. No. 16916

Contig ID 47530\_1.R1040 5'-most EST dpv701098388.h1

Seq. No. 16917

Contig ID 47534 1.R1040

5'-most EST uC-gmrominsoy162f02b1

Method BLASTX
NCBI GI g3157932
BLAST score 205
E value 3.0e-32
Match length 108
% identity 65

NCBI Description (AC002131) Similar to hypothetical protein HYP1 gb Z97338

from A. thaliana. [Arabidopsis thaliana]

Seq. No. 16918

Contig ID 47560 1.R1040

5'-most EST LIB3093-032-Q1-K1-G12

Seq. No. 16919

Contig ID 47566 1.R1040 5'-most EST sat701012692.h1

Method BLASTX
NCBI GI g2829894
BLAST score 331
E value 1.0e-30



```
126
Match length
                  56
% identity
NCBI Description (AC002311) Unknown protein [Arabidopsis thaliana]
                  16920
Seq. No.
                  47571 1.R1040
Contig ID
                  ncj700983065.hl
5'-most EST
                  16921
Seq. No.
                   47571 2.R1040
Contig ID
                   \verb|jC-gms| t02400008f05a1|
5'-most EST
                   BLASTX
Method
                   g4099092
NCBI GI
                   847
BLAST score
                   7.0e-91
E value
                   225
Match length
                   68
% identity
                  (U83179) unknown [Arabidopsis thaliana]
NCBI Description
                   16922
Seq. No.
                   47571_3.R1040
Contig ID
                   LIB3093-032-Q1-K1-G1
5'-most EST
                   BLASTX
Method
                   g4099092
NCBI GI
                   440
BLAST score
                   2.0e-46
E value
                   139
Match length
                   68
% identity
NCBI Description (U83179) unknown [Arabidopsis thaliana]
                   16923
Seq. No.
                   47578 1.R1040
Contig ID
                   LIB3093-032-Q1-K1-E8
5'-most EST
                   BLASTX
Method
                   g2190540
NCBI GI
                   263
BLAST score
                   7.0e-23
E value
Match length
                   87
                   56
% identity
                   (AC001229) Similar to Arabidopsis TFL1 (gb_U77674).
NCBI Description
                    [Arabidopsis thaliana]
                   16924
Seq. No.
                   47594 1.R1040
 Contig ID
 5'-most EST
                   zhf700963970.h1
                   16925
 Seq. No.
                    47609 1.R1040
 Contig ID
                    zhf700962375.h1
 5'-most EST
                   BLASTX
 Method
 NCBI GI
                    g2894378
 BLAST score
                    1158
 E value
                    1.0e-127
```

. 15.

Match length

NCBI Description

% identity

286

73

(Y14573) putative ribophorin I homologue [Hordeum vulgare]



```
Seq. No.
                   16926
Contig ID
                   47620 1.R1040
                  LIB3167-049-P1-K1-G9
5'-most EST
                  BLASTN
Method
NCBI GI
                  g4218522
BLAST score
                  260
E value
                  1.0e-144
                  666
Match length
                  87
% identity
NCBI Description Pisum sativum mRNA for PPF-1 protein
                  16927
Seq. No.
                   47620 2.R1040
Contig ID
5'-most EST
                  LIB3093-032-Q1-K1-C8
Method
                  BLASTN
NCBI GI
                  q4218522
BLAST score
                   255
E value
                  1.0e-141
Match length
                   418
                   90
% identity
NCBI Description Pisum sativum mRNA for PPF-1 protein
Seq. No.
                  16928
Contig ID
                   47624 1.R1040
5'-most EST
                  LIB3093-032-Q1-K1-A12
                  16929
Seq. No.
                   47624 2.R1040
Contig ID
5'-most EST
                  hrw701061503.hl
Seq. No.
                   16930
                   47639 1.R1040
Contig ID
5'-most EST
                   uC-gmropic049c04b1
                  BLASTX
Method
NCBI GI
                   g2598575
BLAST score
                   366
E value
                  1.0e-34
Match length
                  188
% identity
                   38
NCBI Description (Y15293) MtN21 [Medicago truncatula]
Seq. No.
                   16931
Contig ID
                   47639 2.R1040
5'-most EST
                   sat701012973.h1
Method
                  BLASTX
```

NCBI GI q4056506 BLAST score 254 E value 7.0e-22 Match length 108 44 % identity

NCBI Description (AC005896) nodulin-like protein [Arabidopsis thaliana]

16932 Seq. No.

Contig ID 47640 1.R1040

5'-most EST LIB3093-031-Q1-K1-G3

Seq. No. 16933



Contig ID 47641\_1.R1040 5'-most EST zzp700834755.h1

Method BLASTX
NCBI GI g2760830
BLAST score 219
E value 9.0e-18
Match length 48
% identity 88

NCBI Description (AC003105) putative beta-ketoacyl-CoA synthase [Arabidopsis

thaliana]

Seq. No. 16934

Contig ID 47649\_1.R1040 5'-most EST uC-gmronoir026d04b1

Method BLASTX
NCBI GI g3176709
BLAST score 365
E value 2.0e-34
Match length 237
% identity 36

NCBI Description (AC002392) putative anthranilate

N-hydroxycinnamoyl/benzoyltransferase [Arabidopsis

thaliana]

Seq. No. 16935

Contig ID 47655\_1.R1040 5'-most EST gsv701055865.h1

Seq. No. 16936

Contig ID 47660\_1.R1040 5'-most EST leu701147511.h1

Method BLASTX
NCBI GI g2920666
BLAST score 383
E value 2.0e-75
Match length 216
% identity 62

NCBI Description (AF048978) 2,4-D inducible glutathione S-transferase

[Glycine max]

Seq. No. 16937

NCBI Description (AF048978) 2,4-D inducible glutathione S-transferase

[Glycine max]

Seq. No. 16938

Contig ID 47662\_1.R1040 5'-most EST wvk700684318.h1

Seq. No. 16939



Contig ID 47662 2.R1040 5'-most EST pxt700943386.h1

Seq. No. 16940

Contig ID 47665 1.R1040

5'-most EST uC-gmrominsoy245e03b1

Seq. No. 16941

Contig ID 47670\_1.R1040 5'-most EST jex700903701.h1

Method BLASTX
NCBI GI g2921213
BLAST score 617
E value 4.0e-64
Match length 189
% identity 66

NCBI Description (AF026150) beta-ketoacyl-ACP synthase IIIA [Perilla

frutescens]

Seq. No. 16942

Contig ID 47673 1.R1040

5'-most EST LIB3093-031-Q1-K1-C8

Seq. No. 16943

Contig ID 47675 1.R1040

5'-most EST uC-gmflminsoy043f11b1

Method BLASTX
NCBI GI g1174470
BLAST score 268
E value 2.0e-23
Match length 71
% identity 66

NCBI Description OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5)

(INTEGRAL MEMBRANE PROTEIN 1) >gi\_508543 (L34260) integral membrane protein 1 [Mus musculus] >gi\_1588285\_prf\_\_2208301A

integral membrane protein [Mus musculus]

Seq. No. 16944

Contig ID 47675 2.R1040

5'-most EST uC-gmrominsoy128d03b1

Method BLASTX
NCBI GI g1174469
BLAST score 746
E value 3.0e-79
Match length 234
% identity 56

NCBI Description OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5)

(INTEGRAL MEMBRANE PROTEIN 1) >gi 624704 (L38961) putative

transmembrane protein precursor  $[\overline{\text{Homo}} \text{ sapiens}]$ 

>gi 1588286 prf 2208301B integral membrane protein [Homo

sapiens] >gi 4504787\_ref\_NP\_002210.1\_pITM1\_ integral

transmembrane protein

Seq. No. 16945

Contig ID 47679\_1.R1040

5'-most EST uC-gmrominsoy217f01b1

Method BLASTX

```
NCBI GI
                   q4371280
BLAST score
                   583
E value
                   4.0e-60
Match length
                   176
% identity
NCBI Description
                   (AC006260) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   16946
Contig ID
                   47679 2.R1040
5'-most EST
                   ssr700553908.h1
Method
                   BLASTX
NCBI GI
                   g4371280
BLAST score
                   198
E value
                   2.0e-15
Match length
                   51
                   76
% identity
                  (AC006260) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   16947
Contig ID
                   47686 1.R1040
5'-most EST
                   uxk70\overline{0}673365.h1
Seq. No.
                   16948
Contig ID
                   47689 1.R1040
```

5'-most EST LIB3109-052-Q1-K1-E4
Method BLASTX
NCBI GI 93335373

NCBI GI g3335373
BLAST score 210
E value 1.0e-16
Match length 162
% identity 35

NCBI Description (AC003028) putative GTL1 protein [Arabidopsis thaliana]

Seq. No. 16949

Contig ID 47695 1.R1040

5'-most EST uC-gmrominsoy237h02b1

Method BLASTX
NCBI GI g3820531
BLAST score 633
E value 4.0e-66
Match length 195
% identity 59

NCBI Description (AF072736) beta-glucosidase [Pinus contorta]

Seq. No. 16950

Contig ID 47722 1.R1040

5'-most EST jC-gmf102220071a05a1

Method BLASTX
NCBI GI g3021266
BLAST score 1198
E value 1.0e-132
Match length 372
% identity 62

NCBI Description (AL022347) serine/threonine kinase - like protein

[Arabidopsis thaliana] >gi\_3292840\_emb\_CAA19830\_ (AL031018)

serine/threonine kinase - like protein [Arabidopsis

thaliana]

```
Seq. No.
                  16951
                   47734 1.R1040
Contig ID
5'-most EST
                  LIB3093-030-Q1-K1-F6
                  16952
Seq. No.
Contig ID
                   47735 1.R1040
                  LIB3093-030-Q1-K1-F7
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4038055
BLAST score
                  346
E value
                  1.0e-32
Match length
                  113
% identity
                   63
NCBI Description
                  (AC005897) putative cytochrome P450 [Arabidopsis thaliana]
                  >gi_4557077_gb_AAD22516.1 AC007045_16 (AC007045) putative
                  cytochrome p450 [Arabidopsis thaliana]
                  16953
Seq. No.
Contig ID
                  47751 1.R1040
5'-most EST
                  LIB3093-030-Q1-K1-D1
Method
                  BLASTX
NCBI GI
                  g2213600
BLAST score
                  529
E value
                  4.0e-54
Match length
                  147
% identity
                  67
NCBI Description (AC000348) T7N9.20 [Arabidopsis thaliana]
                  16954
Seq. No.
Contig ID
                   47767 1.R1040
                  LIB3093-030-Q1-K1-A6
5'-most EST
                  16955
Seq. No.
Contig ID
                  47780 1.R1040
5'-most EST
                  q4305461
Method
                  BLASTX
NCBI GI
                  q3128208
BLAST score
                  366
                  5.0e-35
E value
Match length
                  104
% identity
                  61
NCBI Description (AC004077) hypothetical protein [Arabidopsis thaliana]
                  16956
Seq. No.
Contig ID
                  47784 2.R1040
5'-most EST
                  LIB3093-029-01-K1-G4
Method
                  BLASTX
NCBI GI
                  g2618684
BLAST score
                  236
                  9.0e-20
E value
                  87
Match length
% identity
                  55
NCBI Description
                  (AC002510) putative
                  UDP-N-acetylglucosamine--dolichyl-phosphate
                  N-acetylglucosaminephosphotransferase [Arabidopsis
```

thaliana] >gi\_3241947 (AC004625) putative 2801



UDP-N-acetylglucosamine--dolichyl-phosphate N-acetylglucosaminephosphotransferase [Arabidopsis thaliana]

16957 Seq. No. 47787 1.R1040 Contig ID  $kmv70\overline{0}743115.h1$ 5'-most EST BLASTX Method g4218120 NCBI GI 217 BLAST score 2.0e-17 E value 122 Match length % identity (AL035353) Proline-rich APG-like protein [Arabidopsis NCBI Description thaliana] 16958 Seq. No. 47791 1.R1040 Contig ID jC-gmst02400061f12d1 5'-most EST BLASTX Method g2213594 NCBI GI BLAST score 112 1.0e-09 E value Match length 93 % identity 37 (AC000348) T7N9.14 [Arabidopsis thaliana] NCBI Description 16959 Seq. No. 47801 1.R1040 Contig ID 5'-most EST LIB3093-029-Q1-K1-E8 16960 Seq. No. 47804 1.R1040 Contig ID 5'-most EST sat701009256.hl BLASTX Method NCBI GI q2392772 BLAST score 169 7.0e-12 E value 40 Match length % identity 78 (AC002534) putative chloroplast prephenate dehydratase NCBI Description [Arabidopsis thaliana] 16961 Seq. No. 47807\_1.R1040 Contig ID kmv700739436.h1 5'-most EST

Method BLASTX
NCBI GI g1652084
BLAST score 304
E value 1.0e-27
Match length 128
% identity 45

NCBI Description (D90902) hypothetical protein [Synechocystis sp.]

Seq. No. Contig ID 16962 47809 1.R1040

5'-most EST

LIB3093-029-Q1-K1-F4



Method BLASTX
NCBI GI g2959767
BLAST score 733
E value 6.0e-78
Match length 167
% identity 42

NCBI Description (AJ002584) AtMRP4 [Arabidopsis thaliana] >gi\_3738292 (AC005309) glutathione-conjugate transporter AtMRP4

[Arabidopsis thaliana]

Seq. No. 16963

Contig ID 47810 1.R1040

5'-most EST jC-gmst02400018d08a1

Method BLASTX
NCBI GI g4512649
BLAST score 740
E value 1.0e-78
Match length 191
% identity 71

NCBI Description (AC007048) hypothetical protein [Arabidopsis thaliana]

Seq. No. 16964

Contig ID 47816\_1.R1040

5'-most EST LIB3138-030-Q1-N1-D11

Method BLASTX
NCBI GI g1175252
BLAST score 161
E value 3.0e-10
Match length 186
% identity 31

NCBI Description HYPOTHETICAL PROTEIN HI0488 >gi\_1074418\_pir\_\_D64008

hypothetical protein HI0488 - Haemophilus influenzae (strain Rd KW20) >gi\_1573468 (U32731) conserved hypothetical protein [Haemophilus influenzae Rd]

Seq. No. 16965

Contig ID 47816\_2.R1040 5'-most EST rca700999809.h1

Seq. No. 16966

Contig ID 47821\_1.R1040 5'-most EST trc700561246.h1

Method BLASTX
NCBI GI g4455210
BLAST score 1023
E value 1.0e-111
Match length 271
% identity 72

NCBI Description (AL035440) putative aspartate-tRNA ligase [Arabidopsis

thaliana]

Seq. No. 16967

Contig ID 47821 2.R1040

5'-most EST LIB3093-002-Q1-K1-C5

Method BLASTX
NCBI GI g4455210
BLAST score 455



E value 2.0e-45 Match length 111 % identity

NCBI Description (AL035440) putative aspartate-tRNA ligase [Arabidopsis

thaliana]

Seq. No. 16968

47822 1.R1040 Contig ID zpv700762357.h1 5'-most EST

BLASTN Method NCBI GI q3510347 BLAST score 39 4.0e-12 E value Match length 320 % identity

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MSJ11, complete sequence [Arabidopsis thaliana]

16969 Seq. No.

Contig ID 47822 2.R1040

5'-most EST LIB3138-016-Q1-N1-D6

16970 Seq. No.

Contig ID 47822 3.R1040 5'-most EST g5677534

16971 Seq. No.

Contig ID 47849 1.R1040

5'-most EST LIB3093-029-Q1-K1-C3

Method BLASTX NCBI GI g399900 BLAST score 688 E value 5.0e-72 Match length 277 54 % identity

NCBI Description HOMEOBOX-LEUCINE ZIPPER PROTEIN HAT5 (HD-ZIP PROTEIN 5) (HD-ZIP PROTEIN ATHB-1) >gi\_99659\_pir\_\_S16325 homeotic

protein Athb-1 - Arabidopsis thaliana

>gi\_16329\_emb\_CAA41625\_ (X58821) Athb-1 protein

[Arabidopsis thaliana]

Seq. No. 16972

47849 2.R1040 Contig ID 5'-most EST vwf700674925.h1

16973 Seq. No.

47852\_1.R1040 Contig ID 5'-most EST fC-gmse700675825a1

Method BLASTX NCBI GI q1170410 BLAST score 578 E value 5.0e-59 Match length 347 % identity 47

NCBI Description HOMEOBOX PROTEIN HAT3.1 >gi 322519 pir\_ S31437 homeotic

protein HAT 3.1 - Arabidopsis thaliana

>gi\_16326\_emb\_CAA49263\_ (X69512) HAT 3.1 [Arabidopsis



```
thaliana]
                   16974
Seq. No.
                   47852 2.R1040
Contig ID
5'-most EST
                   fC-gmse700667947r4
Seq. No.
                   16975
                   47861 1.R1040
Contig ID
                   leu701145644.h1
5'-most EST
Seq. No.
                   16976
Contig ID
                   47866 1.R1040
5'-most EST
                   hrw701061002.hl
Method
                   BLASTX
NCBI GI
                   g2129918
BLAST score
                   743
                   9.0e-79
E value
Match length
                   299
% identity
                   54
```

NCBI Description BPF-1 protein - parsley >gi 396197 emb CAA48413 (X68337)

BPF-1 [Petroselinum crispum] >gi 441310 emb CAA44518

(X62653) BPF-1 [Petroselinum crispum]

Seq. No. Contig ID 47883\_1.R1040 5'-most EST LIB3106-045-Q1-K1-B6 Method BLASTX NCBI GI q3132473 BLAST score 180 6.0e-13 E value 59 Match length 69 % identity

16977

NCBI Description (AC003096) similar to rapb transcription factor

[Arabidopsis thaliana]

Seq. No. 16978

47904 1.R1040 Contig ID

5'-most EST LIB3139-048-P1-N1-B2

Method BLASTN NCBI GI g166411 BLAST score 479 E value 0.0e + 00Match length 1048 87 % identity

NCBI Description Medicago sativa NADH-glutamate synthase mRNA, comlete cds

16979 Seq. No.

Contig ID 47904 2.R1040 5'-most EST trc700562893.h1

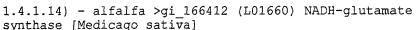
Method BLASTX NCBI GI g417073 BLAST score 336 E value 3.0e-31Match length 94 77 % identity

NCBI Description GLUTAMATE SYNTHASE (NADH) PRECURSOR (NADH-GOGAT)

>gi\_484529\_pir\_\_JQ1977 glutamate synthase (NADH) (EC

2805





16980 Seq. No. 47916 1.R1040 Contig ID 5'-most EST fC-gmro700565944r2 Seq. No. 16981 47922 1.R1040 Contig ID 5'-most EST uC-gmrominsoy0001e08b1 16982 Seq. No. 47935 1.R1040 Contig ID txt700731822.h1 5'-most EST Seq. No. 16983 Contig ID 47941 1.R1040 5'-most EST dpv701099115.h1

Method BLASTX
NCBI GI g2102696
BLAST score 417
E value 2.0e-40
Match length 328
% identity 29

NCBI Description (U72761) karyopherin beta 3 [Homo sapiens]

>gi\_4504909\_ref\_NP\_002262.1\_pKPNB3\_ karyopherin (importin)

beta

Seq. No. 16984

Contig ID 47948\_1.R1040 5'-most EST trc700565535.h1

Method BLASTX
NCBI GI g2275199
BLAST score 518
E value 1.0e-52
Match length 135
% identity 73

NCBI Description (AC002337) hypothetical protein [Arabidopsis thaliana]

Seq. No. 16985

Contig ID 47958\_1.R1040 5'-most EST wvk700681706.h1

Method BLASTX
NCBI GI g2924776
BLAST score 203
E value 2.0e-27
Match length 91
% identity 74

NCBI Description (AC002334) hypothetical protein [Arabidopsis thaliana]

Seq. No. 16986

Contig ID 47959\_1.R1040
5'-most EST g4291793
Method BLASTX
NCBI GI g2961345
BLAST score 481
E value 3.0e-48

2806



Match length 113 77 % identity

(AL022140) hypothetical protein [Arabidopsis thaliana] NCBI Description

Seq. No.

16987 47959 2.R1040

Contig ID 5'-most EST

leu701152429.h1

Method NCBI GI BLASTX q2961345

BLAST score E value

174 1.0e-12 45

Match length % identity

NCBI Description (AL022140) hypothetical protein [Arabidopsis thaliana]

Seq. No.

16988

Contig ID 5'-most EST 47964 1.R1040 fC-gmle7000786857a1

Method BLASTX q3608143

NCBI GI BLAST score 279 1.0e-24 E value 104 Match length % identity 61

NCBI Description (AC005314) unknown protein [Arabidopsis thaliana]

Seq. No.

16989

Contig ID 5'-most EST

47964 3.R1040 ssr700558921.h1

Method BLASTX

NCBI GI q3608143 BLAST score 160 E value 8.0e-11 Match length 56 % identity 61

(AC005314) unknown protein [Arabidopsis thaliana] NCBI Description

Seq. No.

16990

Contig ID

47971 1.R1040

5'-most EST

 $g5606\overline{3}10$ 

Seq. No.

16991

Contig ID

47979 1.R1040

5'-most EST

LIB3093-027-Q1-K1-E10

Seq. No.

16992

Contig ID 5'-most EST 47981 1.R1040 gsv701044426.hl

Method BLASTX NCBI GI g3924848 BLAST score 364 6.0e-34 E value 408 Match length

% identity

31 NCBI Description

(Z81586) cDNA EST yk335d8.5 comes from this gene; cDNA EST yk335d8.3 comes from this gene [Caenorhabditis elegans]



```
16993
Seq. No.
                  47982 1.R1040
Contig ID
                  asn701142122.hl
5'-most EST
                  BLASTX
Method
                  g3201612
NCBI GI
                  1032
BLAST score
                   1.0e-112
E value
                   361
Match length
                   56
% identity
NCBI Description (AC004669) putative 2A6 protein [Arabidopsis thaliana]
                   16994
Seq. No.
                   47982 2.R1040
Contig ID
                   dpv70\overline{1}097369.h1
5'-most EST
                   BLASTX
Method
                   g119640
NCBI GI
                   268
BLAST score
                   1.0e-33
E value
                   136
Match length
                   51
% identity
                   1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE HOMOLOG (PROTEIN
NCBI Description
                   E8) >gi_82109_pir__S01642 ripening protein E8 - tomato
                   >gi_19199_emb_CAA31789_ (X13437) E8 protein [Lycopersicon
                   esculentum]
                   16995
Seq. No.
                   47986 1.R1040
Contig ID
                   jC-gmle01810007h02a1
5'-most EST
                   16996
Seq. No.
                   47988 1.R1040
Contig ID
                   wvk700683746.hl
5'-most EST
                   BLASTX
Method
                   q1483230
NCBI GI
                   441
BLAST score
                   1.0e-43
E value
                   123
Match length
                   72
 % identity
NCBI Description (X99654) MADS4 protein [Betula pendula]
                   16997
 Seq. No.
                   48015 1.R1040
 Contig ID
                   LIB3093-027-Q1-K1-B9
 5'-most EST
 Seq. No.
                   16998
                   48020 1.R1040
 Contig ID
                   LIB3139-113-P1-N1-C6
 5'-most EST
                   16999
 Seq. No.
                    48039 1.R1040
 Contig ID
                   LIB3093-026-Q1-K1-C11
 5'-most EST
                   BLASTX
 Method
                    g2335101
 NCBI GI
```

2808

399

103

71

8.0e-39

BLAST score

Match length

% identity

E value



```
NCBI Description (AC002339) unknown protein [Arabidopsis thaliana]
```

Contig ID 48052 1.R1040

5'-most EST LIB3107-004-Q1-K1-A12

Method BLASTX
NCBI GI g3336903
BLAST score 463
E value 5.0e-46
Match length 118
% identity 75

NCBI Description (Y10809) bZIP DNA-binding protein [Petroselinum crispum]

Seq. No.

17001

Contig ID 48059 1.R1040

5'-most EST LIB3093-025-Q1-K1-F6

Method BLASTX
NCBI GI g2944417
BLAST score 505
E value 4.0e-51
Match length 126
% identity 77

NCBI Description (AF049881) peroxidase FLXPER4 [Linum usitatissimum]

Seq. No.

17002

Contig ID 48067 1.R1040

5'-most EST LIB3093-025-Q1-K1-E5

Method BLASTX
NCBI GI g3096922
BLAST score 297
E value 2.0e-27
Match length 165
% identity 50

NCBI Description (AL023094) putative protein [Arabidopsis thaliana]

Seq. No.

17003

Contig ID 48087 1.R1040

5'-most EST LIB3093-025-Q1-K1-E10

Method BLASTX
NCBI GI g541881
BLAST score 192
E value 1.0e-14
Match length 48
% identity 67

NCBI Description MYB homolog transcription ATMYB2 - Arabidopsis thaliana

>gi\_506189\_dbj\_BAA03534\_ (D14712) ATMYB2 [Arabidopsis
thaliana] >gi 2275197 (AC002337) Atmyb2 [Arabidopsis

thaliana]

Seq. No.

17004

Contig ID

48088 1.R1040

5'-most EST

jC-gmro02910061a05a1

Seq. No.

17005

Contig ID 5'-most EST

48104\_1.R1040 sat701007808.h1



```
17006
Seq. No.
                  48116 1.R1040
Contig ID
                  LIB3093-024-Q1-K1-G8
5'-most EST
                  BLASTX
Method
                  g3292827
NCBI GI
                  306
BLAST score
                  4.0e-45
E value
                  145
Match length
                  71
% identity
NCBI Description (AL031018) putative protein [Arabidopsis thaliana]
                  17007
Seq. No.
                   48117 1.R1040
Contig ID
                  g4405659
5'-most EST
Seq. No.
                   17008
                   48118 1.R1040
Contig ID
                   jC-gmst02400045a12a1
5'-most EST
                   BLASTX
Method
                   g4049517
NCBI GI
                   198
BLAST score
                   5.0e-15
E value
                   200
Match length
                   26
% identity
NCBI Description (AL034563) hypothetical protein [Schizosaccharomyces pombe]
                   17009
Seq. No.
                   48122 1.R1040
Contig ID
                   LIB3093-024-Q1-K1-H3
5'-most EST
                   BLASTX
Method
                   g4490758
NCBI GI
                   172
BLAST score
                   3.0e-12
E value
                   99
Match length
                   33
% identity
                  (AL035708) putative protein [Arabidopsis thaliana]
NCBI Description
                   17010
Seq. No.
                   48124 1.R1040
Contig ID
                   uC-qmrominsoy192c01b1
5'-most EST
                   17011
Seq. No.
                   48124 2.R1040
 Contig ID
                   LIB3093-024-Q1-K1-G11
 5'-most EST
                   17012
Seq. No.
                   48139 1.R1040
 Contig ID
                   LIB3093-024-Q1-K1-E7
 5'-most EST
 Method
                   BLASTX
                   g1946371
 NCBI GI
 BLAST score
                   247
                    5.0e-21
 E value
                   114
 Match length
```

[Arabidopsis thaliana]

(U93215) regulatory protein Viviparous-1 isolog

44

% identity

NCBI Description



Seq. No. 17013 Contig ID 48144

48144\_1.R1040

5'-most EST jC-gmle01810014c11d1

Seq. No. 17014

Contig ID 48144\_3.R1040 5'-most EST wvk700685020.h1

Method BLASTX
NCBI GI g1653954
BLAST score 213
E value 1.0e-16
Match length 106
% identity 42

NCBI Description (D90917) hypothetical protein [Synechocystis sp.]

Seq. No. 17015

Contig ID 48144\_4.R1040 5'-most EST fde700872187.h1

Seq. No. 17016

Contig ID 48184\_1.R1040 5'-most EST uC-gmronoir041f09b1

Method BLASTX
NCBI GI g1272349
BLAST score 340
E value 1.0e-31

Match length 149 % identity 50

NCBI Description (U51740) secreted glycoprotein 3 [Ipomoea trifida]

Seq. No. 17017

Contig ID 48191\_1.R1040 5'-most EST epx701109018.h1

Method BLASTX
NCBI GI g2961357
BLAST score 159
E value 6.0e-17
Match length 78
% identity 67

NCBI Description (AL022140) putative protein [Arabidopsis thaliana]

Seq. No. 17018

Contig ID 48202 1.R1040

5'-most EST LIB3093-023-Q1-K1-F6

Seq. No. 17019

Contig ID 48202\_2.R1040 5'-most EST leu701145196.h1

Seq. No. 17020

Contig ID 48207 1.R1040

5'-most EST LIB $30\overline{9}3-023-Q1-K1-G11$ 

Method BLASTX
NCBI GI g3643192
BLAST score 143
E value 8.0e-09
Match length 53

% identity NCBI Description (AF087435) unknown [Arabidopsis thaliana] Seq. No. 17021 48227 1.R1040 Contig ID 5'-most EST LIB3093-023-Q1-K1-F2 Seq. No. 17022 48233 1.R1040 Contig ID 5'-most EST LIB3093-023-Q1-K1-D12 Method BLASTX NCBI GI q4467098 370 BLAST score 2.0e-35 E value 146 Match length % identity 65 NCBI Description (AL035538) putative protein [Arabidopsis thaliana] Seq. No. 17023 48238 1,R1040 Contig ID 5'-most EST trc700566213.h1 BLASTX Method NCBI GI g2911066 BLAST score 189 E value 6.0e-14 Match length 69 % identity 57 NCBI Description (AL021960) adrenodoxin - like protein [Arabidopsis thaliana] Seq. No. 17024 Contig ID 48246 1.R1040 5'-most EST LIB3093-023-Q1-K1-B5 17025 Seq. No.

Contig ID 48252 1.R1040

5'-most EST LIB3139-073-P1-N1-G4

BLASTX Method NCBI GI g4455335 BLAST score 1059 E value 1.0e-116 Match length 270 % identity 31

NCBI Description (AL035525) putative protein [Arabidopsis thaliana]

17026 Seq. No.

48257\_1.R1040 Contig ID

5'-most EST LIB3170-021-Q1-K1-F4

Method BLASTX NCBI GI g2408068 BLAST score 572 E value 1.0e-58 Match length 288 38 % identity

NCBI Description (Z99165) hypothetical protein [Schizosaccharomyces pombe]

Seq. No. 17027



```
48263 1.R1040
Contig ID
                   bnh70\overline{0}764610.h1
5'-most EST
                   BLASTX
Method
                   q4467359
NCBI GI
                   863
BLAST score
                   4.0e-93
E value
                   172
Match length
                   95
% identity
                   (AJ002685) Phosphatidylinositol 4-kinase [Arabidopsis
NCBI Description
                   thaliana]
                   17028
Seq. No.
                   48266 1.R1040
Contig ID
                   uC-gmrominsoy202b09b1
5'-most EST
                   BLASTX
Method
                   g2505865
NCBI GI
                   318
BLAST score
                   5.0e-29
E value
                   228
Match length
                   17
% identity
NCBI Description (Y12227) putative topoisomerase [Arabidopsis thaliana]
                   17029
Seq. No.
                   48273 1.R1040
Contig ID
                   xzm70\overline{0}763804.h1
5'-most EST
                   17030
Seq. No.
                    48274 1.R1040
Contig ID
                   uC-gmrominsoy042c09b1
5'-most EST
                    BLASTX
Method
                    g4325344
NCBI GI
                    400
BLAST score
                    1.0e-38
E value
                    162
Match length
                    52
% identity
                    (AF128393) similar to beta-transducins (Pfam: PF00400,
NCBI Description
                    Score=71.7, E=1.5e-17, N=6) [Arabidopsis thaliana]
                    17031
Seq. No.
Contig ID
                    48281 1.R1040
                    LIB3093-022-Q1-K1-H11
5'-most EST
                    17032
Seq. No.
                    48284 1.R1040
 Contig ID
                    uxk70\overline{0}668544.h1
 5'-most EST
                    17033
 Seq. No.
                    48287 1.R1040
 Contig ID
                    leu701155105.hl
 5'-most EST
                    BLASTX
 Method
                    g4056552
 NCBI GI
                    177
 BLAST score
                    1.0e-12
 E value
 Match length
                    41
 % identity
                    71
                    (AL034583) putative nucleotide binding protein
 NCBI Description
```

2813

[Schizosaccharomyces pombe]

Contig ID

5'-most EST

```
17034
Seq. No.
                  48287 2.R1040
Contig ID
                  LIB3107-029-Q1-K1-F6
5'-most EST
                  BLASTX
Method
                  g4056552
NCBI GI
                  594
BLAST score
                  2.0e-61
E value
                  159
Match length
                  67
% identity
NCBI Description (AL034583) putative nucleotide binding protein
                  [Schizosaccharomyces pombe]
                  17035
Seq. No.
                  48288 1.R1040
Contig ID
                  LIB3093-022-Q1-K1-G4
5'-most EST
                  BLASTX
Method
                  g3193298
NCBI GI
                   198
BLAST score
                   5.0e-15
E value
                   124
Match length
                   32
% identity
NCBI Description (AF069298) T14P8.17 gene product [Arabidopsis thaliana]
                   17036
Seq. No.
                   48302 1.R1040
Contig ID
                   LIB3093-022-Q1-K1-G3
5'-most EST
                   BLASTX
Method
                   q3252868
NCBI GI
                   501
BLAST score
                   2.0e-50
E value
                   203
Match length
                   48
% identity
                   (AF033536) putative zinc transporter [Arabidopsis thaliana]
NCBI Description
                   17037
Seq. No.
                   48313 1.R1040
Contig ID
                   jC-gmle01810086a12a1
5'-most EST
                   17038
Seq. No.
                   48313 3.R1040
Contig ID
                   zhf700964760.hl
5'-most EST
                   17039
Seq. No.
                   48315 1.R1040
Contig ID
                   LIB3107-031-Q1-K1-G10
 5'-most EST
                   BLASTN
Method
                   g3341467
NCBI GI
                   90
 BLAST score
                   6.0e-43
 E value
                   190
 Match length
                   87
 % identity
 NCBI Description Nicotiana tabacum BBF1 gene
                   17040
```

2814

48347 1.R1040

uaw700660873.hl



Contig ID 48349\_1.R1040

5'-most EST LIB3093-019-Q1-K2-G7

Method BLASTX
NCBI GI g2829870
BLAST score 220
E value 6.0e-18
Match length 99
% identity 48

NCBI Description (AC002396) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 17042

Contig ID 48354 1.R1040

5'-most EST LIB3109-019-Q1-K1-D7

Seq. No. 17043

Contig ID 48355 1.R1040

5'-most EST LIB3093-019-Q1-K2-H7

Seq. No. 17044

Contig ID 48377 1.R1040

5'-most EST jC-gmf102220133d09a1

Method BLASTX
NCBI GI g2961371
BLAST score 227
E value 1.0e-18
Match length 114
% identity 41

NCBI Description (AL022141) hypothetical protein (fragment) [Arabidopsis

thaliana]

Seq. No. 17045

Contig ID 48381\_1.R1040

5'-most EST LIB3093-019-Q1-K1-G4

Seq. No. 17046

Contig ID 48382\_1.R1040 5'-most EST hyd700726484.h1

Method BLASTX
NCBI GI g1346218
BLAST score 243
E value 2.0e-20
Match length 139
% identity 39

NCBI Description PROBABLE GMP SYNTHASE (GLUTAMINE-HYDROLYSING) (GLUTAMINE

AMIDOTRANSFERASE) (GMP SYNTHETASE)

>gi 1001583 dbj BAA10210 (D64000) GMP synthetase

[Synechocystis sp.]

Seq. No. 17047

Contig ID 48400\_1.R1040 5'-most EST zhf700958152.h1

Seq. No. 17048

Contig ID 48402\_1.R1040 5'-most EST g4313506



```
17049
Seq. No.
                  48403 1.R1040
Contig ID
                  g5510222
5'-most EST
                  17050
Seq. No.
                  48403 2.R1040
Contig ID
                  uC-gm\overline{f}lminsoy014f06b1
5'-most EST
                  BLASTX
Method
                  g2911072
NCBI GI
                  1108
BLAST score
                   1.0e-121
E value
                   403
Match length
                   58
% identity
                  (AL021960) putative protein [Arabidopsis thaliana]
NCBI Description
                   17051
Seq. No.
                   48438 1.R1040
Contig ID
                   LIB3093-019-Q1-K1-B11
5'-most EST
                   17052
Seq. No.
                   48447_1.R1040
Contig ID
                   LIB3138-011-Q1-N1-B1
5'-most EST
                   BLASTX
Method
                   g481812
NCBI GI
                   396
BLAST score
                   2.0e-38
E value
                   90
Match length
                   39
% identity
                   DNA-binding protein GT-2 - Arabidopsis thaliana
NCBI Description
                   >gi_416490_emb_CAA51289_ (X72780) GT-2 factor [Arabidopsis
                   thaliana]
                   17053
Seq. No.
                   48447 2.R1040
Contig ID
                   zsq701129820.h1
5'-most EST
                   BLASTX
Method
                   q283004
NCBI GI
                   417
BLAST score
                   8.0e-41
E value
                   115
Match length
% identity
                   DNA-binding protein Gt-2 - rice >gi_20249_emb_CAA48328_
NCBI Description
                   (X68261) gt-2 [Oryza sativa]
                   17054
 Seq. No.
                    48464 1.R1040
 Contig ID
                   uC-gmrominsoy217b01b1
 5'-most EST
```

Contig ID 48471\_1.R1040

5'-most EST g4276939

Seq. No. 17056

Contig ID 48472\_1.R1040

5'-most EST LIB3093-018-Q1-K2-E9

Method BLASTX

```
q3063439
NCBI GI
                  187
BLAST score
                  7.0e-14
E value
                  60
Match length
                  62
% identity
NCBI Description (AC003981) F22013.1 [Arabidopsis thaliana]
                  17057
Seq. No.
                   48484 1.R1040
Contig ID
                  LIB3093-018-Q1-K1-C8
5'-most EST
                  17058
Seq. No.
                   48486 1.R1040
Contig ID
5'-most EST
                  uC-gmropic025c03b1
                   17059
Seq. No.
                   48487 1.R1040
Contig ID
                  LIB3093-018-Q1-K1-D10
5'-most EST
                   17060
Seq. No.
                   48494 1.R1040
Contig ID
                   uC-gmflminsoy029h06b1
5'-most EST
                   BLASTX
Method
                   g2811230
NCBI GI
                   1118
BLAST score
                   1.0e-123
E value
                   275
Match length
                   36
% identity
NCBI Description (AF042670) fimbrin 1 [Arabidopsis thaliana]
                   17061
Seq. No.
                   48495_1.R1040
Contig ID
                   rca701001627.hl
5'-most EST
                   BLASTX
Method
                   g2956717
NCBI GI
                   106
BLAST score
                   4.0e-11
E value
                   108
Match length
                   53
 % identity
                   (Y09722) beta-carotene hydroxylase 2 [Capsicum annuum]
NCBI Description
                   17062
 Seq. No.
                   48498 1.R1040
 Contig ID
                   LIB3093-018-Q1-K2-E2
 5'-most EST
                   17063
 Seq. No.
                   48504 1.R1040
 Contig ID
 5'-most EST
                   LIB3093-018-Q1-K1-B5
 Seq. No.
                   17064
                   48512 1.R1040
 Contig ID
                   uC-qmflminsoy058d01b1
 5'-most EST
```

BLASTX Method g2160138 NCBI GI BLAST score 169 9.0e-12E value 78 Match length

2817



% identity 22

NCBI Description (AC000375) No definition line found [Arabidopsis thaliana]

Seq. No. 17065

Contig ID 48513 1.R1040

5'-most EST LIB3093-018-Q1-K1-C3

Seq. No. 17066

Contig ID 48516\_1.R1040 5'-most EST pmv700893960.h1

Seq. No. 17067

Contig ID 48522 1.R1040

5'-most EST LIB3093-018-Q1-K1-H9

Seq. No. 17068

Contig ID 48528 1.R1040

5'-most EST LIB3093-018-Q1-K2-A5

Method BLASTX
NCBI GI g1208497
BLAST score 161
E value 7.0e-11
Match length 105
% identity 40

NCBI Description (D38125) EREBP-4 [Nicotiana tabacum]

Seq. No. 17069

Contig ID 48541\_1.R1040 5'-most EST kl1701213929.h1

Method BLASTX
NCBI GI g2213600
BLAST score 448
E value 1.0e-44
Match length 151
% identity 58

NCBI Description (AC000348) T7N9.20 [Arabidopsis thaliana]

Seq. No. 17070

Contig ID 48606\_1.R1040

5'-most EST LIB3093-017-Q1-K1-G1

Method BLASTN
NCBI GI g1220521
BLAST score 281
E value 1.0e-156
Match length 441
% identity 91

NCBI Description Glycine max TATA-box binding protein (STBP1) mRNA, complete

cds

Seq. No. 17071

Contig ID 48613\_1.R1040

5'-most EST LIB3093-017-Q1-K1-H2

Method BLASTX
NCBI GI g2731637
BLAST score 151
E value 8.0e-10
Match length 106



```
% identity
NCBI Description (U70667) Fas-ligand associated factor 1 [Homo sapiens]
                   17072
Seq. No.
                   48624 1.R1040
Contig ID
                   fde700871052.hl
5'-most EST
                   17073
Seq. No.
                   48637 1.R1040
Contig ID
                   LIB30\overline{9}3-017-Q1-K2-E10
5'-most EST
                   17074
Seq. No.
                   48638 1.R1040
Contig ID
                   LIB30\overline{9}3-017-Q1-K1-C4
5'-most EST
Method
                   BLASTX
                   g2262105
NCBI GI
                   814
BLAST score
                   3.0e-87
E value
                   221
Match length
                   67
% identity
                  (AC002343) unknown protein [Arabidopsis thaliana]
NCBI Description
                   17075
Seq. No.
                   48639 1.R1040
Contig ID
                   LIB3109-038-Q1-K1-F4
5'-most EST
                   BLASTX
Method
                   g1171577
NCBI GI
                   156
BLAST score
                   3.0e-10
E value
                   123
Match length
                   32
% identity
NCBI Description (X95343) hypersensitivity-related gene [Nicotiana tabacum]
                   17076
Seq. No.
                   48641 1.R1040
Contig ID
                   LIB3093-017-Q1-K2-C7
5'-most EST
                   17077
Seq. No.
                   48643 1.R1040
Contig ID
                   LIB3093-017-Q1-K1-C9
5'-most EST
                   BLASTN
Method
                   q2656026
NCBI GI
BLAST score
                   56
                   1.0e-22
E value
Match length
                   88
                    91
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MDF20
```

Contig ID 48646\_1.R1040 5'-most EST LIB3093-017-Q1-K2-D2

.....

Seq. No. 17079
Contig ID 48649\_1.R1040

5'-most EST g5058341 Method BLASTX

% identity

31



```
NCBI GI
                  g2569938
BLAST score
                  1424
                  1.0e-158
E value
Match length
                  438
% identity
                  66
NCBI Description (Y15193) GAI [Arabidopsis thaliana]
                  17080
Seq. No.
                  48649 2.R1040
Contig ID
                  LIB3170-032-Q1-J1-F7
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2569938
BLAST score
                  299
E value
                  6.0e-27
Match length
                  84
% identity
                  69
NCBI Description (Y15193) GAI [Arabidopsis thaliana]
Seq. No.
                  17081
                  48650 1.R1040
Contig ID
5'-most EST
                  LIB3093-017-Q1-K1-D6
                  17082
Seq. No.
Contig ID
                  48652 1.R1040
5'-most EST
                  LIB3093-017-Q1-K1-D3
                  17083
Seq. No.
Contig ID
                  48653 1.R1040
5'-most EST
                  uC-gmronoir049a02b1
Seq. No.
                  17084
Contig ID
                  48653 2.R1040
5'-most EST
                  LIB3106-063-Q1-K1-G11
Seq. No.
                  17085
Contig ID
                  48662 1.R1040
5'-most EST
                  LIB3093-017-Q1-K1-B4
Method
                  BLASTX
NCBI GI
                  g629561
BLAST score
                  297
                  7.0e-27
E value
Match length
                  136
% identity
                  44
NCBI Description SRG1 protein - Arabidopsis thaliana
                  >gi 479047 emb CAA55654 (X79052) SRG1 [Arabidopsis
                  thaliana]
Seq. No.
                  17086
Contig ID
                  48665 1.R1040
5'-most EST
                  rca700998588.h1
Method
                  BLASTX
NCBI GI
                  g2497217
BLAST score
                  148
E value
                  4.0e-09
Match length
                  137
```

NCBI Description HYPOTHETICAL 59.5 KD PROTEIN IN HDF1-MRPL33 INTERGENIC



REGION >gi\_1078537\_pir\_\_S54592 hypothetical protein YMR285c - yeast (Saccharomyces cerevisiae) >gi\_825551\_emb\_CAA89783\_(Z49704) unknown [Saccharomyces cerevisiae]

Seq. No. 17087

Contig ID 48665 2.R1040

5'-most EST LIB3093-017-Q1-K1-B3

Seq. No. 17088

Contig ID 48667\_1.R1040 5'-most EST fua701040508.h1

Seq. No. 17089

Contig ID 48685\_1.R1040

5'-most EST LIB3093-017-Q1-K1-A12

Method BLASTX
NCBI GI g3513726
BLAST score 303
E value 2.0e-27
Match length 187
% identity 32

NCBI Description (AF080118) F8M12.23 gene product [Arabidopsis thaliana]

>gi 4539354\_emb\_CAB40048.1\_ (AL049525) putative protein

[Arabidopsis thaliana]

Seq. No. 17090

Contig ID 48688 1.R1040

5'-most EST LIB3109-057-Q1-K1-C3

Method BLASTX
NCBI GI g1514649
BLAST score 595
E value 1.0e-85
Match length 216
% identity 59

NCBI Description (X86021) potassium channel [Solanum tuberosum]

Seq. No. 17091

Contig ID 48698\_1.R1040 5'-most EST rca701001056.h1

Method BLASTN
NCBI GI g2924257
BLAST score 479
E value 0.0e+00
Match length 814
% identity 89

NCBI Description Tobacco chloroplast genome DNA

Seq. No. 17092

Contig ID 48708 1.R1040

5'-most EST LIB3093-015-Q1-K1-C7

Method BLASTN
NCBI GI g3334660
BLAST score 118
E value 1.0e-59
Match length 350
% identity 83

NCBI Description G.max mRNA for putative cytochrome P450, clone CP3



Contig ID 48724\_1.R1040

5'-most EST LIB3093-017-Q1-K1-D1

Method BLASTX
NCBI GI g2494151
BLAST score 153
E value 5.0e-10
Match length 44
% identity 68

NCBI Description DNAJ PROTEIN >gi\_2119734\_pir\_\_JC4739 chaperonin dnaJ -

Bacillus stearothermophilus >gi\_1568475\_emb\_CAA62240\_

(X90709) dnaJ [Bacillus stearothermophilus]

Seq. No. 17094

Contig ID 48762\_1.R1040

5'-most EST LIB3093-017-Q1-K1-A9

Seq. No. 17095

48766 1.R1040 Contig ID g5342750 5'-most EST BLASTX Method g1172829 NCBI GI 557 BLAST score 1.0e-56 E value 217 Match length 50 % identity

NCBI Description POLY(A) + RNA EXPORT PROTEIN >gi\_1362233\_pir\_\_A56119 RNA

export protein rael - fission yeast (Schizosaccharomyces

pombe) >gi\_625094 (U14951) polyA+ RNA export

[Schizosaccharomyces pombe] >gi\_2842504\_emb\_CAA16856\_ (AL021748) polya+ rna export protein [Schizosaccharomyces

pombe]

Seq. No. 17096

Contig ID 48769\_1.R1040 5'-most EST crh700851395.h1

Seq. No. 17097

Contig ID 48770 1.R1040

5'-most EST jC-gmle01810087a10a1

Seq. No. 17098

Contig ID 48771\_1.R1040

5'-most EST LIB3093-016-Q1-K2-G10

Method BLASTX
NCBI GI 94220534
BLAST score 155
E value 4.0e-10
Match length 92
% identity 38

NCBI Description (AL035356) putative protein [Arabidopsis thaliana]

Seq. No. 17099

Contig ID 48774\_1.R1040 5'-most EST uC-gmronoir030c01b1

Method BLASTX

```
q3851636
NCBI GI
                  824
BLAST score
                  3.0e-88
E value
                  190
Match length
                  82
% identity
                  (AF098519) unknown [Avicennia marina] >gi_4128206
NCBI Description
                   (AF056316) 40S ribosome protein S7 [Avicennia marina]
                  17100
Seq. No.
                  48780 1.R1040
Contig ID
                  LIB3093-016-Q1-K2-G9
5'-most EST
                  17101
Seq. No.
                  48781 1.R1040
Contig ID
                  LIB3093-016-Q1-K2-H1
5'-most EST
                  BLASTX
Method
                  g1658503
NCBI GI
                  253
BLAST score
                  1.0e-21
E value
                   139
Match length
                   44
% identity
NCBI Description (U75467) Atu [Drosophila melanogaster]
                   17102
Seq. No.
                   48782 1.R1040
Contig ID
                   LIB3093-016-Q1-K1-A11
5'-most EST
                   BLASTX
Method
                   g2213600
NCBI GI
                   249
BLAST score
                   3.0e-21
E value
                   112
Match length
                   45
% identity
NCBI Description (AC000348) T7N9.20 [Arabidopsis thaliana]
                   17103
Seq. No.
Contig ID
                   48787 1.R1040
5'-most EST
                   LIB3093-016-Q1-K2-H3
                   BLASTX
Method
                   q4406764
NCBI GI
BLAST score
                   322
                   6.0e-30
E value
Match length
                   74
                   82
% identity
                   (AC006836) putative uridylyl transferase [Arabidopsis
NCBI Description
                   thaliana]
                   17104
Seq. No.
                   48787 2.R1040
Contig ID
```

LIB3138-080-P1-N1-F8 5'-most EST

Method BLASTX g1146165 NCBI GI 523 BLAST score 3.0e-53 E value 172 Match length % identity 66

NCBI Description (L47479) urophorphyrin III methylase [Arabidopsis thaliana]



Contig ID 48789\_1.R1040 5'-most EST LIB3107-074-Q1-K1-D9

Seq. No. 17106

Contig ID 48789\_2.R1040 5'-most EST ary700764389.h1

Seq. No. 17107

Contig ID 48791\_1.R1040

5'-most EST uC-gmrominsoy268a01b1

Method BLASTX
NCBI GI g3775997
BLAST score 300
E value 4.0e-27
Match length 111
% identity 61

NCBI Description (AJ010462) RNA helicase [Arabidopsis thaliana]

Seg. No. 17108

Contig ID 48791\_2.R1040 5'-most EST kl1701208910.h1

Seq. No. 17109

Contig ID 48797\_1.R1040

5'-most EST LIB3093-016-Q1-K1-C10

Seq. No. 17110

Contig ID 48805\_1.R1040

5'-most EST LIB3093-016-Q1-K2-C7

Method BLASTX
NCBI GI g4454051
BLAST score 162
E value 1.0e-14
Match length 115
% identity 47

NCBI Description (AL035394) putative polygalacturonase [Arabidopsis

thaliana]

Seq. No. 17111

Contig ID 48810 1.R1040

5'-most EST LIB3094-044-Q1-K1-C4

Method BLASTX
NCBI GI g3157943
BLAST score 362
E value 2.0e-34
Match length 135
% identity 53

NCBI Description (AC002131) Contains similarity to BAP31 protein gb\_X81816

from Mus musculus. [Arabidopsis thaliana]

Seq. No. 17112

Contig ID 48810\_2.R1040 5'-most EST taw700660074.h1

Method BLASTX NCBI GI g3157943 BLAST score 293



```
E value
Match length
                   104
% identity
                   53
                   (AC002131) Contains similarity to BAP31 protein gb_X81816
NCBI Description
                   from Mus musculus. [Arabidopsis thaliana]
                   17113
Seq. No.
                   48812 1.R1040
Contig ID
                   LIB3093-016-Q1-K1-D2
5'-most EST
                   17114
Seq. No.
                   48821 1.R1040
Contig ID
5'-most EST
                   LIB3093-016-Q1-K2-C6
Method
                   BLASTX
                   g1732204
NCBI GI
                    299
BLAST score
                    9.0e-27
E value
                    165
Match length
% identity
                    38
                    (U65015) putative aldolase [Vibrio furnissii]
NCBI Description
                    17115
Seq. No.
                    48827 1.R1040
Contig ID
5'-most EST
                    LIB3093-016-Q1-K1-B7
                    BLASTX
Method
                    q585084
NCBI GI
                    633
BLAST score
                    5.0e-66
E value
Match length
                    232
% identity
                    ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G)
NCBI Description
                    >gi_543383_pir__S40780 translation elongation factor G, mitochondrial - rat >gi_310102 (L14684) elongation factor G
                    [Rattus norvegicus]
                    17116
Seq. No.
                    48832 1.R1040
Contig ID
                    zpv700762974.h1
5'-most EST
Method
                    BLASTX
                    g4456758
NCBI GI
BLAST score
                    194
                    7.0e-15
E value
                    97
Match length
% identity
                    45
                   (AJ000691) heat shock protein 17.4 [Quercus suber]
NCBI Description
```

48836 1.R1040 Contig ID

LIB3093-016-Q1-K2-C5 5'-most EST

Method BLASTX q4455232 NCBI GI 215 BLAST score 3.0e-17 E value 51 Match length 73 % identity

(AL035523) putative protein [Arabidopsis thaliana] NCBI Description



```
Seq. No.
                  17118
                  48837 1.R1040
Contig ID
5'-most EST
                  awf700836967.hl
                  BLASTX
Method
                  q3643608
NCBI GI
BLAST score
                  534
                  1.0e-54
E value
                  135
Match length
% identity
NCBI Description (AC005395) hypothetical protein [Arabidopsis thaliana]
                  17119
Seq. No.
Contig ID
                  48837 2.R1040
                  LIB3093-016-Q1-K1-G10
5'-most EST
                  BLASTX
Method
                  a3643608
NCBI GI
                   220
BLAST score
                   7.0e-18
E value
Match length
                   69
                   58
% identity
NCBI Description (AC005395) hypothetical protein [Arabidopsis thaliana]
                   17120
Seq. No.
Contig ID
                   48844 1.R1040
                   LIB3093-016-Q1-K1-H11
5'-most EST
Method
                   BLASTX
                   q1136434
NCBI GI
BLAST score
                   150
                   1.0e-09
E value
                   103
Match length
                   35
% identity
NCBI Description (D80009) KIAA0187 [Homo sapiens]
Seq. No.
                   17121
                   48845 1.R1040
Contig ID
                   LIB3167-078-P1-K2-H12
5'-most EST
Method
                   BLASTX
                   q4262242
NCBI GI
BLAST score
                   519
                   1.0e-52
E value
Match length
                   121
                   80
% identity
NCBI Description (AC006200) NADC homolog [Arabidopsis thaliana]
Seq. No.
                   17122
                   48845 2.R1040
Contig ID
5'-most EST
                   xpa700793925.hl
                   17123
Seq. No.
                   48851 1.R1040
Contig ID
                   LIB3093-016-Q1-K2-A7
5'-most EST
```

Contig ID 48870\_1.R1040 5'-most EST zsg701126036.h1

Seq. No. 17125



```
Contig ID
                  48935 1.R1040
5'-most EST
                  LIB3094-082-Q1-K1-H2
Method
                  BLASTX
NCBI GI
                  g4567282
BLAST score
                  1214
                  1.0e-134
E value
Match length
                  328
                  72
% identity
NCBI Description (AC006841) putative DNAJ protein [Arabidopsis thaliana]
                  17126
Seq. No.
Contig ID
                  48936 1.R1040
5'-most EST
                  fde700870601.h1
                  17127
Seq. No.
Contig ID
                  48938 1.R1040
                  LIB3106-071-P1-K1-D12
5'-most EST
Seq. No.
                  17128
Contig ID
                  48940 1.R1040
5'-most EST
                  kl1701210345.h1
Method
                  BLASTX
NCBI GI
                  g3033375
BLAST score
                  303
E value
                  9.0e-31
Match length
                  118
% identity
NCBI Description (AC004238) putative berberine bridge enzyme [Arabidopsis
                  thaliana]
Seq. No.
                  17129
                  48943 1.R1040
Contig ID
5'-most EST
                  zhf700961810.h1
Method
                  BLASTX
                  g3396079
NCBI GI
BLAST score
                  306
E value
                  7.0e-28
Match length
                  112
                  51
% identity
NCBI Description (AF080173) inositol 1,3,4-trisphosphate 5/6-kinase
                  [Arabidopsis thaliana]
Seq. No.
                  17130
                  48948 1.R1040
Contig ID
5'-most EST
                  LIB3093-015-Q1-K1-G6
Method
                  BLASTX
NCBI GI
                  g2281086
BLAST score
                  229
E value
                  6.0e-19
Match length
                  102
% identity
                  45
NCBI Description (AC002333) indole-3-acetate beta-glucosyltransferase isolog
                  [Arabidopsis thaliana]
```

Contig ID 48950\_1.R1040

5'-most EST LIB30 $\overline{9}$ 3-015-Q1-K2-F4



```
BLASTX
Method
                  g4337001
NCBI GI
BLAST score
                   384
                   4.0e-37
E value
Match length
                   87
                  74
% identity
                  (AF118129) Tsi1-interacting protein TSIP1 [Nicotiana
NCBI Description
                   tabacum]
                   17132
Seq. No.
                   48951 1.R1040
Contig ID
                   LIB3093-015-Q1-K2-F5
5'-most EST
                   BLASTX
Method
                   q4455309
NCBI GI
BLAST score
                   301
                   3.0e-27
E value
Match length
                   82
                   71
% identity
NCBI Description (AL035528) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   17133
                   48957 1.R1040
Contig ID
                   LIB3093-015-Q1-K1-G10
5'-most EST
                   17134
Seq. No.
Contig ID
                   48961 1.R1040
                   fC-qmst700667058f2
5'-most EST
Seq. No.
                   17135
                   48962 1.R1040
Contig ID
                   smc70\overline{0}748845.h1
5'-most EST
                   BLASTX
Method
                   g3411051
NCBI GI
                   1707
BLAST score
                   0.0e+00
E value
                   422
Match length
                   79
% identity
                   (AF032448) ethylene receptor [Malus domestica]
NCBI Description
                   17136
Seq. No.
                   48967 1.R1040
Contig ID
                   uC-gmrominsoy320e02b1
5'-most EST
                   BLASTX
Method
                   g2129655
NCBI GI
BLAST score
                   495
                   7.0e-50
E value
                   153
Match length
 % identity
NCBI Description OBP32pep protein - Arabidopsis thaliana (fragment)
                   >gi_1022799 (U37698) OBP32pep [Arabidopsis thaliana]
                   17137
 Seq. No.
                   48970_1.R1040
 Contig ID
```

5'-most EST LIB3093-014-Q1-K1-E7

Method BLASTX
NCBI GI g4335722
BLAST score 195

2828

Contig ID

5'-most EST



```
7.0e-15
E value
Match length
                  98
% identity
                  (AC006248) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  17138
Seq. No.
                  48970 2.R1040
Contiq ID
                  iC-qmro02910022e07a1
5'-most EST
                  BLASTX
Method
                  g4335722
NCBI GI
                  155
BLAST score
                  3.0e-10
E value
Match length
                  85
                  41
% identity
                  (AC006248) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  17139
                   48971 2.R1040
Contig ID
                  LIB3138-071-P1-N1-G6
5'-most EST
                  BLASTX
Method
                   g4101473
NCBI GI
                   623
BLAST score
                   7.0e-65
E value
                   151
Match length
                   83
% identity
                  (AF003382) KEA1 [Arabidopsis thaliana]
NCBI Description
                   17140
Seq. No.
                   48973 1.R1040
Contig ID
5'-most EST
                   LIB3093-015-Q1-K1-E4
                   BLASTX
Method
                   g1871182
NCBI GI
                   581
BLAST score
                   5.0e-60
E value
Match length
                   134
                   79
% identity
                  (U90439) phospholipase D isolog [Arabidopsis thaliana]
NCBI Description
                   17141
Seq. No.
Contig ID
                   48975 1.R1040
5'-most EST
                   LIB3093-015-Q1-K2-E7
                   17142
Seq. No.
                   48976 1.R1040
Contig ID
5'-most EST
                   ncj700982261.h1
                   BLASTX
Method
                   q2829865
NCBI GI
BLAST score
                   506
E value
                   6.0e-66
Match length
                   162
% identity
                   78
                   (AC002396) N-terminal region similar to DNA-J proteins
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   17143
                   48992 1.R1040
```

2829

LIB3093-015-Q1-K1-D2



Method BLASTX NCBI GI g1575595 BLAST score 155 E value 3.0e-10 Match length 45 67 % identity

NCBI Description (U67717) fimbrin/plastin-like [Triticum aestivum]

Seq. No.

17144

Contig ID 5'-most EST

48999 1.R1040 uaw700663173.hl

BLASTX Method q2909583 NCBI GI BLAST score 450 E value 3.0e-83 Match length 440 % identity

NCBI Description (AL021926) oxcA [Mycobacterium tuberculosis]

Seq. No.

17145

Contig ID 5'-most EST 49001 1.R1040 ssr700554360.hl

Method BLASTX NCBI GI g3142303 BLAST score 1206 1.0e-133 E value Match length 381 % identity 47

NCBI Description

(AC002411) Strong similarity to MRP-like ABC transporter gb U92650 from A. thaliana and canalicular multi-drug

resistance protein gb L49379 from Rattus norvegicus.

[Arabidopsis thaliana]

Seq. No.

17146

Contig ID

49021 1.R1040

5'-most EST

LIB3093-015-Q1-K1-A11

Seq. No.

17147

Contig ID

49025 1.R1040

5'-most EST

LIB3093-015-Q1-K1-A5

Seq. No.

17148

Contig ID

49105\_1.R1040

5'-most EST Method NCBI GI

 $q4290\overline{3}56$ BLASTX q1311536

BLAST score E value Match length 333

% identity

7.0e-3170

NCBI Description (L77969) aquaporin [Spinacia oleracea]

Seq. No.

17149

84

Contig ID 5'-most EST 49107 1.R1040  $qsv70\overline{1}044321.h1$ 

Method NCBI GI BLASTX g2245012



```
BLAST score
                  4.0e-14
E value
                  49
Match length
                  71
% identity
NCBI Description (Z97341) hypothetical protein [Arabidopsis thaliana]
                  17150
Seq. No.
                   49107 2.R1040
Contig ID
                  LIB3093-014-Q1-K1-H2
5'-most EST
                   17151
Seq. No.
                   49108 1.R1040
Contig ID
5'-most EST
                  LIB3139-011-P1-N1-C11
Seq. No.
                   17152
                   49109 1.R1040
Contig ID
                   LIB3093-014-Q1-K1-H4
5'-most EST
                   17153
Seq. No.
                   49110 1.R1040
Contig ID
                   LIB31\overline{0}6-068-P1-K1-B11
5'-most EST
                   17154
Seq. No.
Contig ID
                   49111_1.R1040
                   gsf700698425.hl
5'-most EST
                   BLASTX
Method
                   g4567262
NCBI GI
                   603
BLAST score
                   1.0e-62
E value
                   143
Match length
                   78
% identity
                  (AC006841) putative ubiquitin [Arabidopsis thaliana]
NCBI Description
                   17155
Seq. No.
                   49112 1.R1040
Contig ID
5'-most EST
                   LIB3093-014-Q1-K2-H9
Method
                   BLASTX
                   q1778145
NCBI GI
                   270
BLAST score
E value
                   1.0e-23
                   76
Match length
                   68
% identity
                   (U66402) phosphate/phosphoenolpyruvate translocator
NCBI Description
                   precursor [Nicotiana tabacum]
                   17156
Seq. No.
                   49133 1.R1040
Contig ID
5'-most EST
                   kl1701204861.hl
Method
                   BLASTX
NCBI GI
                   g2245108
                   626
BLAST score
```

6.0e-65 E value 211 Match length 59 % identity

NCBI Description (Z97343) EREBP-4 homolog [Arabidopsis thaliana]

17157 Seq. No.



49140 1.R1040 Contig ID uC-gmflminsoy078d10b1 5'-most EST BLASTN Method q452360 NCBI GI 410 BLAST score E value 0.0e + 00Match length 730 89 % identity V.faba mRNA for guanine nucleotide regulatory protein NCBI Description 17158 Seq. No. Contig ID 49146 1.R1040 LIB3093-014-Q1-K1-D9 5'-most EST 17159 Seq. No. 49151 1.R1040 Contig ID 5'-most EST LIB3093-014-Q1-K1-E2 Method BLASTX g4240169 NCBI GI BLAST score 222 5.0e-18 E value 153 Match length 10 % identity (AB020647) KIAA0840 protein [Homo sapiens] NCBI Description 17160 Seq. No. 49155 1.R1040 Contig ID 5'-most EST LIB3093-014-Q1-K1-E6 17161 Seq. No. 49159 1.R1040 Contig ID LIB3093-014-Q1-K1-B8 5'-most EST Method BLASTX q4544394 NCBI GI BLAST score 167 E value 2.0e-11 Match length 168 33 % identity (AC007047) hypothetical protein [Arabidopsis thaliana] NCBI Description 17162 Seq. No. 49166 1.R1040 Contig ID 5'-most EST LIB3093-014-Q1-K1-C4 17163 Seq. No.

49170 1.R1040 Contig ID

LIB3093-014-Q1-K1-D1 5'-most EST

17164 Seq. No.

49171 1.R1040 Contig ID

LIB3093-014-Q1-K1-D11 5'-most EST

17165 Seq. No.

49171 2.R1040 Contig ID crh700850093.hl 5'-most EST



Contig ID 49183\_1.R1040

5'-most EST jC-gmro02910041071a1

Method BLASTX
NCBI GI g2352998
BLAST score 173
E value 3.0e-12
Match length 104
% identity 31

NCBI Description (AF014461) EXO70 protein [Mus musculus]

Seq. No. 17167

Contig ID 49185\_1.R1040 5'-most EST zsg701119049.h1

Seq. No. 17168

Contig ID 49185 2.R1040

5'-most EST uC-gmrominsoy208a11b1

Method BLASTX
NCBI GI g4454050
BLAST score 377
E value 5.0e-36
Match length 151
% identity 54

NCBI Description (AL035394) putative protein [Arabidopsis thaliana]

Seq. No. 17169

Contig ID 49200\_1.R1040

5'-most EST LIB3093-014-Q1-K1-H6

Seq. No. 17170

Contig ID 49264\_1.R1040

5'-most EST uC-gmrominsoy168c02b1

Seq. No. 17171

Contig ID 49265\_1.R1040 5'-most EST rlr700900395.h1

Seq. No.

Contig ID 49276\_1.R1040

5'-most EST LIB3093-013-Q1-K1-H3

17172

Method BLASTX
NCBI GI g2498864
BLAST score 152
E value 1.0e-09
Match length 48
% identity 58

NCBI Description RRP5 PROTEIN HOMOLOG (KIAA0185) >gi\_1136430\_dbj\_BAA11502\_

(D80007) similar to hypothetical protein YM9959.11C of

S.cerevisiae. [Homo sapiens]

Seq. No. 17173

Contig ID 49280 1.R1040

5'-most EST LIB3093-013-Q1-K2-G2

Method BLASTX
NCBI GI g4008010
BLAST score 261



E value 1.0e-22 Match length 125 % identity 46

NCBI Description (AF084036) receptor-like protein kinase [Arabidopsis

thaliana]

Seq. No. 17174

Contig ID 49281\_1.R1040

5'-most EST LIB3093-013-Q1-K2-G3

Seq. No. 17175

Contig ID 49282\_1.R1040

5'-most EST LIB3093-013-Q1-K1-G4

Seq. No. 17176

Contig ID 49282\_2.R1040

5'-most EST LIB3139-073-P1-N1-H7

Seq. No. 17177

Contig ID 49288\_1.R1040

5'-most EST jC-gmle01810094f03a1

Method BLASTX
NCBI GI g4454458
BLAST score 266
E value 3.0e-23
Match length 73

% identity 75

NCBI Description (AC006234) unknown protein [Arabidopsis thaliana]

Seq. No. 17178

Contig ID 49291 1.R1040

5'-most EST jC-gmst02400065e05a2

Seq. No. 17179

Contig ID 49291\_2.R1040

5'-most EST jC-gmst02400076c11a1

Method BLASTX
NCBI GI g3880585
BLAST score 166
E value 3.0e-11
Match length 114
% identity 32

NCBI Description (Z79758) cDNA EST EMBL:D34582 comes from this gene; cDNA EST EMBL:D37744 comes from this gene; cDNA EST EMBL:D64724 comes from this gene; cDNA EST EMBL:D67838 comes from this

gene; cDNA EST yk355g10.3 comes from this gene; cDNA

Seq. No. 17180

Contig ID 49291 3.R1040

5'-most EST uC-gmrominsoy033h09b1

Method BLASTX
NCBI GI g3643105
BLAST score 174
E value 2.0e-12
Match length 87
% identity 37

NCBI Description (AF077950) protein inhibitor of activated STAT protein



```
PIAS1 [Mus musculus]
```

Contig ID 49293\_1.R1040

5'-most EST LIB3093-013-Q1-K2-E2

Seq. No. 17182

Contig ID 49293\_2.R1040 5'-most EST fjg700968486.h1

Seq. No. 17183

Contig ID 49294\_1.R1040

5'-most EST LIB3093-013-Q1-K1-E3

Seq. No. 17184

Contig ID 49295\_1.R1040

5'-most EST LIB3093-013-Q1-K1-E5

Seq. No. 17185

Contig ID 49301\_1.R1040 5'-most EST gsv701056267.h1

Method BLASTX
NCBI GI g2832685
BLAST score 539
E value 5.0e-55
Match length 191
% identity 60

NCBI Description (AL021712) putative protein [Arabidopsis thaliana]

Seq. No. 17186

Contig ID 49304\_1.R1040

5'-most EST LIB3093-013-Q1-K1-F5

Seq. No. 17187

Contig ID 49311\_1.R1040
5'-most EST g5510376
Method BLASTX
NCBI GI q4559377

NCBI GI G4559377
BLAST score 1402
E value 1.0e-156
Match length 343
% identity 75

NCBI Description (AC006526) putative photomorphogenesis repressor protein

COP1 [Arabidopsis thaliana]

Seq. No. 17188

Contig ID 49311 2.R1040

5'-most EST jC-gmst02400065d06a2

Seq. No. 17189

Contig ID 49316 1.R1040

5'-most EST LIB3093-013-Q1-K2-D3

Seq. No. 17190

Contig ID 49317\_1.R1040

5'-most EST LIB3093-013-Q1-K2-D4



```
17191
Seq. No.
                  49317 2.R1040
Contig ID
                  bnc700605528.h2
5'-most EST
                  BLASTX
Method
                  q299703
NCBI GI
                  152
BLAST score
                  7.0e-10
E value
                  94
Match length
                  19
% identity
                  (S58544) 75 kda infertility-related sperm protein [human,
NCBI Description
                  testis, Peptide Partial, 528 aa] [Homo sapiens]
                  17192
Seq. No.
                   49323 1.R1040
Contig ID
                  LIB3093-013-Q1-K1-E10
5'-most EST
                   17193
Seq. No.
                   49324 1.R1040
Contig ID
                  bth700845584.hl
5'-most EST
Seq. No.
                   17194
                   49330 1.R1040
Contig ID
                   g5753636
5'-most EST
                   BLASTX
Method
                   g3287695
NCBI GI
BLAST score
                   470
                   2.0e-46
E value
Match length
                   338
% identity
                   38
                   (AC003979) Similar to hypothetical protein C34B7.2
NCBI Description
                   gb 1729503 from C. elegans cosmid gb_Z83220. [Arabidopsis
                   thaliana]
                   17195
Seq. No.
                   49330_3.R1040
Contig ID
                   fde700875013.hl
5'-most EST
                   BLASTX
Method
                   g3287695
NCBI GI
BLAST score
                   152
                   4.0e-10
E value
Match length
                   76
                   43
% identity
                   (AC003979) Similar to hypothetical protein C34B7.2
NCBI Description
                   gb 1729503 from C. elegans cosmid gb_Z83220. [Arabidopsis
                   thaliana]
                   17196
Seq. No.
                   49332 1.R1040
Contig ID
5'-most EST
                   fde700872894.hl
                   BLASTX
Method
NCBI GI
                   q2688619
                   184
BLAST score
                   3.0e-28
E value
Match length
                   153
```

2836

(AE001169) conserved hypothetical protein [Borrelia

43

burgdorferi]

% identity

NCBI Description



```
17197
Seq. No.
                  49335 1.R1040
Contig ID
                  LIB3093-013-Q1-K1-C12
5'-most EST
                  BLASTX
Method
NCBI GI
                  g4512714
BLAST score
                  347
                  1.0e-32
E value
                  81
Match length
                  85
% identity
NCBI Description (AC006569) hypothetical protein [Arabidopsis thaliana]
                  17198
Seq. No.
Contig ID
                  49346 1.R1040
5'-most EST
                  jC-gmst02400014e09a1
                  17199
Seq. No.
                  49346 2.R1040
Contig ID
                  LIB3093-013-Q1-K1-A10
5'-most EST
                  17200
Seq. No.
                  49349_1.R1040
Contig ID
5'-most EST
                  taw700659888.h1
Method
                  BLASTX
                  g4204288
NCBI GI
                  596
BLAST score
                  1.0e-61
E value
                  198
Match length
                  56
% identity
                  (AC003027) 1cl prt seq No definition line found
NCBI Description
                   [Arabidopsis thaliana]
                  17201
Seq. No.
                   49350 1.R1040
Contig ID
5'-most EST
                  jC-gmle01810094h10a1
Seq. No.
                   17202
                   49401 1.R1040
Contig ID
5'-most EST
                  ncj700980514.h1
                   17203
Seq. No.
                   49446 1.R1040
Contig ID
                   eep700868863.hl
5'-most EST
Method
                   BLASTX
                   g1362017
NCBI GI
                   179
BLAST score
                   9.0e-13
E value
Match length
                   115
% identity
                   46
                   zinc finger protein 4 - Arabidopsis thaliana >gi_790679
NCBI Description
                   (L39647) zinc finger protein [Arabidopsis thaliana]
```

Contig ID 49446\_2.R1040 5'-most EST uC-gmropic018b10b1

Seq. No. 17205



```
49456 1.R1040
Contig ID
5'-most EST
                  uC-gmropic037h04b1
                  BLASTX
Method
NCBI GI
                  q1361983
BLAST score
                  811
                  8.0e-87
E value
                  235
Match length
% identity
                  63
                  ARP protein - Arabidopsis thaliana >gi_886434 emb_CAA89858_
NCBI Description
                  (Z49776) ARP protein [Arabidopsis thaliana]
                  17206
Seq. No.
                  49457 1.R1040
Contig ID
                  LIB3106-036-Q1-K1-G10
5'-most EST
                  BLASTX
Method
                  q2739369
NCBI GI
                  338
BLAST score
                  2.0e-31
E value
                  129
Match length
                   60
% identity
                  (AC002505) putative pectinesterase [Arabidopsis thaliana]
NCBI Description
                  17207
Seq. No.
                   49460 1.R1040
Contig ID
5'-most EST
                  pcp700994914.hl
                   17208
Seq. No.
                   49467_1.R1040
Contig ID
5'-most EST
                   q5677428
Method
                   BLASTX
NCBI GI
                   g128392
                   227
BLAST score
                   2.0e-18
E value
Match length
                   111
% identity
                   NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP)
NCBI Description
                   (PHOSPHOLIPID TRANSFER PROTEIN) (PLTP) >gi_170117 (M58635)
                   lipid transfer protein [Spinacia oleracea]
                   >gi_228406_prf__1803519A lipid transfer protein [Spinacia
                   oleracea]
                   17209
Seq. No.
                   49468 1.R1040
Contig ID
5'-most EST
                   LIB3093-005-Q1-K1-G5
                   BLASTX
Method
                   g2224547
NCBI GI
BLAST score
                   485
E value
                   3.0e-50
                   219
Match length
% identity
                   50
```

(AB002301) KIAA0303 [Homo sapiens] NCBI Description

17210 Seq. No.

49468 2.R1040 Contig ID uaw700666326.h1 5'-most EST

17211 Seq. No.

NCBI Description



```
49468 3.R1040
Contig ID
                  fC-gmle700873886r1
5'-most EST
Seq. No.
                  17212
                  49480 1.R1040
Contig ID
                  fua701042706.hl
5'-most EST
                  BLASTX
Method
                  g3367568
NCBI GI
                  374
BLAST score
                  2.0e-35
E value
                  109
Match length
% identity
                  60
                   (AL031135) protein kinase - like protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  17213
Contig ID
                   49482 1.R1040
                  V4L-01-Q1-B1-B2
5'-most EST
Method
                  BLASTX
                  g3878874
NCBI GI
BLAST score
                   159
                   1.0e-10
E value
Match length
                   81
% identity
                   41
NCBI Description (Z69793) R03A10.3 [Caenorhabditis elegans]
                   17214
Seq. No.
                   49483 1.R1040
Contig ID
                   kmv700739084.hl
5'-most EST
Seq. No.
                   17215
                   49489 1.R1040
Contig ID
                   zsg701125943.hl
5'-most EST
                   17216
Seq. No.
                   49490 1.R1040
Contig ID
5'-most EST
                   LIB3093-012-Q1-K1-C9
Method
                   BLASTX
                   q1418331
NCBI GI
BLAST score
                   295
                   1.0e-26
E value
                   138
Match length
                   46
% identity
                   (X95909) receptor like protein kinase [Arabidopsis
NCBI Description
                   thaliana]
                   17217
Seq. No.
                   49491 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400037d03a1
                   BLASTX
Method
NCBI GI
                   q3702641
BLAST score
                   255
E value
                   5.0e-22
Match length
                   112
                   42
% identity
                   (AL031825) similar to human 75k autoantigen
```

[Schizosaccharomyces pombe]



₹\$. - : L

```
17218
Seq. No.
Contig ID
                  49494 1.R1040
                  uC-gmrominsoy220d10b1
5'-most EST
                  BLASTX
Method
                  g4335751
NCBI GI
                  1394
BLAST score
                  1.0e-155
E value
Match length
                  432
                  60
% identity
                  (AC006284) putative methyltransferase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  17219
                  49518 1.R1040
Contig ID
                  LIB3093-011-Q1-K1-H2
5'-most EST
                  17220
Seq. No.
                  49527 1.R1040
Contig ID
                  sat701003812.hl
5'-most EST
Method
                  BLASTX
                  g1931653
NCBI GI
BLAST score
                  165
E value
                   4.0e-11
Match length
                   48
% identity
                  73
NCBI Description (U95973) unknown protein [Arabidopsis thaliana]
                  17221
Seq. No.
                   49539 1.R1040
Contig ID
                  LIB3093-011-Q1-K1-F8
5'-most EST
Seq. No.
                   17222
Contig ID
                   49546 1.R1040
5'-most EST
                   zhf700953404.h1
Seq. No.
                   17223
Contig ID
                   49549 1.R1040
5'-most EST
                   bth700847859.h1
Seq. No.
                   17224
                   49549 2.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy041b07b1
Seq. No.
                   17225
                   49550 1.R1040
Contig ID
5'-most EST
                   LIB3107-061-Q1-K1-F11
Method
                   BLASTX
                   g4580468
NCBI GI
BLAST score
                   558
                   2.0e-57
E value
                   164
Match length
                   62
% identity
                   (AC006081) putative protein kinase; similar to human PKX1
NCBI Description
                   and Drosophila DC2 [Arabidopsis thaliana]
```

17226 .



```
49553 1.R1040
Contig ID
                   g4313716
5'-most EST
Sea. No.
                   17227
                   49556 1.R1040
Contig ID
                   vzy70\overline{0}753463.h1
5'-most EST
                   BLASTX
Method
                   g2982456
NCBI GI
                   591
BLAST score
                   5.0e-61
E value
                   206
Match length
                   64
% identity
                  (AL022223) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   17228
                   49557 1.R1040
Contig ID
                   leu701144587.h1
5'-most EST
                   BLASTX
Method
                   g1064883
NCBI GI
                   298
BLAST score
                   1.0e-26
E value
                   64
Match length
                   39
% identity
NCBI Description (X92976) ZAP1 [Arabidopsis thaliana]
                   17229
Seq. No.
                   49564 1.R1040
Contig ID
                   uaw70\overline{0}663701.h1
5'-most EST
                   BLASTN
Method
                   q556901
NCBI GI
                   400
BLAST score
                   0.0e+00
E value
                   972
Match length
                   85
% identity
NCBI Description L.esculentum (UC82-B) mRNA for 54-kD signal recognition
                   particle (SRP) specific protein
                   17230
Seq. No.
                    49566 1.R1040
Contig ID
5'-most EST
                    zzp700835553.hl
                    17231
Seq. No.
                    49566 2.R1040
 Contig ID
                    uC-gmropic016e06b1
 5'-most EST
                    17232
 Seq. No.
                    49569 1.R1040
 Contig ID
                    smc700744231.hl
 5'-most EST
 Seq. No.
                    17233
                    49572 1.R1040
 Contig ID
                    uC-gmropic104g07b1
 5'-most EST
                    BLASTX
 Method
                    g4049353
 NCBI GI
 BLAST score
                    1110
```

1.0e-121

334

E value

Match length



```
% identity
NCBI Description (AL034567) putative protein [Arabidopsis thaliana]
                  17234
Seq. No.
                  49581 1.R1040
Contig ID
                  awf700841030.hl
5'-most EST
                  17235
Seq. No.
                  49582 1.R1040
Contig ID
                  uC-gmflminsoy058a08b1
5'-most EST
                  BLASTN
Method
                  g1255447
NCBI GI
                  39
BLAST score
                  1.0e-12
E value
Match length
                  111
                  85
% identity
NCBI Description Arabidopsis thaliana mRNA for mitogen-activated protein
                  kinase, complete cds
                  17236
Seq. No.
                  49597_1.R1040
Contig ID
                  LIB3093-011-Q1-K1-B5
5'-most EST
                  17237
Seq. No.
Contig ID
                  49601_1.R1040
                  uC-gmronoir043a07b1
5'-most EST
                  BLASTX
Method
                  q2522534
NCBI GI
BLAST score
                   235
                   3.0e-19
E value
                  77
Match length
                   41
% identity
NCBI Description (AF027302) TNF-alpha stimulated ABC protein [Homo sapiens]
                   17238
Seq. No.
                   49601 2.R1040
Contig ID
5'-most EST
                  LIB3138-046-Q1-N1-E5
                   17239
Seq. No.
                   49610 1.R1040
Contig ID
                   jC-qmle01810051e03a1
5'-most EST
                   BLASTX
Method
                   g1507699
NCBI GI
BLAST score
                   155
                   6.0e-10
E value
Match length
                   69
% identity
                   26
                   (L81119) COL2 [Arabidopsis thaliana] >gi 1507701 (L81120)
NCBI Description
                   COL2 [Arabidopsis thaliana]
                   17240
Seq. No.
                   49612 1.R1040
Contig ID
```

5'-most EST LIB3093-010-Q1-K1-H4

Method BLASTX
NCBI GI G3927831

NCBI GI g3927831 BLAST score 949 E value 1.0e-103

2842



Match length 235 % identity 54

NCBI Description (AC005727) similar to mouse ankyrin 3 [Arabidopsis

thaliana]

Seq. No. 17241

Contig ID 49627\_1.R1040

5'-most EST LIB3093-010-Q1-K1-F2

Method BLASTN
NCBI GI g2351066
BLAST score 38
E value 5.0e-12
Match length 82
% identity 87

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MOP9, complete sequence [Arabidopsis thaliana]

Seq. No. 17242

Contig ID 49629 1.R1040

5'-most EST uC-gmflminsoy069g06b1

Seq. No. 17243

Contig ID 49632\_1.R1040

5'-most EST LIB3093-010-Q1-K1-E12

Seq. No. 17244

Match length 127 % identity 57

NCBI Description (AL021890) heat shock protein - like [Arabidopsis thaliana]

Seq. No. 17245

Contig ID 49638\_1.R1040 5'-most EST eep700866065.h1

Method BLASTX
NCBI GI g2801536
BLAST score 505
E value 6.0e-51
Match length 139
% identity 68

NCBI Description (AF039531) lysophospholipase homolog [Oryza sativa]

Seq. No. 17246

Contig ID 49638 2.R1040 5'-most EST uxk700669254.h1

Method BLASTX
NCBI GI g2801536
BLAST score 182
E value 8.0e-14
Match length 74
% identity 54

NCBI Description (AF039531) lysophospholipase homolog [Oryza sativa]

```
17247
Seq. No.
                  49653 1.R1040
Contig ID
                  LIB3093-010-Q1-K1-B6
5'-most EST
                  BLASTX
Method
                  q3063444
NCBI GI
                  596
BLAST score
                  1.0e-61
E value
                  155
Match length
                  72
% identity
NCBI Description (AC003981) F22013.5 [Arabidopsis thaliana]
                  17248
Seq. No.
                  49658 1.R1040
Contig ID
                  LIB3093-010-Q1-K1-C11
5'-most EST
                  17249
Seq. No.
                   49662 1.R1040
Contig ID
                   eep700865070.hl
5'-most EST
                   BLASTX
Method
                   g1174621
NCBI GI
                   550
BLAST score
                   4.0e-56
E value
                   205
Match length
                   55
% identity
                   T-COMPLEX PROTEIN 1, THETA SUBUNIT (TCP-1-THETA)
NCBI Description
                   (CCT-THETA) >gi_1083259_pir__JC4073 TCP-1 containing
                   cytosolic chaperonin (CCT) theta chain - mouse
                   >gi 695625 emb CAA85521_ (Z37164) CCTtheta, theta subunit
                   of the chaperonin containing TCP-1 (CCT) [Mus musculus]
                   17250
Seq. No.
                   49668 1.R1040
Contig ID
5'-most EST
                   LIB3093-009-Q1-K1-H7
                   17251
Seq. No.
                   49672 1.R1040
Contig ID
                   dpv701099116.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q1800147
                   331
BLAST score
                   6.0e-45
E value
                   199
Match length
                   59
 % identity
                   (U83655) membrane associated protein [Arabidopsis thaliana]
NCBI Description
                   17252
Seq. No.
                   49672 2.R1040
 Contig ID
                   jC-gmf102220053b03a1
 5'-most EST
                   BLASTX
Method
                   q3080389
 NCBI GI
                   376
 BLAST score
```

2844

(AL022603) putative membrane associated protein

4.0e-36

[Arabidopsis thaliana]

111

69

E value Match length

% identity

NCBI Description



Contig ID 49680 1.R1040 5'-most EST rca701002007.h1

Seq. No. 17254

Contig ID 49682\_1.R1040

5'-most EST LIB3093-009-Q1-K1-H3

Method BLASTX
NCBI GI g2492597
BLAST score 190
E value 6.0e-14
Match length 112
% identity 38

NCBI Description HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN SLL0182

>gi 1001688 dbj BAA10424\_ (D64002) ABC transporter

[Synechocystis sp.]

Seq. No. 17255

Contig ID 49699 1.R1040

5'-most EST LIB3109-015-Q1-K1-E8

Method BLASTX
NCBI GI g4538920
BLAST score 250
E value 3.0e-21
Match length 64
% identity 38

NCBI Description (AL049483) nitrogen fixation like protein [Arabidopsis

thaliana]

Seq. No. 17256

Contig ID 49699\_2.R1040 5'-most EST zsg701124482.h1

Method BLASTX
NCBI GI g4538920
BLAST score 380
E value 2.0e-36
Match length 134
% identity 47

NCBI Description (AL049483) nitrogen fixation like protein [Arabidopsis

thaliana]

Seq. No. 17257

Contig ID 49708 1.R1040

5'-most EST LIB $30\overline{9}3-009-Q1-K1-F1$ 

Seq. No. 17258

Contig ID 49719 1.R1040

5'-most EST LIB3093-009-Q1-K1-D1

Method BLASTX
NCBI GI g2465923
BLAST score 435
E value 1.0e-42
Match length 191
% identity 50

NCBI Description (AF024648) receptor-like serine/threonine kinase

[Arabidopsis thaliana]



```
17259
Seq. No.
                   49730 2.R1040
Contig ID
                   jC-gm\overline{f}102220082g03a1
5'-most EST
                  BLASTX
Method
                  g3785978
NCBI GI
                   318
BLAST score
                   4.0e-29
E value
                   67
Match length
                   79
% identity
                  (AC005560) unknown protein [Arabidopsis thaliana]
NCBI Description
                   17260
Seq. No.
Contig ID
                   49746 1.R1040
                   LIB3093-009-Q1-K1-B12
5'-most EST
                   BLASTN
Method
                   g255572
NCBI GI
                   81
BLAST score
                   1.0e-37
E value
                   157
Match length
                   88
% identity
                   small auxin up RNA gene cluster: orf 15A [Glycine
NCBI Description
                   max=soybeans, cv. Wayne, Genomic, 637 nt]
Seq. No.
                   17261
                   49752_1.R1040
Contig ID
                   zhf700963111.h1
5'-most EST
                   BLASTX
Method
                   q3914801
NCBI GI
BLAST score
                   410
                   5.0e-40
E value
                   171
Match length
                   49
% identity
                   DNA-DIRECTED RNA POLYMERASE I 135 KD POLYPEPTIDE (RNA
NCBI Description
                   POLYMERASE I SUBUNIT 2) (RPA135) (RNA POLYMERASE I 127 KD
                   SUBUNIT) >gi_2739048 (AF025424) RNA polymerase I 127 kDa
                   subunit [Rattus norvegicus]
                   17262
Seq. No.
                   49757 1.R1040
Contig ID
                   jC-gmro02910046g02a1
5'-most EST
                   BLASTX
Method
                   q3005931
NCBI GI
BLAST score
                   1787
E value
                   0.0e+00
                   533
Match length
```

% identity 64

(AJ005016) ABC transporter [Homo sapiens] NCBI Description

Seq. No. 17263 49763 1.R1040 Contig ID leu701151240.hl 5'-most EST BLASTX Method g3075397 NCBI GI BLAST score 166 1.0e-11 E value

Match length 48



```
% identity
NCBI Description (AC004484) hypothetical protein [Arabidopsis thaliana]
                  17264
Seq. No.
                  49765 1.R1040
Contig ID
                  jC-gm\overline{f}102220065g07a1
5'-most EST
Seq. No.
                  17265
                   49770 1.R1040
Contig ID
                  pcp700989705.hl
5'-most EST
                   BLASTX
Method
                   q3128217
NCBI GI
BLAST score
                   941
E value
                   1.0e-102
                   275
Match length
                   69
% identity
                   (AC004077) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   >gi 3337374 (AC004481) hypothetical protein [Arabidopsis
                   thaliana]
                   17266
Seq. No.
                   49782 1.R1040
Contig ID
                   txt700735461.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g103313
                   263
BLAST score
                   9.0e-23
E value
                   105
Match length
                   49
% identity
                   probable cell cycle control protein crn - fruit fly
NCBI Description
                   (Drosophila melanogaster) >gi_2827496_emb_CAA15705_
                   (AL009195) EG:30B8.1 [Drosophila melanogaster]
                   17267
Seq. No.
                   49787 1.R1040
Contig ID
5'-most EST
                   LIB3093-008-Q1-K1-E8
Method
                   BLASTX
                   q4508074
NCBI GI
BLAST score
                   215
E value
                   4.0e-17
                   163
Match length
                   38
% identity
                   (AC005882) 45341 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   17268
                   49794 1.R1040
Contig ID
                   rlr700898006.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2335100
BLAST score
                   531
                   5.0e-54
E value
                   143
Match length
% identity
                   69
                   (AC002339) unknown protein [Arabidopsis thaliana]
NCBI Description
```

17269

49797 1.R1040

Seq. No.

Contig ID

% identity

44



```
q4277038
5'-most EST
                  BLASTX
Method
                  g4454468
NCBI GI
                  383
BLAST score
                  5.0e-37
E value
                  136
Match length
% identity
                  (AC006234) putative NADH dehydrogenase [Arabidopsis
NCBI Description
                  thaliana]
                  17270
Seq. No.
                  49802 1.R1040
Contig ID
                  LIB3093-008-Q1-K1-D10
5'-most EST
                  BLASTN
Method
NCBI GI
                  q1498314
BLAST score
                  109
                   3.0e-54
E value
                   314
Match length
                   85
% identity
                  Pisum sativum import intermediate associated protein 100
NCBI Description
                   mRNA, nuclear gene encoding chloroplast protein, complete
                   17271
Seq. No.
                   49810 1.R1040
Contig ID
                   epx701108526.h1
5'-most EST
                   BLASTX
Method
                   g2947070
NCBI GI
                   364
BLAST score
                   2.0e-34
E value
                   127
Match length
                   39
% identity
                  (AC002521) putative Ser/Thr protein kinase [Arabidopsis
NCBI Description
                   thaliana]
                   17272
Seq. No.
                   49810 2.R1040
Contig ID
                   rca701001009.hl
5'-most EST
                   17273
Seq. No.
                   49810 3.R1040
Contig ID
                   fde700874894.hl
5'-most EST
                   17274
Seq. No.
                   49813 1.R1040
Contig ID
                   LIB3093-008-Q1-K1-E10
5'-most EST
                   17275
Seq. No.
                   49824 1.R1040
Contig ID
                   uaw700666259.h1
 5'-most EST
Method
                   BLASTX
                   g100226
NCBI GI
BLAST score
                   334
                   3.0e-31
E value
Match length
                   139
```

NCBI Description hypothetical protein - tomato >gi\_19275\_emb\_CAA78112\_



(Z12127) protein of unknown function [Lycopersicon esculentum] >gi\_445619\_prf\_\_1909366A Leu zipper protein [Lycopersicon esculentum]

17276 Seq. No.

49833 1.R1040 Contig ID

5'-most EST LIB3093-008-Q1-K1-A9

17277 Seq. No.

49844 1.R1040 Contig ID

5'-most EST LIB3093-008-Q1-K1-A2

Seq. No. 17278

49848 1.R1040 Contig ID

LIB3093-008-Q1-K1-A5 5'-most EST

17279 Seq. No.

49849 1.R1040 Contig ID leu701151025.h1 5'-most EST

17280 Seq. No.

49850 1.R1040 Contig ID

5'-most EST jC-gmf102220084g03d1

Seq. No. 17281

49851 1.R1040 Contig ID

LIB3170-038-Q1-K1-G5 5'-most EST

Seq. No. 17282

49851 2.R1040 Contig ID

5'-most EST LIB3093-008-Q1-K1-A8

Seq. No. 17283

49859 1.R1040 Contig ID 5'-most EST pmv700893094.hl

Method BLASTX g4335773 NCBI GI BLAST score 164 E value 4.0e-11 Match length 131

% identity 38

NCBI Description (AC006284) unknown protein [Arabidopsis thaliana]

Seq. No. 17284

49859 2.R1040 Contig ID 5'-most EST zsg701121163.h1

17285 Seq. No.

49860 1.R1040 Contig ID

LIB3093-007-Q1-K1-G11 5'-most EST

17286 Seq. No.

49861 1.R1040 Contig ID

5'-most EST g5607<u>1</u>21

Seq. No. 17287

49864\_1.R1040 Contig ID



```
LIB3093-007-01-K1-G4
5'-most EST
Method
                  BLASTX
                  q4580456
NCBI GI
BLAST score
                  173
                  3.0e-12
E value
                  115
Match length
                  43
% identity
NCBI Description (AC006081) unknown protein [Arabidopsis thaliana]
                  17288
Seq. No.
                  49871 1.R1040
Contig ID
5'-most EST
                  bth700849494.hl
                  17289
Seq. No.
                  49875 1.R1040
Contig ID
5'-most EST
                  jC-qmro02910014e05a1
                  17290
Seq. No.
                  49885 1.R1040
Contig ID
                  jC-gmle01810012b09a1
5'-most EST
                  17291
Seq. No.
                  49893 1.R1040
Contig ID
5'-most EST
                  LIB3106-015-Q1-K1-G4
                  17292
Seq. No.
                  49903 1.R1040
Contig ID
5'-most EST
                  LIB3093-007-Q1-K1-A7
                  BLASTX
Method
                  g2494144
NCBI GI
                   191
BLAST score
E value
                   2.0e-14
Match length
                   125
% identity
                  (AC002329) predicted leucine-rich protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   17293
                   49905 1.R1040
Contig ID
                   LIB3093-007-Q1-K1-A9
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2253579
BLAST score
                   208
E value
                   5.0e-16
Match length
                   73
                   60
% identity
NCBI Description (U78721) hypothetical protein [Arabidopsis thaliana]
                   17294
Seq. No.
                   49907 1.R1040
Contig ID
                   jC-gmro02800033e12a1
5'-most EST
                   BLASTX
Method
                   g3021272
NCBI GI
BLAST score
                   254
                   1.0e-33
E value
```

118

62

Match length

% identity



NCBI Description (AL022347) serine /threonine kinase - like protein [Arabidopsis thaliana]

Seq. No. 17295

Contig ID 49912\_1.R1040 5'-most EST leu701152368.h1

Method BLASTX
NCBI GI g2194142
BLAST score 617
E value 1.0e-124
Match length 349
% identity 61

NCBI Description (AC002062) ESTs gb\_N38288, gb\_T43486, gb\_AA395242 come from

this gene. [Arabidopsis thaliana]

Seq. No. 17296

Contig ID 49913\_1.R1040

5'-most EST LIB3093-007-Q1-K1-B7

Method BLASTX
NCBI GI g3449041
BLAST score 264
E value 6.0e-23
Match length 96
% identity 46

NCBI Description (U73462) carbonic anhydrase [Arabidopsis thaliana]

Seq. No. 17297

Contig ID 49928\_1.R1040

5'-most EST LIB3093-006-Q1-K1-H9

Method BLASTX
NCBI GI g4220462
BLAST score 726
E value 6.0e-77
Match length 183
% identity 82

NCBI Description (AC006216) Strong similarity to gb\_Z50851 HD-zip (athb-8) gene from Arabidopsis thaliana containing Homeobox PF\_00046

and bZIP PF\_00170 domains. [Arabidopsis thaliana]

Seq. No. 17298

Contig ID 49932 1.R1040 5'-most EST ssr700554481.h1

Method BLASTX
NCBI GI g131289
BLAST score 2309
E value 0.0e+00
Match length 473
% identity 91

NCBI Description PHOTOSYSTEM II 44 KD REACTION CENTRE PROTEIN (P6 PROTEIN) (CP43) >gi 72709 pir F2NT44 photosystem II chlorophyll

a-binding protein psbC - common tobacco chloroplast

>gi 225285 prf 1211235W photosystem II 44kD protein

[Nicotiana tabacum]

Seq. No. 17299

Contig ID 49934\_1.R1040

5'-most EST LIB3093-007-Q1-K1-A4



17301

```
17300
Seq. No.
                   49934 2.R1040
Contig ID
5'-most EST
                  g5509258
```

Seq. No. 49938 1.R1040 Contig ID smc700747277.hl 5'-most EST BLASTX Method g2129626 NCBI GI 256 BLAST score 1.0e-36 E value

116 Match length 60 % identity

J-domain protein - Arabidopsis thaliana NCBI Description

>gi 928936 emb\_CAA89204\_ (Z49238) J-domain protein

[Arabidopsis thaliana] >gi 1585434\_prf\_\_2124427A diamide

resistance gene [Arabidopsis thaliana]

17302 Seq. No.

49945 1.R1040 Contig ID leu701144974.h1 5'-most EST

17303 Seq. No.

49946 1.R1040 Contig ID

LIB3093-006-Q1-K1-G6 5'-most EST

BLASTX Method g3461846 NCBI GI BLAST score 213 9.0e-25 E value 99 Match length 31 % identity

(AC005315) putative zinc-finger protein [Arabidopsis NCBI Description

thaliana]

17304 Seq. No.

49953 1.R1040 Contig ID

LIB3106-106-Q1-K1-F11 5'-most EST

17305 Seq. No.

49964 1.R1040 Contig ID seb700649623.hl 5'-most EST

BLASTX Method q730934 NCBI GI BLAST score 247 E value 1.0e-20 72 Match length % identity

QUEUINE TRNA-RIBOSYLTRANSFERASE (TRNA-GUANINE NCBI Description TRANSGLYCOSYLASE) (GUANINE INSERTION ENZYME)

>gi\_2137015\_pir\_\_S68430 queuine tRNA-ribosyltransferase (EC 2.4.2.29),  $\overline{60}$ K  $\overline{\text{ch}}$ ain - rabbit >gi\_623547 (L37420) queuine

tRNA-ribosyltransferase [Oryctolagus cuniculus]

17306 Seq. No.

49964 2.R1040 Contig ID

jC-gmf102220054b10d1 5'-most EST



54

91

Match length

% identity

```
17307
Seq. No.
                  49972 1.R1040
Contig ID
                  xpa700796005.h1
5'-most EST
                  BLASTX
Method
                  g3935170
NCBI GI
                  186
BLAST score
                  1.0e-22
E value
                  130
Match length
                  52
% identity
NCBI Description (AC004557) F17L21.13 [Arabidopsis thaliana]
                   17308
Seq. No.
                   49972 2.R1040
Contig ID
                  LIB3109-034-Q1-K1-B7
5'-most EST
                   17309
Seq. No.
                   49984 1.R1040
Contig ID
                   xpa700794716.hl
5'-most EST
                   BLASTX
Method
                   g1418990
NCBI GI
                   338
BLAST score
                   3.0e - 31
E value
                   172
Match length
                   42
% identity
                   (Z75524) unknown [Lycopersicon esculentum]
NCBI Description
                   17310
Seq. No.
                   49990 1.R1040
Contig ID
                   LIB3093-006-Q1-K1-B9
5'-most EST
                   17311
Seq. No.
                   49999 2.R1040
Contig ID
5'-most EST
                   LIB3106-102-Q1-K1-B2
                   17312
Seq. No.
                   50010 1.R1040
Contig ID
                   gsv701049022.h1
5'-most EST
                   BLASTX
Method
                   g3128181
NCBI GI
                   473
BLAST score
E value
                   2.0e-47
                   116
Match length
                   83
% identity
                   (AC004521) unknown protein [Arabidopsis thaliana]
NCBI Description
 Seq. No.
                   17313
                   50010 2.R1040
 Contig ID
                   yz1700966994.h1
 5'-most EST
Method
                   BLASTX
                   g3128181
 NCBI GI
                   236
 BLAST score
                   1.0e-19
 E value
```

NCBI Description (AC004521) unknown protein [Arabidopsis thaliana]



Contig ID 50017\_1.R1040

5'-most EST LIB3093-005-Q1-K1-G11

Seq. No. 17315

Contig ID 50017\_2.R1040 5'-most EST pxt700944692.h1

Seq. No. 17316

Contig ID 50020\_1.R1040 5'-most EST gsv701044420.h1

Seq. No. 17317

Contig ID 50023\_1.R1040 5'-most EST kl1701208213.h1

Method BLASTX
NCBI GI g2894610
BLAST score 211
E value 1.0e-16
Match length 59
% identity 73

NCBI Description (AL021889) putative protein [Arabidopsis thaliana]

Seq. No. 17318

Contig ID 50023 2.R1040

5'-most EST uC-gmflminsoy109h05b1

Method BLASTX
NCBI GI g4204697
BLAST score 1004
E value 1.0e-109
Match length 328
% identity 62

NCBI Description (AF117063) putative inositol polyphosphate 5-phosphatase

At5P2 [Arabidopsis thaliana]

Seq. No. 17319

Contig ID 50024 1.R1040

5'-most EST LIB3093-005-Q1-K1-G7

Seq. No. 17320

Contig ID 50024\_2.R1040 5'-most EST vzy700752324.h1

Seq. No. 17321

Contig ID 50029 1.R1040

5'-most EST LIB3093-005-Q1-K1-H2

Seq. No. 17322

Contig ID 50050\_1.R1040 5'-most EST uC-gmropic012d02b1

Method BLASTN
NCBI GI g2264309
BLAST score 37
E value 5.0e-11

Match length 101 % identity 84

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:



MJJ3, complete sequence [Arabidopsis thaliana]

Seq. No. 17323

Contig ID 50053\_1.R1040

5'-most EST LIB3093-005-Q1-K1-D2

Seq. No. 17324

Contig ID 50059\_1.R1040

5'-most EST LIB3093-005-Q1-K1-D9

Method BLASTX
NCBI GI g2832402
BLAST score 162
E value 4.0e-11
Match length 33
% identity 88

NCBI Description (Y15055) dihydroxypolyprenylbenzoate methyltransferase

[Arabidopsis thaliana]

Seq. No. 17325

Contig ID 50062\_1.R1040

5'-most EST LIB3093-005-Q1-K1-E11

Method BLASTN
NCBI GI g4456681
BLAST score 175
E value 1.0e-93
Match length 446
% identity 85

NCBI Description Medicago sativa mRNA for MAP kinase, complete CDS

Seq. No. 17326

Contig ID 50066\_1.R1040

5'-most EST uC-gmrominsoy182e04b1

Method BLASTX
NCBI GI g2842493
BLAST score 379
E value 3.0e-36
Match length 118
% identity 60

NCBI Description (AL021749) predicted protein [Arabidopsis thaliana]

Seq. No. 17327

Contig ID 50066\_2.R1040 5'-most EST uC-gmropic047d10b1

Seq. No. 17328

Contig ID 50067\_1.R1040

5'-most EST jC-gmro02910026e03d1

Method BLASTX
NCBI GI g100225
BLAST score 457
E value 5.0e-45
Match length 195
% identity 52

NCBI Description heat shock transcription factor 8 - tomato

>gi\_19260\_emb\_CAA47868\_ (X67599) heat stress transcription

factor 8 [Lycopersicon esculentum]



```
17329
Seq. No.
Contig ID
                  50071 1.R1040
                  LIB3093-005-Q1-K1-B9
5'-most EST
                  17330
Seq. No.
                  50075 1.R1040
Contig ID
                  zpv70\overline{0}760126.h1
5'-most EST
Method
                  BLASTX
                  g3695408
NCBI GI
BLAST score
                  266
                   4.0e-23
E value
Match length
                   86
% identity
                   62
                   (AF096373) contains similarity to Solanum lycopersicum
NCBI Description
                   (tomato) wound-induced protein (GB:X59882) [Arabidopsis
                  thaliana] >gi_4538956_emb_CAB39780.1_ (AL049488) probable
                   wound-induced protein [Arabidopsis thaliana]
Seq. No.
                   17331
                   50079 1.R1040
Contig ID
                   LIB3093-005-Q1-K1-C7
5'-most EST
                   17332
Seq. No.
                   50082_1.R1040
Contig ID
                   leu701154802.hl
5'-most EST
Method
                   BLASTX
                   q3550661
NCBI GI
                   407
BLAST score
E value
                   1.0e-39
Match length
                   96
% identity
                   41
                   (AJ001310) 39 kDa EF-Hand containing protein [Solanum
NCBI Description
                   tuberosum]
                   17333
Seq. No.
                   50100 1.R1040
Contig ID
5'-most EST
                   LIB3093-004-Q1-K1-F3
Seq. No.
                   17334
                   50101 1.R1040
Contig ID
                   LIB3093-004-Q1-K1-F5
5'-most EST
Method
                   BLASTX
                   g3249098
NCBI GI
BLAST score
                   352
                   6.0e-33
E value
Match length
                   176
% identity
                   50
                   (AC003114) ESTs gb T04610, gb N38459, gb_T45174, gb_R30481
NCBI Description
                   and gb N64971 come from this gene. [Arabidopsis thaliana]
                   17335
Seq. No.
                   50124_1.R1040
Contig ID
```

 $seb70\overline{0}651235.h1$ 5'-most EST BLASTX Method

g3413706 NCBI GI 574 BLAST score E value 7.0e-59



```
207
Match length
                  51
% identity
NCBI Description (AC004747) hypothetical protein [Arabidopsis thaliana]
                  17336
Seq. No.
                  50149 1.R1040
Contig ID
5'-most EST
                  sat701004741.hl
                  BLASTX
Method
                  g3068714
NCBI GI
                  150
BLAST score
                  1.0e-09
E value
                  85
Match length
                  18
% identity
NCBI Description (AF049236) unknown [Arabidopsis thaliana]
                   17337
Seq. No.
                   50149 2.R1040
Contig ID
                   epx701109705.h1
5'-most EST
                   BLASTX
Method
                   g2804436
NCBI GI
                   146
BLAST score
                   3.0e-09
E value
                   79
Match length
                   22
% identity
                  (AF043695) Similar to mitochondrial carrier protein
NCBI Description
                   [Caenorhabditis elegans]
                   17338
Seq. No.
Contig ID
                   50157 1.R1040
                   LIB3093-004-Q1-K1-A5
5'-most EST
                   17339
Seq. No.
                   50164 1.R1040
Contig ID
                   LIB3093-003-Q1-K1-H5
5'-most EST
                   17340
Seq. No.
                   50167 1.R1040
Contig ID
                   LIB3093-003-Q1-K1-G10
5'-most EST
                   BLASTX
Method
                   q3540201
NCBI GI
BLAST score
                   409
                   7.0e-40
E value
                   98
Match length
                   83
 % identity
                   (AC004260) Putative nuclear protein [Arabidopsis thaliana]
NCBI Description
                   17341
Seq. No.
                   50178 1.R1040
 Contig ID
                   LIB3093-003-Q1-K1-H12
 5'-most EST
                   BLASTX
 Method
                   q3170174
 NCBI GI
                   211
 BLAST score
                   8.0e-17
 E value
                   115
 Match length
```

(AF039687) antigen NY-CO-1 [Homo sapiens]

40

% identity

NCBI Description



```
Seq. No. 17342
Contig ID 50195 1.R1040
```

5'-most EST jC-gmst02400025e08a1

Method BLASTX
NCBI GI g2982320
BLAST score 226
E value 2.0e-18
Match length 73
% identity 55

NCBI Description (AF051245) hypothetical protein [Picea mariana]

Seq. No. 17343

Contig ID 50204 1.R1040

5'-most EST LIB3093-003-Q1-K1-D7

Seq. No. 17344

Contig ID 50209\_1.R1040 5'-most EST uC-gmropic097b04b1

Seq. No. 17345

Contig ID 50210\_1.R1040 5'-most EST ssr700555328.h1

Seq. No. 17346

Contig ID 50222 1.R1040

5'-most EST jC-gmfl02220090b03a1

Method BLASTN
NCBI GI g170059
BLAST score 364
E value 0.0e+00
Match length 853
% identity 97

NCBI Description Soybean (G.max L.) beta-tubulin (S-beta-1) gene, complete

cds

Seq. No. 17347

Contig ID 50222\_2.R1040 5'-most EST uC-gmropic075c02b1

Method BLASTN
NCBI GI g170059
BLAST score 447
E value 0.0e+00
Match length 447
% identity 100

NCBI Description Soybean (G.max L.) beta-tubulin (S-beta-1) gene, complete

cds

Seq. No. 17348

Contig ID 50234\_1.R1040

5'-most EST jC-gmro02910051d11a1

Seq. No. 17349

Contig ID 50236\_1.R1040

5'-most EST jC-gmst02400026a08a1

Method BLASTX
NCBI GI g3298542
BLAST score 394



```
E value
                  4.0e-38
Match length
                  132
% identity
NCBI Description
                  (AC004681) putative cellulose synthase [Arabidopsis
                  thaliana]
Seq. No.
                  17350
                  50237 1.R1040
Contig ID
5'-most EST
                  gsv701046092.h1
Method
                  BLASTX
NCBI GI
                  g2739004
BLAST score
                  415
E value
                  1.0e-40
Match length
                  116
% identity
                  59
NCBI Description (AF022461) CYP82C1p [Glycine max]
Seq. No.
                  17351
Contig ID
                  50241 1.R1040
5'-most EST
                  LIB3093-003-Q1-K1-A6
Seq. No.
                  17352
Contig ID
                  50242 1.R1040
5'-most EST
                  LIB3093-003-Q1-K1-A7
Seq. No.
                  17353
                  50256 1.R1040
Contig ID
5'-most EST
                  ssr700557766.h1
Method
                  BLASTX
NCBI GI
                  g4200165
BLAST score
                  974
E value
                  1.0e-106
Match length
                  214
% identity
                  80
NCBI Description (Y16262) neutral invertase [Daucus carota]
Seq. No.
                  17354
Contig ID
                  50262 1.R1040
5'-most EST
                  LIB3093-002-Q1-K1-H11
Method
                  BLASTX
                  g3913952
NCBI GI
BLAST score
                  179
E value
                  5.0e-13
Match length
                  56
% identity
                  66
NCBI Description ADENYLATE KINASE (ATP-AMP TRANSPHOSPHORYLASE) >gi 2351578
                  (U82330) adenylate kinase homolog [Prunus armeniaca]
Seq. No.
                  17355
Contig ID
                  50262 2.R1040
                  gsv701046565.hl
```

5'-most EST

Method BLASTX NCBI GI q3913952 BLAST score 201 E value 7.0e-16 Match length 92 % identity 53



NCBI Description ADENYLATE KINASE (ATP-AMP TRANSPHOSPHORYLASE) >gi\_2351578 (U82330) adenylate kinase homolog [Prunus armeniaca]

Seq. No. 17356

Contig ID 50271\_1.R1040 5'-most EST leu701150465.h1

Method BLASTX
NCBI GI g4455242
BLAST score 432
E value 2.0e-42
Match length 118
% identity 66

NCBI Description (AL035523) geranylgeranylated protein ATGP4 [Arabidopsis

thaliana]

Seq. No. 17357

Contig ID 50271\_2.R1040 5'-most EST epx701110139.h1

Method BLASTX
NCBI GI g4455242
BLAST score 367
E value 5.0e-35
Match length 96
% identity 69

NCBI Description (AL035523) geranylgeranylated protein ATGP4 [Arabidopsis

thaliana]

Seq. No. 17358

Contig ID 50292 1.R1040

5'-most EST uC-gmrominsoy141d03b1

Method BLASTX
NCBI GI g1171579
BLAST score 353
E value 8.0e-41
Match length 198
% identity 43

NCBI Description (X95342) cytochrome P450 [Nicotiana tabacum]

Seq. No. 17359

Contig ID 50293\_1.R1040 5'-most EST pcp700990376.h1

Method BLASTX
NCBI GI g1805654
BLAST score 284
E value 4.0e-25
Match length 129
% identity 62

NCBI Description (X99972) calmodulin-stimulated calcium-ATPase [Brassica

oleracea]

Seq. No. 17360

Contig ID 50301\_1.R1040 5'-most EST sat701009538.h1

Method BLASTX NCBI GI g3757522 BLAST score 431 E value 4.0e-42



```
Match length
                  60
% identity
                  (AC005167) putative splicing factor [Arabidopsis thaliana]
NCBI Description
                  17361
Seq. No.
                  50301 2.R1040
Contig ID
                  uC-gmronoir071g03b1
5'-most EST
                  BLASTX
Method
                  g3757522
NCBI GI
                  210
BLAST score
                  2.0e-16
E value
                  103
Match length
                  59
% identity
                  (AC005167) putative splicing factor [Arabidopsis thaliana]
NCBI Description
                  17362
Seq. No.
                  50301 4.R1040
Contig ID
                  uC-gmrominsoy174h06b1
5'-most EST
                  BLASTX
Method
                   g3757522
NCBI GI
                   187
BLAST score
                   4.0e-14
E value
                   45
Match length
                   80
% identity
                  (AC005167) putative splicing factor [Arabidopsis thaliana]
NCBI Description
                   17363
Seq. No.
                   50314 1.R1040
Contig ID
                   LIB3093-002-Q1-K1-C10
5'-most EST
                   BLASTX
Method
                   g2492526
NCBI GI
BLAST score
                   438
                   5.0e-56
E value
Match length
                   267
% identity
                   HYPOTHETICAL 93.1 KD PROTEIN YLL034C
NCBI Description
                   >gi_2131732_pir__S64785 hypothetical protein YLL034c -
                   yeast (Saccharomyces cerevisiae) >gi_1360222_emb_CAA97483_
                   (Z73139) ORF YLL034c [Saccharomyces cerevisiae]
Seq. No.
                   17364
                   50329 1.R1040
Contig ID
                   leu701151179.hl
 5'-most EST
                   BLASTX
Method
                   g3341687
NCBI GI
 BLAST score
                   262
 E value
                   1.0e-22
```

Match length 91 57 % identity

(AC003672) putative ras protein [Arabidopsis thaliana] NCBI Description

17365 Seq. No.

50338 1.R1040 Contig ID

LIB3093-001-Q1-K1-G4 5'-most EST

17366 Seq. No.

50343 1.R1040 Contig ID



```
jC-gmst02400052g04d1
5'-most EST
                  17367
Seq. No.
                   50346 1.R1040
Contig ID
                  LIB3093-001-Q1-K1-E4
5'-most EST
                  BLASTX
Method
NCBI GI
                   g3892052
                   359
BLAST score
                   3.0e - 34
E value
                   83
Match length
% identity
                   (AC002330) predicted protein of unknown function
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   17368
                   50347 1.R1040
Contig ID
5'-most EST
                   LIB3093-001-Q1-K1-E5
                   17369
Seq. No.
                   50370 1.R1040
Contig ID
5'-most EST
                   uC-gmropic088c11b1
                   BLASTX
Method
NCBI GI
                   q3367596
BLAST score
                   339
                   9.0e-32
E value
                   94
Match length
% identity
                   (AL031135) putative protein [Arabidopsis thaliana]
NCBI Description
                   17370
Seq. No.
                   50370 2.R1040
Contig ID
                   fua701041218.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3367596
BLAST score
                   217
                   2.0e-32
E value
                   103
Match length
                   77
% identity
NCBI Description (AL031135) putative protein [Arabidopsis thaliana]
                   17371
Seq. No.
                   50372 1.R1040
Contig ID
                   jC-gmro02910017a07a1
5'-most EST
                   BLASTX
Method
                   g1491776
NCBI GI
                   833
BLAST score
                   2.0e-89
E value
                   219
Match length
% identity
                   (M37636) cationic peroxidase [Arachis hypogaea]
NCBI Description
Seq. No.
                   17372
                   50377 1.R1040
Contig ID
                   fde700872527.h1
5'-most EST
                   BLASTX
Method
                   q4204265
NCBI GI
```

2862

129

BLAST score



17373

2.0e-10 E value Match length 57 59

% identity (AC005223) 45643 [Arabidopsis thaliana] NCBI Description

Seq. No.

50380 1.R1040 Contig ID pmv700889747.h1 5'-most EST

17374 Seq. No.

50381 1.R1040 Contig ID uC-gmropic101e12b1 5'-most EST

17375 Seq. No.

50381 2.R1040 Contig ID uC-gmropic087f01b1 5'-most EST

17376 Seq. No.

50386 1.R1040 Contig ID

LIB3093-001-Q1-K1-C5 5'-most EST

17377 Seq. No.

50388 1.R1040 Contig ID

LIB3093-001-Q1-K1-C7 5'-most EST

17378 Seq. No.

50409 1.R1040 Contig ID zzp700833282.hl 5'-most EST

BLASTX Method q2388564 NCBI GI 331 BLAST score 3.0e-30 E value 286 Match length

16 % identity

NCBI Description (AC000098) ESTs gb\_AA042402,gb\_ATTS1380 come from this

gene. [Arabidopsis thaliana]

17379 Seq. No.

Contig ID 50413 1.R1040 5'-most EST vwf700679255.h1

17380 Seq. No.

50422 1.R1040 Contig ID 5'-most EST pmv700890339.h1

17381 Seq. No.

50425 1.R1040 Contig ID

jC-gmle01810030a07a2 5'-most EST

Method BLASTX NCBI GI g2982272 222 BLAST score 5.0e-18 E value 64 Match length

61 % identity

(AF051220) hypothetical protein [Picea mariana] NCBI Description

17382 Seq. No.

```
50436 1.R1040
Contig ID
5'-most EST
                   smc70\overline{0}745278.h1
Method
                   BLASTX
NCBI GI
                   q3135256
BLAST score
                   262
E value
                   1.0e-22
Match length
                   150
% identity
                   43
                  (AC003058) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   17383
                   50443 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220114b12d1
Seq. No.
                   17384
Contig ID
                   50451 1.R1040
5'-most EST
                   LIB3093-014-Q1-K1-A9
                   BLASTX
Method
NCBI GI
                   g4539454
BLAST score
                   272
E value
                   5.0e-24
Match length
                   66
% identity
                   74
NCBI Description
                  (AL049500) contains EST gb:AA728416 [Arabidopsis thaliana]
                   17385
Seq. No.
Contig ID
                   50469 1.R1040
5'-most EST
                   LIB3093-017-01-K1-A2
Method
                   BLASTX
                   g1465770
NCBI GI
BLAST score
                   189
E value
                   2.0e-26
Match length
                   280
% identity
                   34
                  (U61233) cofactor D [Bos taurus]
NCBI Description
Seq. No.
                   17386
Contig ID
                   50475 1.R1040
5'-most EST
                   LIB3139-092-P1-N1-G1
Seq. No.
                   17387
Contig ID
                   50487 1.R1040
5'-most EST
                   hrw701063209.h1
Method
                   BLASTX
NCBI GI
                   q129808
BLAST score
                   407
E value
                   2.0e-39
Match length
                   128
                   66
% identity
                   CATIONIC PEROXIDASE 2 PRECURSOR >gi_99873_pir__B38265
NCBI Description
```

peroxidase (EC 1.11.1.7) precursor, cationic (clone PNC2) -

peanut >gi 166475 (M37637) cationic peroxidase [Arachis

hypogaea]

Seq. No.

17388

Contig ID

50491 1.R1040

5'-most EST

uC-gmrominsoy109g11b1



Contig ID 50494\_1.R1040 5'-most EST ary700764414.h1

Method BLASTX
NCBI GI g3738302
BLAST score 692
E value 9.0e-73
Match length 162
% identity 80

NCBI Description (AC005309) tubby-like protein [Arabidopsis thaliana]

>gi\_4249398 (AC006072) putative tubby protein [Arabidopsis

thaliana]

Seq. No. 17390

Contig ID 50499\_1.R1040 5'-most EST uxk700673162.h1

Seq. No. 17391

Contig ID 50517\_1.R1040 5'-most EST wrg700790028.h2

Method BLASTX
NCBI GI g2982783
BLAST score 184
E value 1.0e-13
Match length 117
% identity 37

NCBI Description (AE000670) 3-hydroxyisobutyrate dehydrogenase [Aquifex

aeolicus]

Seq. No. 17392

Contig ID 50527\_1.R1040

5'-most EST LIB3093-035-Q1-K1-H12

Seq. No. 17393

Contig ID 50546\_1.R1040 5'-most EST pxt700941016.h1

Seq. No. 17394

Contig ID 50552\_1.R1040

5'-most EST jC-gmro02910001e08d1

Seq. No. 17395

Contig ID 50554\_1.R1040 5'-most EST ncj700984605.h1

Method BLASTX
NCBI GI g3264757
BLAST score 159
E value 1.0e-10
Match length 48
% identity 65

NCBI Description (AF071888) zeaxanthin epoxidase [Prunus armeniaca]

Seq. No. 17396

Contig ID 50554 2.R1040 5'-most EST wvk700683655.h1



```
Seq. No.
                  50565 1.R1040
Contig ID
5'-most EST
                  LIB3139-095-P1-N1-E7
                  BLASTX
Method
NCBI GI
                  q3334144
BLAST score
                  764
E value
                  3.0e-81
Match length
                  213
% identity
                  71
NCBI Description
                  G1/S-SPECIFIC CYCLIN C-TYPE >gi 1695698 dbj BAA13181
                  (D86925) C-type cyclin [Oryza sativa]
                  17398
Seq. No.
                  50565 4.R1040
Contig ID
5'-most EST
                  jsh701065285.h1
Seq. No.
                  17399
                  50593 1.R1040
Contig ID
5'-most EST
                  txt700733958.hl
Method
                  BLASTX
NCBI GI
                  g2459440
                  274
BLAST score
E value
                  8.0e-24
Match length
                  153
% identity
                  37
                  (AC002332) putative receptor kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  17400
                  50595 1.R1040
Contig ID
5'-most EST
                  LIB3094-033-Q1-K1-F5
Method
                  BLASTN
NCBI GI
                  g3821780
BLAST score
                  33
E value
                  6.0e-09
Match length
                  37
                  97
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  17401
Seq. No.
                   50601 1.R1040
Contig ID
5'-most EST
                  LIB3094-104-Q1-K1-G7
Method
                  BLASTX
NCBI GI
                  q3176664
BLAST score
                  164
                  5.0e-11
E value
Match length
                  150
% identity
                  36
                  (ACO04393) Contains similarity to beta scruin gb_Z47541
NCBI Description
                  from Limulus polyphemus. ESTs gb_T04493 and gb_AA585955
```

50601 2.R1040 Contig ID 5'-most EST hyd700730323.h1

Seq. No. 17403

50601\_3.R1040 Contig ID

come from this gene. [Arabidopsis thaliana]

E value Match length



```
seb700653969.hl
5'-most EST
                  17404
Seq. No.
                  50607 1.R1040
Contig ID
                  LIB3094-026-Q1-K1-B11
5'-most EST
                  17405
Seq. No.
                  50613 1.R1040
Contig ID
                  LIB3094-091-Q1-K1-H6
5'-most EST
                  17406
Seq. No.
                  50615 1.R1040
Contig ID
                  LIB3094-087-Q1-K1-F2
5'-most EST
Seq. No.
                  17407
                  50637 1.R1040
Contig ID
                  LIB3094-085-Q1-K1-E12
5'-most EST
                  BLASTX
Method
                  q509810
NCBI GI
                   536
BLAST score
                   2.0e-54
E value
                   257
Match length
% identity
                   45
NCBI Description (L08468) envelope Ca2+-ATPase [Arabidopsis thaliana]
                   17408
Seq. No.
                   50640 1.R1040
Contig ID
                   uC-gmrominsoy172d02b1
5'-most EST
                   17409
Seq. No.
                   50640 2.R1040
Contig ID
                   LIB3094-023-Q1-K1-H9
5'-most EST
                   17410
Seq. No.
                   50658_1.R1040
Contig ID
                   leu701153375.h1
5'-most EST
                   BLASTX
Method
                   g4469020
NCBI GI
                   342
BLAST score
                   6.0e-32
E value
                   97
Match length
                   72
% identity
                   (AL035602) putative protein (fragment) [Arabidopsis
NCBI Description
                   thaliana]
                   17411
Seq. No.
                   50658 2.R1040
 Contig ID
                   LIB3109-035-Q1-K1-G6
 5'-most EST
 Seq. No.
                   17412
                   50658 8.R1040
 Contig ID
                   uC-gmrominsoy114c09b1
 5'-most EST
                   BLASTX
 Method
                   g4469020
 NCBI GI
 BLAST score
                   151
                   7.0e-10
```



% identity (AL035602) putative protein (fragment) [Arabidopsis NCBI Description thaliana] 17413 Seq. No. Contig ID 50662 1.R1040 LIB3094-025-Q1-K1-H5 5'-most EST

Seq. No. 50662 2.R1040 Contig ID LIB3138-053-Q1-N1-B2 5'-most EST

17414

17415 Seq. No.

50672 1.R1040 Contig ID

LIB3094-051-Q1-K1-G5 5'-most EST

17416 Seq. No.

50761 1.R1040 Contig ID LIB3170-074-Q1-J1-A5 5'-most EST

BLASTX Method NCBI GI g3551075 316 BLAST score 3.0e-49 E value 151 Match length 65 % identity

NCBI Description (AB011974) maturase [Rosa persica]

17417 Seq. No.

50762 1.R1040 Contig ID

5'-most EST LIB3094-100-Q1-K1-E4

Method BLASTX q3426045 NCBI GI BLAST score 243 E value 2.0e-20 75 Match length % identity

(AC005168) hypothetical protein [Arabidopsis thaliana] NCBI Description

17418 Seq. No.

50768 1.R1040 Contig ID rlr700900569.h1 5'-most EST

Method BLASTX NCBI GI q4467154 BLAST score 201 3.0e-29 E value Match length 82 77 % identity

(AL035540) putative thaumatin-like protein [Arabidopsis NCBI Description

thaliana]

17419 Seq. No.

50777 1.R1040 Contig ID

jC-gmle01810063f07a1 5'-most EST

BLASTX Method g2244999 NCBI GI 898 BLAST score 1.0e-96 E value



```
398
Match length
                  48
% identity
                  (Z97341) similarity to phaseolin G-box binding protein PG2
NCBI Description
                  [Arabidopsis thaliana]
                  17420
Seq. No.
                  50779 1.R1040
Contig ID
                  LIB3094-087-Q1-K1-F7
5'-most EST
                  BLASTX
Method
                  g4218114
NCBI GI
                  180
BLAST score
                  5.0e-13
E value
                  94
Match length
                   50
% identity
NCBI Description (AL035353) putative protein [Arabidopsis thaliana]
                   17421
Seq. No.
                   50789 1.R1040
Contig ID
                  LIB3094-100-Q1-K1-C6
5'-most EST
                  BLASTX
Method
                   g2578823
NCBI GI
                   449
BLAST score
                   2.0e-44
E value
                   156
Match length
% identity
                   54
                  (AB000835) similar to YGR200c [Arabidopsis thaliana]
NCBI Description
                   17422
Seq. No.
                   50790 1.R1040
Contig ID
                   LIB3107-015-Q1-K1-C7
5'-most EST
                   BLASTX
Method
                   g3036795
NCBI GI
                   675
BLAST score
                   7.0e-71
E value
                   244
Match length
                   55
% identity
                   (AL022373) putative protein [Arabidopsis thaliana]
NCBI Description
                   >gi 3805857_emb_CAA21477_ (AL031986) putative protein
                   [Arabidopsis thaliana]
                   17423
Seq. No.
                   50792 1.R1040
Contig ID
5'-most EST
                   zhf700952780.h1
                   17424
Seq. No.
                   50821 1.R1040
 Contig ID
                   LIB3094-069-Q1-K1-H4
 5'-most EST
                   BLASTX
Method
NCBI GI
                   g3176710
                   333
BLAST score
                   5.0e-31
E value
                   136
 Match length
```

NCBI Description (AC002392) unknown protein [Arabidopsis thaliana]

% identity

Seq. No.

Contig ID 50821\_2.R1040

47

17425



```
jC-gmst02400054h09a1
  5'-most EST
                     BLASTX
  Method
                     q3176710
  NCBI GI
  BLAST score
                     239
                     2.0e-20
  E value
                     78
  Match length
                     56
  % identity
                     (AC002392) unknown protein [Arabidopsis thaliana]
  NCBI Description
                     17426
Seq. No.
                     50855 1.R1040
  Contig ID
                     uC-gmrominsoy054d02b1
  5'-most EST
                     BLASTX
  Method
                     q4417267
  NCBI GI
  BLAST score
                     212
                     1.0e-16
  E value
                     110
  Match length
                     38
  % identity
  NCBI Description (AC007019) hypothetical protein [Arabidopsis thaliana]
                     17427
  Seq. No.
                     50864 1.R1040
  Contig ID
                     uxk700668841.h1
  5'-most EST
                      17428
  Seq. No.
                      50864 2.R1040
  Contig ID
                     uC-qmrominsoy298a11b1
   5'-most EST
                      17429
   Seq. No.
                      50902 1.R1040
   Contig ID
                      zsg701124903.h1
   5'-most EST
                      BLASTX
   Method
                      g2809246
   NCBI GI
   BLAST score
                      761
   E value
                      3.0e-97
                      215
   Match length
                      78
   % identity
                      (AC002560) F2401.15 [Arabidopsis thaliana]
   NCBI Description
                      17430
   Seq. No.
                      50908 1.R1040
   Contig ID
                      jC-gmro02910064g08a1
   5'-most EST
                      BLASTX
   Method
                      q3434971
   NCBI GI
   BLAST score
                      281
                      1.0e-24
   E value
                      128
   Match length
                      55
   % identity
                      (AB008105) ethylene responsive element binding factor 3
   NCBI Description
                      [Arabidopsis thaliana]
                      17431
   Seq. No.
                      50908 2.R1040
   Contig ID
   5'-most EST
                      jC-qmst02400050e06a1
```

Method BLASTX q3434971 NCBI GI BLAST score 316



1.0e-28 E value 150 Match length 51 % identity (AB008105) ethylene responsive element binding factor 3 NCBI Description [Arabidopsis thaliana] 17432 Seq. No. 50910 1.R1040 Contig ID LIB3094-090-Q1-K1-C10 5'-most EST Seq. No. 17433 50919 1.R1040 Contig ID LIB3094-047-Q1-K1-E12 5'-most EST 17434 Seq. No. 50936 1.R1040 Contig ID LIB3094-010-Q1-K1-B6 5'-most EST 17435 Seq. No. 50947 1.R1040 Contig ID LIB3094-096-Q1-K1-H6 5'-most EST Seq. No. 17436 50971 1.R1040 Contig ID 5'-most EST wrg700791813.hl 17437 Seq. No. 50971 2.R1040 Contig ID LIB3094-092-Q1-K1-F10 5'-most EST 17438 Seq. No. 50973 1.R1040 Contig ID LIB3094-014-Q1-K1-C10 5'-most EST 17439 Seq. No. 50990 1.R1040 Contig ID LIB3094-089-Q1-K1-E9 5'-most EST BLASTX Method g4538624 NCBI GI 343 BLAST score 1.0e-40 E value 116 Match length 73 % identity NCBI Description (AJ133502) hypothetical protein [Nicotiana tabacum] 17440 Seq. No. 51005 1.R1040 Contig ID

LIB3094-065-Q1-K1-F7 5'-most EST

Method BLASTN g19394 NCBI GI 50 BLAST score 4.0e-19 E value 98 Match length % identity 72

Tomato U3 small nuclear RNA gene NCBI Description

Seq. No. 17441



Contig ID 51005\_3.R1040

5'-most EST LIB3094-034-Q1-K1-B11

Method BLASTN
NCBI GI g19394
BLAST score 50
E value 4.0e-19
Match length 98
% identity 72

NCBI Description Tomato U3 small nuclear RNA gene

Seq. No.

17442 51035 1.R1040

Contig ID 5'-most EST

jC-qmle01810020b12a1

Seq. No.

17443

Contig ID

51044\_1.R1040

5'-most EST

LIB3094-094-Q1-K1-E4

Seq. No.

17444

Contig ID 51060 1.R1040

5'-most EST

LIB3094-027-Q1-K1-C11

Seq. No.

17445

Contig ID 5'-most EST

51060\_2.R1040 tku700646351.h1

Seq. No.

17446

Contig ID

51072\_1.R1040

5'-most EST

LIB3094-093-Q1-K1-F2 BLASTX

Method NCBI GI BLAST score

g3157936 140

E value Match length 1.0e-08

% identity

68 38

NCBI Description

(AC002131) Contains similarity to NFATc3 gb\_U28807 from Mus

musculus. [Arabidopsis thaliana]

Seq. No.

17447

Contig ID

51082 1.R1040

5'-most EST

LIB3094-041-Q1-K1-E11

Seq. No.

17448

Contig ID

51197 1.R1040

5'-most EST

LIB3094-090-Q1-K1-H4

Seq. No.

17449

Contig ID

51213\_1.R1040

5'-most EST

jC-gmst02400007f05a1

Seq. No.

17450

Contig ID 5'-most EST

51313\_1.R1040 fde700874737.h1

Seq. No.

17451

Contig ID

51346 1.R1040

5'-most EST

LIB3094-009-Q1-K1-F3

51392\_1.R1040 Contig ID

5'-most EST LIB3094-087-Q1-K1-C7

BLASTX Method NCBI GI g2498329 BLAST score 472 2.0e-47 E value Match length 143 % identity 67

NCBI Description PATTERN FORMATION PROTEIN EMB30 >gi 2129665\_pir\_\_S65571 pattern-formation protein GNOM - Arabidopsis thaliana

>gi\_1209633 (U36433) GNOM gene product [Arabidopsis

thaliana] >gi 1335997 (U56140) similar to the Saccharomyces cerevisiae Sec7 protein, GenBank Accession Number J03918 [Arabidopsis thaliana] >gi 1335999 (U56141) similar to the Saccharomyces cerevisiae Sec7 protein, GenBank Accession

Number J03918 [Arabidopsis thaliana]

17453 Seq. No.

Contig ID 51471 1.R1040

LIB3094-022-Q1-K1-C8 5'-most EST

Seq. No. 17454

51511 1.R1040 Contig ID

5'-most EST LIB3094-054-Q1-K1-H7

Method BLASTX NCBI GI g2541876 BLAST score 170 E value 6.0e-12 Match length 109 % identity 41

(D26015) CND41, chloroplast nucleoid DNA binding protein NCBI Description

[Nicotiana tabacum]

17455 Seq. No.

Contig ID 51583 1.R1040

5'-most EST LIB3094-064-Q1-K1-C11

Seq. No. 17456

51583 2.R1040 Contia ID 5'-most EST g4313305

Seq. No.

17457

51595 1.R1040 Contig ID

5'-most EST LIB3094-081-Q1-K1-F6

Method BLASTX NCBI GI g3786007 BLAST score 522 2.0e-57 E value 185 Match length 64 % identity

NCBI Description (AC005499) hypothetical protein [Arabidopsis thaliana]

Seq. No. 17458

Contig ID 51638 1.R1040

5'-most EST LIB3138-022-Q1-N1-E9



70

Method NCBI GI BLAST score E value

Match length

BLASTX g3695379 700 7.0e-74202

% identity

NCBI Description

(AF096370) contains similarity to a C. elegans hypothetical protein F44G4.1 (GB:Z49910) and several yeast hypothetical proteins such as 35.1 KD protein in NAM8-GAR1 intergenic

region (SP:P38805) [Arabidopsis thaliana]

Seq. No.

Contig ID 5'-most EST

% identity

51638 2.R1040 qsv701051351.h1

Method NCBI GI BLAST score E value Match length

509 2.0e-51 188 60

BLASTX

g3695379

17459

NCBI Description

(AF096370) contains similarity to a C. elegans hypothetical protein F44G4.1 (GB:Z49910) and several yeast hypothetical proteins such as 35.1 KD protein in NAM8-GAR1 intergenic region (SP:P38805) [Arabidopsis thaliana]

Seq. No.

Contig ID

17460

17461

17462

51669 1.R1040

5'-most EST

LIB3094-030-Q1-K1-B8

Seq. No.

Contig ID

51705 1.R1040

5'-most EST

LIB3094-078-01-K1-E8

Seq. No.

Contig ID

51736 1.R1040

5'-most EST

LIB3094-077-Q1-K1-H10

Seg. No.

17463

Contig ID

51737 1.R1040

5'-most EST

LIB3094-077-Q1-K1-C7

Seq. No.

17464

Contig ID

51829 1.R1040

5'-most EST

LIB3094-037-Q1-K1-D7

Seq. No.

17465

Contig ID

51859 1.R1040

5'-most EST

LIB3094-028-Q1-K1-H12

Seq. No.

17466

Contig ID 5'-most EST 51928 1.R1040 pmv700889483.h1

Seq. No.

17467

Contig ID 5'-most EST 51979 1.R1040 epx701108436.hl

Method

BLASTX



```
q2981439
NCBI GI
                   257
BLAST score
                   5.0e-22
E value
                   154
Match length
% identity
                   40
NCBI Description (AF051853) t-SNARE SED5 [Arabidopsis thaliana]
                   17468
Seq. No.
                   51979 2.R1040
Contig ID
                   LIB3094-072-Q1-K1-C7
5'-most EST
                   17469
Seq. No.
                   51989 1.R1040
Contig ID
                   uC-gmrominsoy081f04b1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g4097573
BLAST score
                   155
E value
                   7.0e-10
                   72
Match length
                   42
% identity
NCBI Description (U64917) GMFP7 [Glycine max]
                   17470
Seq. No.
                   51989 3.R1040
Contig ID
                   hyd70\overline{0}725021.h1
5'-most EST
Seq. No.
                   17471
                   52099 1.R1040
Contig ID
                   LIB3094-069-Q1-K1-C11
5'-most EST
                   17472
Seq. No.
Contig ID
                   52132 1.R1040
                   LIB3094-067-Q1-K1-F9
5'-most EST
                   17473
Seq. No.
                   52138_1.R1040
Contig ID
                   kl1701206244.h1
5'-most EST
                   17474
 Seq. No.
                   52138 2.R1040
 Contig ID
                   kl1701205654.h1
 5'-most EST
                   17475
 Seq. No.
                   52153 1.R1040
 Contig ID
                   LIB3107-018-Q1-K1-D3
 5'-most EST
                   BLASTX
 Method
                    g203550
 NCBI GI
                    109
 BLAST score
                    1.0e-08
 E value
                    108
 Match length
```

40 % identity

(L07281) carboxypeptidase E [Rattus norvegicus] NCBI Description

Seq. No.

17476

Contig ID

52168 1.R1040

5'-most EST LIB3094-019-Q1-K1-H7



Contig ID 52214\_1.R1040

5'-most EST jC-gmle01810085e03a1

Method BLASTX
NCBI GI g3184113
BLAST score 203
E value 3.0e-15
Match length 134
% identity 33

NCBI Description (AL023780) zinc finger protein [Schizosaccharomyces pombe]

Seq. No. 17478

Contig ID 52233\_1.R1040 5'-most EST taw700657431.h1

Seq. No. 17479

Contig ID 52296\_1.R1040

5'-most EST LIB3094-063-Q1-K1-H5

Method BLASTX
NCBI GI g3080398
BLAST score 432
E value 2.0e-42
Match length 159
% identity 56

NCBI Description (AL022603) putative protein [Arabidopsis thaliana]

Seq. No. 17480

Contig ID 52319\_1.R1040 5'-most EST zsg701126379.h1

Method BLASTX
NCBI GI g1703386
BLAST score 494
E value 8.0e-50
Match length 182
% identity 51

NCBI Description ACETYLORNITHINE DEACETYLASE (ACETYLORNITHINASE) (AO)

(N-ACETYLORNITHINASE) (NAO) >gi\_763048 (U23957)

 ${\tt N-acetylornithine\ deacetylase\ [\overline{\tt Dictyostelium\ discoideum]}}$ 

Seq. No. 17481

Contig ID 52327\_1.R1040 5'-most EST hyd700728012.h1

Seq. No. 17482

Contig ID 52374\_1.R1040 5'-most EST jex700909093.h1

Method BLASTX
NCBI GI g161752
BLAST score 161
E value 1.0e-10
Match length 146
% identity 11

NCBI Description (L03710) cnjB [Tetrahymena thermophila]

>gi 737494 prf\_ 1922371A cnjB gene [Tetrahymena

thermophila]

Seq. No. 17483



```
Contig ID
                  52389 1.R1040
5'-most EST
                  LIB3094-022-Q1-K1-B6
Seq. No.
                  17484
Contig ID
                  52414 1.R1040
5'-most EST
                  uaw700666005.h1
                  17485
Seq. No.
                  52474_2.R1040
Contig ID
                  gsv701046510.hl
5'-most EST
Method
                  BLASTN
                  g2624382
NCBI GI
BLAST score
                  173
E value
                  1.0e-92
Match length
                  301
% identity
                  89
NCBI Description P.vulgaris mRNA for cinnamate 4-hydroxylase
Seq. No.
                  17486
Contig ID
                  52498 1.R1040
5'-most EST
                  LIB3107-025-Q1-K1-F5
Method
                  BLASTN
                  g2924257
NCBI GI
BLAST score
                  183
E value
                  6.0e-98
Match length
                  857
% identity
                  88
NCBI Description Tobacco chloroplast genome DNA
Seq. No.
                  17487
Contig ID
                  52530 1.R1040
5'-most EST
                  LIB3094-056-Q1-K1-F2
                  BLASTX
Method
NCBI GI
                  q4417267
BLAST score
                  338
E value
                  1.0e-31
Match length
                  128
% identity
                  59
                  (AC007019) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  17488
Seq. No.
Contig ID
                  52533 1.R1040
5'-most EST
                  LIB3094-007-Q1-K1-H9
Method
                  BLASTX
NCBI GI
                  g3540182
BLAST score
                  158
```

E value 3.0e-10 Match length 122 % identity

NCBI Description (AC004122) Unknown protein [Arabidopsis thaliana]

Seq. No.

17489

Contig ID

52536 1.R1040

5'-most EST

LIB3094-048-Q1-K1-G2

Seq. No.

17490

Contig ID

52536 2.R1040



uC-qmflminsoy027d04b1 5'-most EST

17491 Seq. No.

52609 1.R1040 Contig ID

5'-most EST uC-qmronoir050h11b1

Method BLASTX q3420054 NCBI GI 314 BLAST score 3.0e-28 E value 335 Match length % identity

NCBI Description (AC004680) unknown protein [Arabidopsis thaliana]

17492 Seq. No.

52642 1.R1040 Contig ID

LIB3094-053-Q1-K1-A8 5'-most EST

BLASTX Method NCBI GI q3062806 464 BLAST score 2.0e-46 E value 124 Match length % identity

(D86198) dolichol-phosphate-mannose synthase [Homo sapiens] NCBI Description

>gi 4503363 ref\_NP\_003850.1\_pDPM1\_ UNKNOWN

17493 Seq. No.

52751 1.R1040 Contig ID

LIB3094-050-Q1-K1-C1 5'-most EST

BLASTX Method NCBI GI q3924612 416 BLAST score 8.0e-41 E value 131 Match length 68 % identity

(AF069442) mitochondrial elongation factor Tu [Arabidopsis NCBI Description

thaliana] >gi\_4263511\_gb\_AAD15337\_ (AC004044) mitochondrial

elongation factor Tu [Arabidopsis thaliana]

17494 Seq. No.

52892 1.R1040 Contig ID

LIB3094-046-Q1-K1-D6 5'-most EST

17495 Seq. No.

52939 1.R1040 Contig ID uC-gmropic059c12b1 5'-most EST

17496 Seq. No.

52952 1.R1040 Contig ID  $ncj70\overline{0}978478.h1$ 5'-most EST

17497 Seq. No.

52999 1.R1040 Contig ID

LIB3094-026-Q1-K1-H10 5'-most EST

17498 Seq. No.

53018 1.R1040 Contig ID

jC-gmst02400042f11a1 5'-most EST



```
BLASTX
Method
                  g2739008
NCBI GI
                  1432
BLAST score
                  1.0e-159
E value
                  387
Match length
                  73
% identity
NCBI Description (AF022463) CYP78A3p [Glycine max]
                  17499
Seq. No.
                  53129 1.R1040
Contig ID
5'-most EST
                  pxt700942841.h1
                  BLASTN
Method
                  g2827538
NCBI GI
BLAST score
                  41
                  1.0e-13
E value
                   65
Match length
% identity
                   91
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T12H17
NCBI Description
                   (ESSAII project)
                   17500
Seq. No.
                   53167 1.R1040
Contig ID
                  LIB3094-035-Q1-K1-G6
5'-most EST
                   17501
Seq. No.
                   53179 1.R1040
Contig ID
5'-most EST
                   LIB3106-090-Q1-K1-F12
                   17502
Seq. No.
Contig ID
                   53179 2.R1040
5'-most EST
                   leu701154473.h1
Seq. No.
                   17503
                   53318 1.R1040
Contig ID
                   LIB3094-013-Q1-K1-E6
5'-most EST
Seq. No.
                   17504
                   53434 1.R1040
Contig ID
                   LIB3094-026-Q1-K1-D2
5'-most EST
                   BLASTX
Method
                   q4415937
NCBI GI
BLAST score
                   153
                   5.0e-10
E value
                   38
Match length
                   76
% identity
                   (AC006418) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   17505
Seq. No.
                   53495 1.R1040
Contig ID
5'-most EST
                   uC-gmropic029d06b1
                   17506
```

53538 1.R1040 Contig ID

LIB3170-073-Q1-J1-D6 5'-most EST

17507 Seq. No.

53538\_2.R1040 Contig ID

Method

NCBI GI

BLASTX

g3395758



```
vzy700756038.h1
5'-most EST
                   17508
Seq. No.
Contig ID
                   53541 1.R1040
5'-most EST
                   epx701108607.h1
Method
                   BLASTX
                   g4567247
NCBI GI
BLAST score
                   542
                   2.0e-55
E value
Match length
                   157
% identity
                  (AC007070) unknown protein [Arabidopsis thaliana]
NCBI Description
                   17509
Seq. No.
Contig ID
                   53713 1.R1040
5'-most EST
                   vzy700752340.hl
Method
                   BLASTX
                   g2462748
NCBI GI
BLAST score
                   629
                   9.0e-66
E value
Match length
                   134
% identity
                   88
                   (AC002292) putative Clathrin Coat Assembly protein
NCBI Description
                   [Arabidopsis thaliana]
                   17510
Seq. No.
                   53713 2.R1040
Contig ID
5'-most EST
                   LIB3138-124-Q1-N1-E3
Method
                   BLASTX
                   g2462748
NCBI GI
                   491
BLAST score
                   2.0e-49
E value
                   105
Match length
                   87
% identity
                   (AC002292) putative Clathrin Coat Assembly protein
NCBI Description
                   [Arabidopsis thaliana]
                   17511
Seq. No.
Contig ID
                   53731 1.R1040
                   ek170\overline{0}968166.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4567275
BLAST score
                   302
                   1.0e-27
E value
                   85
Match length
                   23
% identity
                   (AC006841) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   17512
Seq. No.
                   53751 1.R1040
Contig ID
5'-most EST
                   LIB3094-019-Q1-K1-B12
                   17513
Seq. No.
                   53824 1.R1040
Contig ID
5'-most EST
                   pmv700892980.hl
```



```
BLAST score 662
E value 2.0e-69
Match length 181
% identity 69
NCBI Description (U76300) unknown [Arabidopsis thaliana]
```

Contig ID 53879\_1.R1040 5'-most EST zhf700953571.h1

Seq. No. 17515

Contig ID 54077\_1.R1040 5'-most EST kl1701211489.h1

Seq. No. 17516

Contig ID 54077\_2.R1040

5'-most EST jC-gmro02800029d10a1

Seq. No. 17517

Contig ID 54077\_3.R1040

5'-most EST uC-gmronoir051e10b1

Seq. No. 17518

Contig ID 54288\_1.R1040 5'-most EST gsv701050009.h1

Method BLASTX
NCBI GI g1903019
BLAST score 433
E value 1.0e-42
Match length 92
% identity 89

NCBI Description (Y10580) polycomb group [Arabidopsis thaliana]

Seq. No. 17519

Contig ID 54373\_1.R1040 5'-most EST wvk700685642.h1

Seq. No. 17520

Contig ID 54412\_1.R1040

5'-most EST LIB3094-002-Q1-K1-D4

Method BLASTX
NCBI GI g3668093
BLAST score 223
E value 5.0e-18
Match length 82
% identity 55

NCBI Description (AC004667) unknown protein [Arabidopsis thaliana]

Seq. No.

17521

Contig ID 54469\_1.R1040

5'-most EST LIB3094-025-Q1-K1-F9

Seq. No.

17522

Contig ID 54487 1.R1040

5'-most EST LIB3094-018-Q1-K1-H12

Seq. No.



54504 1.R1040 Contig ID LIB3094-028-Q1-K1-C1 5'-most EST 17524 Seq. No. Contig ID 54529 1.R1040 leu701155846.hl 5'-most EST BLASTX Method g4510385 NCBI GI BLAST score 168 E value 1.0e-11 Match length 71 41 % identity (AC007017) unknown protein [Arabidopsis thaliana] NCBI Description 17525 Seq. No. Contig ID 54542 1.R1040 LIB3094-060-Q1-K1-C7 5'-most EST 17526 Seq. No. 54669 1.R1040 Contig ID 5'-most EST jC-qmle01810088g11a1 17527 Seq. No. Contig ID 54671 1.R1040 LIB3106-116-Q1-K1-G9 5'-most EST BLASTN Method g2264314 NCBI GI BLAST score 46 E value 1.0e-16 Match length 125 % identity 84 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MQK4, complete sequence [Arabidopsis thaliana] 17528 Seq. No. 54678 1.R1040 Contig ID LIB3106-116-Q1-K1-G11 5'-most EST BLASTX Method g4218120 NCBI GI 394 BLAST score 6.0e-38 E value Match length 101 % identity (AL035353) Proline-rich APG-like protein [Arabidopsis NCBI Description thaliana] 17529 Seq. No. 54680 1.R1040 Contig ID hrw701060402.hl 5'-most EST Method BLASTX NCBI GI q3080401 BLAST score 568 2.0e-58 E value

160 Match length 65 % identity

(AL022603) putative protein [Arabidopsis thaliana] NCBI Description >gi 4455265 emb CAB36801.1 (AL035527) putative protein



## [Arabidopsis thaliana]

```
      Seq. No.
      17530

      Contig ID
      54688_1.R1040

      5'-most EST
      kl1701205216.h1
```

Seq. No. 17531

Contig ID 54689\_1.R1040

5'-most EST LIB3106-116-Q1-K1-E1

Seq. No. 17532

Contig ID 54691\_1.R1040

5'-most EST LIB3106-108-Q1-K1-E12

Seq. No. 17533

Contig ID 54692 1.R1040 5'-most EST pmv700889182.h1

Method BLASTX
NCBI GI 94580394
BLAST score 569
E value 1.0e-58
Match length 163
% identity 63

NCBI Description (AC007171) putative fatty acid elongase [Arabidopsis

thaliana]

Seq. No. 17534

Contig ID 54696\_1.R1040 5'-most EST leu701157526.h1

Seq. No. 17535

Contig ID 54720\_1.R1040 5'-most EST uC-gmropic105h12b1

Method BLASTX

NCBI GI g3688185 BLAST score 254 E value 7.0e-22

Match length 71 % identity 75

NCBI Description (AL031804) putative protein [Arabidopsis thaliana]

Seq. No. 17536

Contig ID 54744\_1.R1040

5'-most EST LIB3106-116-Q1-K1-A5

Method BLASTX
NCBI GI g3080440
BLAST score 252
E value 1.0e-21
Match length 85
% identity 54

NCBI Description (AL022605) hypothetical protein [Arabidopsis thaliana]

Seq. No.

Contig ID 54745\_2.R1040 5'-most EST sat701005941.h1

17537

Seq. No. 17538

% identity

NCBI Description

thaliana]



```
54748 1.R1040
Contig ID
                  bth700844939.h1
5'-most EST
                  BLASTX
Method
                  q1362015
NCBI GI
BLAST score
                   179
                   6.0e-13
E value
                   95
Match length
                   46
% identity
                   zinc finger protein 1 - Arabidopsis thaliana
NCBI Description
                   >gi 2129779_pir__S71240 zinc finger protein 1 - Arabidopsis
                   thaliana >gi_790673 (L39644) zinc finger protein
                   [Arabidopsis thaliana] >gi_1297186 (U53501) zinc finger
                   protein 1 [Arabidopsis thaliana]
                   17539
Seq. No.
Contig ID
                   54748 2.R1040
                   pmv700893905.hl
5'-most EST
Method
                   BLASTX
                   g1362017
NCBI GI
BLAST score
                   152
                   4.0e-10
E value
Match length
                   34
                   76
% identity
                   zinc finger protein 4 - Arabidopsis thaliana >gi_790679
NCBI Description
                   (L39647) zinc finger protein [Arabidopsis thaliana]
Seq. No.
                   17540
                   54756 1.R1040
Contig ID
                   fde700871366.hl
5'-most EST
                   BLASTX
Method
                   g1001311
NCBI GI
BLAST score
                   309
                   5.0e-28
E value
                   216
Match length
                   33
% identity
                   (D64006) hypothetical protein [Synechocystis sp.]
NCBI Description
                   17541
Seq. No.
                   54765 1.R1040
Contig ID
                   leu70\overline{1}156153.h1
 5'-most EST
                   17542
Seq. No.
                   54770 1.R1040
 Contig ID
                   ssr700556714.h1
 5'-most EST
                   17543
Seq. No.
                   54776 1.R1040
 Contig ID
                   LIB3106-115-Q1-K1-D4
 5'-most EST
                   BLASTX
 Method
                   q3790571
 NCBI GI
 BLAST score
                   156
                   3.0e-10
 E value
                   46
 Match length
```

2884

(AF078823) RING-H2 finger protein RHA2b [Arabidopsis



```
Seq. No. 17544
Contig ID 54790_1.R1040
```

LIB3106-115-Q1-K1-C10

5'-most EST LIB3106-1
Method BLASTX
NCBI GI g3915964

BLAST score 221 E value 1.0e-17 Match length 244 % identity 26

NCBI Description HYPOTHETICAL 112.2 KD PROTEIN IN TIF35-NPL3 INTERGENIC REGION (ORF1) >gi\_2131486\_pir\_S69711 hypothetical protein

YDR430c - yeast (Saccharomyces cerevisiae) >gi\_927711 (U33007) Ydr430cp; CAI: 0.15 [Saccharomyces cerevisiae]

Seq. No. 17545

Contig ID 54814\_1.R1040

5'-most EST jC-gmro02910030g11a1

Method BLASTX
NCBI GI g2244785
BLAST score 421
E value 3.0e-41
Match length 95
% identity 78

NCBI Description (Z97335) hypothetical protein [Arabidopsis thaliana]

Seq. No. 17546

Contig ID 54821\_1.R1040 5'-most EST trc700565965.h1

Method BLASTX
NCBI GI g3249577
BLAST score 335
E value 5.0e-31
Match length 150
% identity 45

NCBI Description (AF055573) fragile histidine triad protein [Mus musculus] >gi 3264590 (AF047699) fragile histidine triad protein [Mus

musculus]

Seq. No. 17547

Contig ID 54838\_1.R1040

5'-most EST jC-gmst02400004d11a1

Method BLASTX
NCBI GI g1946372
BLAST score 379
E value 4.0e-36
Match length 118
% identity 61

NCBI Description (U93215) yeast hypothetical protein YDB1\_SCHPO isolog

[Arabidopsis thaliana]

Seq. No. 17548

Contig ID 54843\_1.R1040

5'-most EST jC-gmst02400060c08d1

Method BLASTX
NCBI GI g3080420
BLAST score 996
E value 1.0e-108



Match length % identity 69

NCBI Description

(AL022604) putative sugar transporter protein [Arabidopsis

thaliana]

Seq. No.

17549

Contig ID 5'-most EST

54845 1.R1040 LIB3106-114-Q1-K1-F2

Method NCBI GI BLASTX g1717755 295

BLAST score E value Match length

1.0e-26 83

% identity

NCBI Description

TROPINONE REDUCTASE HOMOLOG (P29X) >gi 539028\_pir C48674

tropinone reductase homolog - jimsonweed >gi\_424158 (L20475) 29kDa protein; high homology to aa sequence of

tropinone reductases [Datura stramonium]

Seq. No.

17550

Contig ID

54849 1.R1040

5'-most EST

LIB3106-114-Q1-K1-G1

Method BLASTX g3880399 NCBI GI BLAST score 152 E value 6.0e-10 Match length 82

% identity

NCBI Description

(Z71267) predicted using Genefinder; cDNA EST yk275h2.3 comes from this gene; cDNA EST yk309g11.3 comes from this gene; cDNA EST yk309g11.5 comes from this gene; cDNA EST yk275h2.5 comes from this gene [Caenorhabditis elegans]

Seq. No.

17551

39

Contig ID 5'-most EST 54862 1.R1040 art700605410.h2

Seq. No.

17552

Contig ID

54874 1.R1040

5'-most EST

LIB3106-114-Q1-K1-C1

Method BLASTX g4056461 NCBI GI 367 BLAST score 4.0e-35 E value Match length 82

% identity

NCBI Description

(AC005990) F508.34 [Arabidopsis thaliana]

Seq. No.

17553

Contig ID

54888 1.R1040

5'-most EST

g5676857

Seq. No.

17554

Contig ID 5'-most EST

54894 1.R1040 ncj700981513.hl

Seq. No.



54894 2.R1040 Contig ID gsv701056196.h1 5'-most EST Seq. No. 17556 54897 1.R1040 Contig ID epx701105103.hl 5'-most EST BLASTX Method q282994 NCBI GI 654 BLAST score 2.0e-68 E value

Seq. No. 17557

Match length

Contig ID 54911 1.R1040

5'-most EST LIB3106-113-Q1-K1-E1

231

Method BLASTX
NCBI GI g2500980
BLAST score 470
E value 7.0e-47
Match length 136
% identity 67

NCBI Description GLUTAMYL-TRNA SYNTHETASE (GLUTAMATE--TRNA LIGASE) (GLURS)

>gi\_1076718\_pir\_\_S51684 glutamate--tRNA ligase (EC
6.1.1.17) precursor - barley >gi\_603849\_emb\_CAA58505\_
(X83523) glutamate--tRNA ligase [Hordeum vulgare]

Seq. No. 17558

Contig ID 54937 1.R1040

5'-most EST LIB3106-113-Q1-K1-D3

Seq. No. 17559

Contig ID 54949 1.R1040

5'-most EST jC-gmle01810071g07a1

Seq. No. 17560

Contig ID 54961\_1.R1040

5'-most EST LIB3106-112-Q1-K1-G7

Seq. No. 17561

Contig ID 54962\_1.R1040 5'-most EST fua701039791.h1

Method BLASTX
NCBI GI g3426064
BLAST score 394
E value 4.0e-38
Match length 149
% identity 56

NCBI Description (AJ007588) monooxygenase [Arabidopsis thaliana]

>gi\_4467141\_emb\_CAB37510\_ (AL035540) monooxygenase 2 (MO2)

[Arabidopsis thaliana]

Seq. No. 17562

Contig ID 54969 1.R1040

5'-most EST LIB3106-112-Q1-K1-H5



```
17563
Seq. No.
                   54972 1.R1040
Contig ID
5'-most EST
                   LIB31\overline{0}6-112-Q1-K1-H9
Seq. No.
                   17564
                   54994 1.R1040
Contig ID
5'-most EST
                   LIB3106-112-Q1-K1-E10
Seq. No.
                   17565
Contig ID
                   54998 1.R1040
                   uC-gmflminsoy026h10b1
5'-most EST
                   BLASTX
Method
                   q3688600
NCBI GI
                   2570
BLAST score
E value
                   0.0e + 00
Match length
                   534
% identity
                   85
                  (AB009030) beta-Amyrin Synthase [Panax ginseng]
NCBI Description
                   17566
Seq. No.
Contig ID
                   54998 2.R1040
5'-most EST
                   fC-qmf1700905218j1
                   BLASTX
Method
                   g3688600
NCBI GI
BLAST score
                   423
E value
                   9.0e-42
                   116
Match length
% identity
                   (AB009030) beta-Amyrin Synthase [Panax ginseng]
NCBI Description
Seq. No.
                   17567
                   55004 1.R1040
Contig ID
                   LIB3106-112-Q1-K1-B4
5'-most EST
                   BLASTX
Method
                   g3600059
NCBI GI
BLAST score
                   416
                   8.0e-41
E value
Match length
                   135
                   61
% identity
                   (AF080120) contains similarity to WB domains, G-beta
NCBI Description
                   repeats (Pfam: G-beta.hmm, score: 14.83 and 23.03)
                   [Arabidopsis thaliana]
                   17568
Seq. No.
Contig ID
                   55012 1.R1040
                   hyd700727781.h1
5'-most EST
                   BLASTX
Method
                   g3445207
NCBI GI
BLAST score
                   413
```

E value 2.0e-41 174 Match length % identity 55

(AC004786) unknown protein [Arabidopsis thaliana] NCBI Description

Seq. No. 17569

Contig ID 55019 1.R1040

E value

Match length

% identity

1.0e-15

50 70



```
jC-gmle01810033a09a2
5'-most EST
                  BLASTX
Method
                  q3850111
NCBI GI
BLAST score
                  494
E value
                  1.0e-49
                  148
Match length
                  56
% identity
                  (AL033388) hypothetical integral membrane protein, putative
NCBI Description
                  involvement in lipid metabolism [Schizosaccharomyces pombe]
                  17570
Seq. No.
                  55020_1.R1040
Contig ID
                  zsg701121529.h1
5'-most EST
Seq. No.
                  17571
Contig ID
                  55049 1.R1040
                  LIB3170-022-Q1-J1-E11
5'-most EST
Method
                  BLASTN
                  g2656031
NCBI GI
BLAST score
                  53
E value
                  1.0e-20
Match length
                  178
% identity
                  86
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MXC20
                  17572
Seq. No.
                  55051 1.R1040
Contig ID
5'-most EST
                  vzy700756286.h1
                  BLASTX
Method
                  q3386598
NCBI GI
                  2036
BLAST score
                  0.0e+00
E value
                  525
Match length
                  73
% identity
                  (AC004665) putative cytochrome p450 [Arabidopsis thaliana]
NCBI Description
                  17573
Seq. No.
                   55051 2.R1040
Contig ID
5'-most EST
                  rlr700902064.h1
Method
                  BLASTX
                   q3386598
NCBI GI
BLAST score
                   472
E value
                   3.0e-47
Match length
                   141
% identity
                   65
                  (AC004665) putative cytochrome p450 [Arabidopsis thaliana]
NCBI Description
                   17574
Seq. No.
                   55051 3.R1040
Contig ID
5'-most EST
                   zhf700965146.h1
                   BLASTX
Method
NCBI GI
                   q3702348
BLAST score
                   198
```



NCBI Description (AC005397) putative cytochrome P450, 3' partial [Arabidopsis thaliana]

Seq. No. 17575

Contig ID 55059\_1.R1040

5'-most EST LIB3106-078-P1-K1-E3

Seq. No. 17576

Contig ID 55059 2.R1040

5'-most EST LIB3167-078-P1-K2-A5

Seq. No. 17577

Contig ID 55066 1.R1040

5'-most EST LIB3106-111-Q1-K1-C4

Seq. No. 17578

Contig ID 55079 1.R1040 5'-most EST jex700903269.h1

Seq. No. 17579

Contig ID 55094 1.R1040

5'-most EST jC-gmst02400064c06d1

Seq. No. 17580

Contig ID 55098 1.R1040

5'-most EST uC-gmrominsoy189b10b1

Method BLASTX
NCBI GI g3021270
BLAST score 750
E value 2.0e-79
Match length 261
% identity 55

NCBI Description (AL022347) serine/threonine kinase -like protein

[Arabidopsis thaliana]

Seq. No. 17581

Contig ID 55098 2.R1040 5'-most EST jex700904449.h1

Seq. No. 17582

Contig ID 55103 1.R1040 5'-most EST fde700874424.h1

Method BLASTX
NCBI GI g1169302
BLAST score 175
E value 2.0e-12
Match length 134
% identity 32

NCBI Description ISOCHORISMATASE (2,3 DIHYDRO-2,3 DIHYDROXYBENZOATE

SYNTHASE) (SUPEROXIDE-INDUCIBLE PROTEIN 1) (SOI1)

>gi 837333 (U26444) isochorismatase [Bacillus subtilis]

>gi\_2635694\_emb\_CAB15187\_ (Z99120) isochorismatase

[Bacillus subtilis]

Seq. No. 17583

Contig ID 55105 1.R1040

5'-most EST LIB3106-019-Q1-K1-C8



```
17584
Seq. No.
Contig ID
                  55110 1.R1040
                  LIB3106-110-Q1-K1-H10
5'-most EST
                  BLASTX
Method
                  g3522957
NCBI GI
BLAST score
                  327
                  7.0e-59
E value
Match length
                  143
                  79
% identity
NCBI Description (AC004411) unknown protein [Arabidopsis thaliana]
                  17585
Seq. No.
Contig ID
                  55118 1.R1040
                  ssr700556992.h1
5'-most EST
                  BLASTX
Method
                  q431162
NCBI GI
BLAST score
                  233
                   4.0e-28
E value
Match length
                  126
                  56
% identity
NCBI Description (D21822) ORF [Lilium longiflorum]
                  17586
Seq. No.
Contig ID
                  55145 1.R1040
5'-most EST
                  LIB3106-110-Q1-K1-D11
                  BLASTX
Method
                   g4490756
NCBI GI
BLAST score
                   346
                   2.0e-32
E value
Match length
                   103
% identity
                   67
                  (AL035708) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   17587
Seq. No.
Contiq ID
                   55147_1.R1040
5'-most EST
                  LIB3106-110-Q1-K1-D3
                   17588
Seq. No.
Contig ID
                   55150 1.R1040
5'-most EST
                   jC-qmf102220090g11a1
Seq. No.
                   17589
Contig ID
                   55150 2.R1040
5'-most EST
                   zsg701125064.h1
Seq. No.
                   17590
                   55157 1.R1040
Contig ID
5'-most EST
                   k1170\overline{1}208235.h1
                   17591
Seq. No.
```

55195 1.R1040 Contig ID 5'-most EST zsg701123955.h1

Seq. No.

55203 1.R1040 Contig ID

5'-most EST LIB3106-109-Q1-K1-G9

17592



```
17593
Seq. No.
Contig ID
                   55203 2.R1040
5'-most EST
                   rca700998704.h1
                   17594
Seq. No.
                   55204 1.R1040
Contig ID
                   LIB3106-021-Q1-K1-H3
5'-most EST
Seq. No.
                   17595
                   55205 1.R1040
Contig ID
                   crh70\overline{0}854496.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3135268
BLAST score
                   440
E value
                   1.0e-43
Match length
                   116
% identity
                   28
                   (AC003058) putative RNA-binding protein [Arabidopsis
NCBI Description
                   thaliana]
                   17596
Seq. No.
Contig ID
                   55213 1.R1040
                   LIB3106-005-Q1-K2-B2
5'-most EST
Method
                   BLASTN
NCBI GI
                   g169190
BLAST score
                   217
                   1.0e-118
E value
Match length
                   221
                   100
% identity
                  P.hybrida 5-enolpyruvylshikimate 3-phosphate synthase mRNA,
NCBI Description
                   complete cds
                   17597
Seq. No.
Contig ID
                   55220 1.R1040
5'-most EST
                   uC-gmropic063e01b1
Seq. No.
                   17598
                   55229 1.R1040
Contig ID
5'-most EST
                   jC-gmro02800039h11a1
                   17599
Seq. No.
                   55231 1.R1040
Contig ID
                   wvk700680056.h2
5'-most EST
Seq. No.
                   17600
                   55238 1.R1040
Contig ID
                   zzp700830974.h1
5'-most EST
Method
                   BLASTX
```

Method BLASTX
NCBI GI 94512698
BLAST score 882
E value 2.0e-95
Match length 187
% identity 89

17601

NCBI Description (AC006569) hypothetical protein [Arabidopsis thaliana]

Seq. No.



```
Contig ID
                  55239 1.R1040
5'-most EST
                  hyd700726855.h1
                  17602
Seq. No.
                  55245 1.R1040
Contig ID
                  uC-gmropic067g01b1
5'-most EST
Method
                  BLASTX
                  g3033375
NCBI GI
BLAST score
                  581
                  1.0e-60
E value
Match length
                  208
                  56
% identity
                  (AC004238) putative berberine bridge enzyme [Arabidopsis
NCBI Description
                  thaliana]
                  17603
Seq. No.
                  55248 1.R1040
Contig ID
5'-most EST
                  uC-gmropic105d07b1
Method
                  BLASTX
                  g3668089
NCBI GI
BLAST score
                  348
E value
                  1.0e-36
Match length
                  99
% identity
                  81
                  (AC004667) unknown protein [Arabidopsis thaliana]
NCBI Description
                  17604
Seq. No.
                  55256 1.R1040
Contig ID
5'-most EST
                  nsy700645679.h1
Method
                  BLASTX
                  g1076274
NCBI GI
                  473
BLAST score
                  4.0e-58
E value
Match length
                  275
                  47
% identity
                  cucumisin (EC 3.4.21.25) precursor - muskmelon (fragment)
NCBI Description
Seq. No.
                  17605
Contig ID
                  55265 1.R1040
5'-most EST
                  LIB3109-048-Q1-K1-E9
Method
                  BLASTX
NCBI GI
                  g2655008
                  694
BLAST score
E value
                   6.0e-73
Match length
                  272
% identity
                   49
NCBI Description
                   (AF017144) (1-4)-beta-mannan endohydrolase [Lycopersicon
                   esculentum]
Seq. No.
                  17606
```

55265 3.R1040 Contig ID 5'-most EST uC-gmronoir038f08b1

Seq. No. 17607

55266 1.R1040 Contig ID

LIB3106-108-Q1-K1-F12 5'-most EST



Contig ID 55277\_1.R1040 5'-most EST zhf700964423.h1

Seq. No. 17609

Contig ID 55282 1.R1040 5'-most EST fde700871751.h1

Seq. No. 17610

Contig ID 55284 1.R1040

5'-most EST LIB3138-081-P1-N1-F5

Seq. No. 17611

Contig ID 55286 1.R1040

5'-most EST jC-gmle01810093c06a1

Seq. No. 17612

Contig ID 55293 1.R1040 5'-most EST zsg701121003.h1

Method BLASTX
NCBI GI g2982445
BLAST score 218
E value 2.0e-17
Match length 67
% identity 63

NCBI Description (AL022224) putative protein [Arabidopsis thaliana]

Seq. No. 17613

Contig ID 55300\_1.R1040 5'-most EST rlr700897401.h1

Method BLASTX
NCBI GI 94454012
BLAST score 972
E value 1.0e-105
Match length 269
% identity 67

NCBI Description (AL035396) Pollen-specific protein precursor like

[Arabidopsis thaliana]

Seq. No. 17614

Contig ID 55303 1.R1040

5'-most EST jC-gmle01810043g02a1

17615

Method BLASTX
NCBI GI g3928085
BLAST score 271
E value 9.0e-24
Match length 93
% identity 60

NCBI Description (AC005770) unknown protein [Arabidopsis thaliana]

Seq. No.

Contig ID 55313\_1.R1040 5'-most EST seb700653088.h1

Seq. No. 17616

Contig ID 55330\_1.R1040 5'-most EST pxt700945653.h1



```
17617
Seq. No.
Contig ID
                  55334 1.R1040
5'-most EST
                  LIB31\overline{0}6-107-Q1-K1-H8
Method
                  BLASTX
                  g3080390
NCBI GI
BLAST score
                  237
                  1.0e-19
E value
                  66
Match length
                  68
% identity
                  (AL022603) putative protein [Arabidopsis thaliana]
NCBI Description
                  17618
Seq. No.
Contig ID
                  55349 1.R1040
5'-most EST
                  gsv701047861.h1
Method
                  BLASTX
                  q2465923
NCBI GI
BLAST score
                  238
                   8.0e-20
E value
                   96
Match length
                   51
% identity
                   (AF024648) receptor-like serine/threonine kinase
NCBI Description
                   [Arabidopsis thaliana]
                   17619
Seq. No.
Contig ID
                   55350 1.R1040
5'-most EST
                  LIB3106-107-Q1-K1-G2
Seq. No.
                   17620
                   55361 1.R1040
Contig ID
                   LIB3106-107-Q1-K1-E12
5'-most EST
Method
                   BLASTX
                   q4371280
NCBI GI
                   203
BLAST score
                   9.0e-16
E value
                   65
Match length
                   58
% identity
                  (AC006260) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   17621
                   55368 1.R1040
Contig ID
                   taw700659009.h1
5'-most EST
                   BLASTX
Method
                   q2897942
NCBI GI
BLAST score
                   157
E value
                   1.0e-10
                   93
Match length
                   39
% identity
                   (AF003938) thioredoxin-like protein [Homo sapiens]
NCBI Description
                   >gi_2961254 (AF051896) thioredoxin homolog [Homo sapiens]
                   >gi_2970689 (AF052659) thioredoxin-related protein [Homo
                   sapiens]
```

Contig ID 55369 1.R1040

5'-most EST LIB3106-107-Q1-K1-B6

17622

Method BLASTX



```
g2253119
NCBI GI
BLAST score
                  987
                  1.0e-107
E value
                  389
Match length
% identity
                  50
NCBI Description (AF007099) chalcone synthase [Bromheadia finlaysoniana]
                  17623
Seq. No.
                  55373 1.R1040
Contig ID
                  epx701104458.h1
5'-most EST
                  BLASTX
Method
                  g1175703
NCBI GI
                  220
BLAST score
                  1.0e-17
E value
Match length
                  91
                   44
% identity
                  HYPOTHETICAL 30.3 KD PROTEIN IN PSAC-ACCA INTERGENIC REGION
NCBI Description
                   (ORF 277) >gi 493471 emb CAA83938 (Z33874) unknown
                   [Antithamnion sp.]
                   17624
Seq. No.
                   55374 1.R1040
Contig ID
                   zhf700958744.h1
5'-most EST
                   17625
Seq. No.
                   55374 2.R1040
Contig ID
5'-most EST
                   jC-gmro02910022c11a1
                   17626
Seq. No.
                   55381 1.R1040
Contig ID
5'-most EST
                  LIB3106-107-Q1-K1-D11
                   17627
Seq. No.
                   55384 1.R1040
Contig ID
                   pxt700943342.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3164115
                   282
BLAST score
                   9.0e-25
E value
Match length
                   153
% identity
                   (AJ224145) major latex-like protein [Rubus idaeus]
NCBI Description
                   17628
Seq. No.
Contig ID
                   55386 1.R1040
                   LIB3106-107-Q1-K1-A12
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3935165
BLAST score
                   320
E value
                   3.0e-29
Match length
                   114
% identity
                   63
NCBI Description (AC004557) F17L21.8 [Arabidopsis thaliana]
Seq. No.
                   17629
```

2896

55387 1.R1040

 $jex70\overline{0}908229.h1$ 

Contig ID

5'-most EST



```
BLASTX
Method
                  q4454051
NCBI GI
BLAST score
                  519
E value
                  8.0e-53
Match length
                  113
% identity
                  85
                  (AL035394) putative polygalacturonase [Arabidopsis
NCBI Description
                  thaliana]
                  17630
Seq. No.
                  55390 1.R1040
Contig ID
                  sat701003583.h1
5'-most EST
Method
                  BLASTX
                   g1495251
NCBI GI
BLAST score
                  342
E value
                   4.0e-32
Match length
                  76
% identity
                  87
                  (Z70314) heat-shock protein [Arabidopsis thaliana]
NCBI Description
                   17631
Seq. No.
                   55396 1.R1040
Contig ID
                  LIB3170-079-Q1-J1-C7
5'-most EST
Method
                  BLASTX
                   g4220461
NCBI GI
BLAST score
                   171
                   5.0e-12
E value
Match length
                   77
% identity
                   56
                   (AC006216) ESTs gb T75642 and gb_AA650997 come from this
NCBI Description
                   gene. [Arabidopsis thaliana]
                   17632
Seq. No.
                   55403_1.R1040
Contig ID
5'-most EST
                   gsv701056492.h1
                   BLASTX
Method
                   g1616609
NCBI GI
BLAST score
                   458
                   2.0e-45
E value
                   157
Match length
% identity
                   55
                   (Y08641) PR10-1 protein [Medicago truncatula]
NCBI Description
                   17633
Seq. No.
Contig ID
                   55405 1.R1040
                   jC-gmro02910047g06a1
5'-most EST
                   BLASTX
Method
                   q4262226
NCBI GI
BLAST score
                   355
                   5.0e-33
E value
Match length
                   150
% identity
                   (AC006200) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                   17634
Seq. No.
```

2897

55405 2.R1040

jC-gmle01810056h02a1

Contig ID

5'-most EST



```
17635
Seq. No.
                   55408 2.R1040
Contig ID
                   smc70\overline{0}744580.h1
5'-most EST
                   17636
Seq. No.
                   55420 1.R1040
Contig ID
                   LIB3106-106-Q1-K1-F5
5'-most EST
                   BLASTX
Method
                   g2894599
NCBI GI
                   179
BLAST score
                   5.0e-13
E value
Match length
                   97
% identity
                   39
                  (AL021889) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   17637
                   55430 1.R1040
Contig ID
                   dpv701097705.hl
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4406819
BLAST score
                   246
E value
                   1.0e-20
Match length
                   164
                   38
% identity
                   (AC006201) unknown protein [Arabidopsis thaliana]
NCBI Description
                   17638
Seq. No.
Contig ID
                   55430 2.R1040
                   zpv700760014.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4406819
                   169
BLAST score
                   6.0e-12
E value
                   94
Match length
                   39
% identity
                  (AC006201) unknown protein [Arabidopsis thaliana]
NCBI Description
                   17639
Seq. No.
                   55430 3.R1040
Contig ID
                   kl1701213960.h1
5'-most EST
                   BLASTX
Method
                   g4406819
NCBI GI
                   180
BLAST score
                   3.0e-13
E value
Match length
                   91
                   45
% identity
                   (AC006201) unknown protein [Arabidopsis thaliana]
NCBI Description
                   17640
Seq. No.
```

Contig ID 55434\_1.R1040

5'-most EST LIB3167-027-P1-K1-D2

Seq. No. 17641

Contig ID 55438 1.R1040

5'-most EST jC-gmst02400032d03d1



```
Seq. No.
                  17642
Contig ID
                  55472 1.R1040
                  jC-gmf102220071e09a1
5'-most EST
                  17643
Seq. No.
                  55482 1.R1040
Contig ID
5'-most EST
                  LIB3106-105-Q1-K1-G9
Method
                  BLASTX
                  g2342723
NCBI GI
BLAST score
                  192
E value
                  4.0e-14
                  107
Match length
                  34
% identity
                  (AC002341) unknown protein [Arabidopsis thaliana]
NCBI Description
                  17644
Seq. No.
                  55485 1.R1040
Contig ID
5'-most EST
                  LIB3106-105-Q1-K1-H2
                  BLASTX
Method
                  g3395436
NCBI GI
BLAST score
                  239
                  1.0e-19
E value
                  159
Match length
                  33
% identity
NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]
                  17645
Seq. No.
                  55487 1.R1040
Contig ID
5'-most EST
                  txt700737325.h1
Method
                  BLASTN
NCBI GI
                   q4218522
                  135
BLAST score
E value
                  1.0e-69
Match length
                   415
% identity
                   86
NCBI Description Pisum sativum mRNA for PPF-1 protein
Seq. No.
                   17646
Contig ID
                   55512 1.R1040
5'-most EST
                   fC-qmst700662684f6
Method
                   BLASTX
NCBI GI
                   g2916917
BLAST score
                   249
E value
                   3.0e-21
Match length
                   137
```

% identity 42

NCBI Description (AL022004) hypothetical protein Rv0858c [Mycobacterium

tuberculosis]

Seq. No. 17647

55515 1.R1040 Contig ID leu701157552.h1 5'-most EST

BLASTX Method NCBI GI g3342552 BLAST score 272 8.0e-24 E value Match length 97



% identity 57

NCBI Description (AF076979) putative strictosidine synthase [Arabidopsis thaliana]

Seq. No. 17648

Contig ID 55533\_1.R1040

51-most FST LIB3106-105-01-K1-C5

5'-most EST LIB31 $\overline{0}$ 6-105-Q1-K1-C5

Seq. No. 17649

Contig ID 55535\_1.R1040 5'-most EST zhf700952513.h1

Method BLASTX
NCBI GI g2980773
BLAST score 723
E value 8.0e-83
Match length 363
% identity 32

NCBI Description (AL022198) putative protein [Arabidopsis thaliana]

Seq. No. 17650

Contig ID 55550\_1.R1040 5'-most EST eep700864088.h1

Seq. No. 17651

Contig ID 55561\_1.R1040 5'-most EST fC-gmse7000752125d1

Method BLASTX
NCBI GI g2501647
BLAST score 743
E value 5.0e-79
Match length 154
% identity 90

NCBI Description UROPORPHYRINOGEN DECARBOXYLASE PRECURSOR (UPD)

>gi\_1362120\_pir\_\_S55732 uroporphyrinogen decarboxylase -

common tobacco >gi\_1009429\_emb\_CAA58040\_ (X82833) uroporphyrinogen decarboxylase [Nicotiana tabacum]

Seq. No. 17652

Contig ID 55562 1.R1040

5'-most EST LIB3106-104-Q1-K1-H11

Method BLASTX
NCBI GI g2145356
BLAST score 951
E value 1.0e-103
Match length 215
% identity 83

NCBI Description (Y11122) HD-Zip protein [Arabidopsis thaliana] >gi\_3132474 (AC003096) homeobox protein, ATHB-14 [Arabidopsis thaliana]

Seq. No. 17653

Contig ID 55565\_1.R1040 5'-most EST g5605943

 Method
 BLASTX

 NCBI GI
 g2213611

 BLAST score
 607

 E value
 4.0e-63

 Match length
 164



NCBI Description (AC000103) F21J9.5 [Arabidopsis thaliana]

Seq. No. 17654

% identity

Contig ID 55571\_1.R1040 5'-most EST leu701145294.h1

Method BLASTX
NCBI GI g2262159
BLAST score 696
E value 3.0e-73
Match length 187
% identity 67

NCBI Description (AC002329) predicted protein similar to S.pombe protein

C5H10.03 [Arabidopsis thaliana]

Seq. No. 17655

Contig ID 55576\_1.R1040 5'-most EST zzp700835611.h1

Method BLASTX
NCBI GI g4234955
BLAST score 183
E value 3.0e-13
Match length 73
% identity 49

NCBI Description (AF098971) NBS-LRR-like protein cD8 [Phaseolus vulgaris]

Seq. No. 17656

Contig ID 55596\_1.R1040 5'-most EST epx701109076.h1

Seq. No.

17657

Contig ID 55600 1.R1040

5'-most EST LIB3 $\overline{0}$ 6-104-Q1-K1-C4

Method BLASTX
NCBI GI g1076421
BLAST score 390
E value 8.0e-38
Match length 133
% identity 56

NCBI Description transcription factor TGA3 - Arabidopsis thaliana >qi 304113

(L10209) transcription factor [Arabidopsis thaliana]

Seq. No.

17658

Contig ID 55614 1.R1040 5'-most EST vzy700756233.h1

Method BLASTX
NCBI GI g2961346
BLAST score 1716
E value 0.0e+00
Match length 422
% identity 74

NCBI Description (AL022140) pectinesterase like protein [Arabidopsis

thaliana]

Seq. No.

17659

Contig ID 55617 1.R1040

5'-most EST jC-gmst02400027h04a1



Method BLASTX
NCBI GI g3212852
BLAST score 280
E value 8.0e-25
Match length 58
% identity 86

NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]

Seq. No. 17660

Contig ID 55618 1.R1040

5'-most EST LIB3106-104-Q1-K1-B12

Method BLASTN
NCBI GI g3821780
BLAST score 33
E value 6.0e-09
Match length 33
% identity 58

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 17661

Contig ID 55619 1.R1040

5'-most EST uC-gmrominsoy127a10b1

Method BLASTX
NCBI GI g3193293
BLAST score 450
E value 2.0e-44
Match length 269
% identity 44

NCBI Description (AF069298) contains a short region of similarity to another

Arabidopsis hypothetical protein F19K23.8 (GB:AC000375)

[Arabidopsis thaliana]

Seq. No. 17662

Contig ID 55620\_1.R1040 5'-most EST gsv701054025.h1

Seq. No. 17663

Contig ID 55632\_1.R1040 5'-most EST kl1701209260.h1

Method BLASTX
NCBI GI g3914467
BLAST score 250
E value 3.0e-21
Match length 121
% identity 50

NCBI Description 26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)

>gi\_1864003\_dbj\_BAA19252\_ (AB001422) 21D7 [Nicotiana

tabacum]

Seq. No. 17664

Contig ID 55641\_1.R1040

5'-most EST LIB3106-103-Q1-K1-F11

Method BLASTX
NCBI GI g2460203
BLAST score 217
E value 2.0e-17
Match length 116



% identity 42
NCBI Description (AF021244) coronatine-induced protein 1 [Arabidopsis thaliana]

Seq. No. 17665

Contig ID 55644\_1.R1040

5'-most EST LIB3106-103-Q1-K1-F5

Method BLASTX
NCBI GI 94006848
BLAST score 240
E value 3.0e-20
Match length 78
% identity 56

NCBI Description (AJ131433) selenocysteine methyltransferase [Astragalus

bisulcatus]

Seq. No. 17666

Contig ID 55656 1.R1040

5'-most EST LIB31 $\overline{0}$ 6-103-Q1-K1-D4

Seq. No. 17667

Contig ID 55658 1.R1040

5'-most EST jC-gmro02910020h05a1

Seq. No. 17668

Contig ID 55668\_1.R1040 5'-most EST jex700906346.h1

Seq. No. 17669

Contig ID 55668\_2.R1040 5'-most EST wrg700786485.h1

Seq. No. 17670

Contig ID 55673 1.R1040 5'-most EST fde700875958.h1

Method BLASTX
NCBI GI g3420052
BLAST score 264
E value 5.0e-23
Match length 63
% identity 78

NCBI Description (AC004680) putative ubiqinone reductase [Arabidopsis

thaliana]

Seq. No. 17671

Contig ID 55678 1.R1040

5'-most EST LIB3106-103-Q1-K1-C7

Seq. No. 17672

Contig ID 55679\_1.R1040

5'-most EST jC-gmf102220076e02a1

Method BLASTX
NCBI GI g2507455
BLAST score 2148
E value 0.0e+00
Match length 618
% identity 87



NCBI Description FORMATE--TETRAHYDROFOLATE LIGASE (FORMYLTETRAHYDROFOLATE

SYNTHETASE) (FHS) (FTHFS) >gi\_322401\_pir\_ A43350

formate--tetrahydrofolate ligase (EC 6.3.4.3) - spinach >gi\_170145 (M83940) 10-formyltetrahydrofolate synthetase [Spinacia oleracea]

Seq. No. 17673

Contig ID 55679 2.R1040

5'-most EST uC-gmrominsoy109a12b1

85

Method BLASTX
NCBI GI g2507455
BLAST score 455
E value 2.0e-45
Match length 102

NCBI Description FORMATE--TETRAHYDROFOLATE LIGASE (FORMYLTETRAHYDROFOLATE

SYNTHETASE) (FHS) (FTHFS) >gi\_322401\_pir\_A43350

formate--tetrahydrofolate ligase (EC 6.3.4.3) - spinach >gi\_170145 (M83940) 10-formyltetrahydrofolate synthetase

[Spinacia oleracea]

Seq. No. 17674

% identity

Contig ID 55679\_3.R1040 5'-most EST vwf700676443.h1

Method BLASTX
NCBI GI g2507455
BLAST score 223
E value 1.0e-18
Match length 53
% identity 79

% identity 79

NCBI Description FORMATE--TETRAHYDROFOLATE LIGASE (FORMYLTETRAHYDROFOLATE

SYNTHETASE) (FHS) (FTHFS) >gi\_322401\_pir\_A43350

formate--tetrahydrofolate ligase (EC 6.3.4.3) - spinach >gi\_170145 (M83940) 10-formyltetrahydrofolate synthetase

[Spinacia oleracea]

Seq. No. 17675

Contig ID 55685\_1.R1040 5'-most EST zsg701119584.h1

Method BLASTN
NCBI GI g18376
BLAST score 346
E value 0.0e+00
Match length 411
% identity 99

NCBI Description Glycine max PAL1 gene for phenylalanine ammonia lyase (EC

4.3.1.5)

Seq. No. 17676

Contig ID 55697 1.R1040 5'-most EST vzy700756474.h1

Seq. No. 17677 Contig ID 55701

55701 1.R1040

5'-most EST LIB3139-089-P1-N1-D8

Method BLASTX NCBI GI g4206210



BLAST score 566 E value 4.0e-58 Match length 162 % identity 65

NCBI Description (AF071527) putative calcium channel [Arabidopsis thaliana]

>gi\_4263043\_gb\_AAD15312 (AC005142) putative calcium

channel [Arabidopsis thaliana]

Seq. No. 17678

Contig ID 55701 2.R1040

5'-most EST jC-gmro02800031a01a1

Method BLASTX NCBI GI q4206210 BLAST score 600 E value 4.0e-62 Match length 188 % identity

(AF071527) putative calcium channel [Arabidopsis thaliana] NCBI Description

>gi\_4263043 gb\_AAD15312\_ (AC005142) putative calcium

channel [Arabidopsis thaliana]

Seq. No. 17679

Contig ID 55705 2.R1040

5'-most EST LIB3170-059-Q1-J1-C6

Seq. No. 17680

Contig ID 55712 1.R1040

5'-most EST g5688321

Seq. No. 17681

Contig ID 55717 1.R1040

5'-most EST LIB3106-102-Q1-K1-F12

Method BLASTN NCBI GI q2688829 BLAST score 141 E value 2.0e-73 Match length 341 % identity 85

NCBI Description Prunus armeniaca putative sugar transporter mRNA, complete

cds

Seq. No. 17682

Contig ID 55734 1.R1040

5'-most EST LIB3106-085-Q1-K1-B9

Method BLASTX NCBI GI g3193330 BLAST score 336 2.0e-31 E value Match length 125 % identity 54

NCBI Description (AF069299) contains similarity to Medicago sativa corC

(GB:L22305) [Arabidopsis thaliana]

Seq. No. 17683

55756 1.R1040 Contig ID 5'-most EST pcp700988887.h1

Method BLASTX



NCBI GI g4097585 BLAST score 472 E value 3.0e-47 Match length 148 % identity 62

NCBI Description (U64925) NTGP4 [Nicotiana tabacum]

Seq. No.

17684

Contig ID

55763 1.R1040

5'-most EST LIB3106-102-Q1-K1-A7

Seq. No. 17685

Contig ID 55763\_2.R1040 5'-most EST kl1701213211.h1

Seq. No. 17686

Contig ID 55764\_1.R1040 5'-most EST uC-gmropic110g07b1

Method BLASTX
NCBI GI g2739371
BLAST score 622
E value 9.0e-65
Match length 219
% identity 60

NCBI Description (AC002505) unknown protein [Arabidopsis thaliana]

Seq. No.

17687

Contig ID 5'-most EST

55768\_1.R1040 LIB3106-102-Q1-K1-A10

Method BLASTX NCBI GI g2213590

NCBI GI G2213590
BLAST score 422
E value 2.0e-41
Match length 149
% identity 54

NCBI Description (AC000348) T7N9.10 [Arabidopsis thaliana]

Seq. No. 17688

Contig ID 55775\_1.R1040 5'-most EST epx701104147.h1

Method BLASTX
NCBI GI g3928083
BLAST score 154
E value 5.0e-10
Match length 49
% identity 69

NCBI Description (AC005770) unknown protein [Arabidopsis thaliana]

Seq. No.

17689

Contig ID 55775\_2.R1040

5'-most EST LIB3106-101-Q1-K1-G6

Method BLASTX
NCBI GI g3928083
BLAST score 166
E value 2.0e-11
Match length 68
% identity 57



NCBI Description (AC005770) unknown protein [Arabidopsis thaliana]

Seq. No. 17690 Contig ID 55775

Contig ID 55775\_3.R1040 5'-most EST cfl700863584.h1

Method BLASTX
NCBI GI g3928083
BLAST score 484
E value 1.0e-48
Match length 137
% identity 66

NCBI Description (AC005770) unknown protein [Arabidopsis thaliana]

Seq. No. 17691

Contig ID 55794 1.R1040

5'-most EST LIB3106-101-Q1-K1-F11

Seq. No. 17692

Contig ID 55796 1.R1040

5'-most EST uC-gmrominsoy126a02b1

Seq. No. 17693

Contig ID 55797 1.R1040

5'-most EST LIB3106-101-Q1-K1-F4

Seq. No. 17694

Contig ID 55804\_1.R1040 5'-most EST zsg701129983.h1

Seq. No. 17695

Contig ID 55807 1.R1040

5'-most EST LIB3106-101-Q1-K1-D6

Method BLASTN
NCBI GI g255576
BLAST score 86
E value 2.0e-40
Match length 239
% identity 84

NCBI Description small auxin up RNA gene cluster: orf 6B [Glycine

max=soybeans, cv. Wayne, Genomic, 665 nt]

Seq. No. 17696

Contig ID 55810 1.R1040

5'-most EST jC-gmle01810004e03a1 Method BLASTX

Method BLASTX
NCBI GI 94056506
BLAST score 256
E value 7.0e-37
Match length 125
% identity 68

NCBI Description (AC005896) nodulin-like protein [Arabidopsis thaliana]

Seq. No.

17697

Contig ID 55823\_1.R1040

5'-most EST LIB3106-101-Q1-K1-C2

Seq. No. 17698



Contig ID 55833\_1.R1040

5'-most EST jC-gmst02400043g05a1

Method BLASTX
NCBI GI g4544399
BLAST score 843
E value 2.0e-90
Match length 306
% identity 54

NCBI Description (AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis

thaliana]

Seq. No. 17699

Contig ID 55850 1.R1040

5'-most EST LIB31 $\overline{0}$ 6-100-Q1-K1-G3

Method BLASTX
NCBI GI g1931640
BLAST score 474
E value 2.0e-47
Match length 154
% identity 60

NCBI Description (U95973) Serine carboxypeptidase isolog [Arabidopsis

thaliana]

Seq. No. 17700

Contig ID 55853\_1.R1040 5'-most EST fde700871136.h1

Method BLASTX
NCBI GI g3176675
BLAST score 345
E value 4.0e-32
Match length 173
% identity 45

NCBI Description (AC003671) F1707.4 [Arabidopsis thaliana]

Seq. No. 17701

Contig ID 55853\_2.R1040 5'-most EST trc700563369.h1

Seq. No. 17702

Contig ID 55859 1.R1040 5'-most EST wvk700686568.h1

Seq. No. 17703

Contig ID 55862\_1.R1040

5'-most EST uC-gmronoir063b06b1

Seq. No. 17704

Contig ID 55864\_1.R1040 5'-most EST jex700907682.h1

Method BLASTX
NCBI GI g2979555
BLAST score 535
E value 2.0e-54
Match length 225
% identity 49

NCBI Description (AC003680) unknown protein [Arabidopsis thaliana]

```
Seq. No.
                   17705
Contig ID
                   55865 1.R1040
5'-most EST
                   LIB3106-100-Q1-K1-E9
Method
                   BLASTN
NCBI GI
                   g4220640
BLAST score
                   36
E value
                   1.0e-10
Match length
                   44
% identity
                   48
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                   MPE11, complete sequence [Arabidopsis thaliana]
Seq. No.
                   17706
Contig ID
                   55878 1.R1040
                   LIB3106-100-Q1-K1-D10
5'-most EST
Seq. No.
                   17707
Contig ID
                   55879 1.R1040
5'-most EST
                   pmv700892043.hl
Method
                   BLASTX
NCBI GI
                   q3152598
BLAST score
                   205
E value
                   5.0e-16
Match length
                   61
% identity
                   67
NCBI Description
                   (AC002986) Contains similarity to C2-HC type zinc finger
                   protein C.e-MyT1 gb U67079 from C. elegans and to
                   hypersensitivity-related gene 201 isolog T28M21.14 from A.
                   thaliana BAC gb_AF002109. [Arabidopsis thaliana]
Seq. No.
                   17708
Contig ID
                   55882 1.R1040
5'-most EST
                   uC-gmropic113b12b1
Method
                  BLASTX
NCBI GI
                   g3176874
BLAST score
                   315
E value
                   6.0e-29
Match length
                  101
% identity
                   (AF065639) cucumisin-like serine protease [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  17709
Contig ID
                  55886_1.R1040
5'-most EST
                  jsh701069702.h1
Seq. No.
                  17710
Contig ID
                  55893 1.R1040
```

Contig ID 55893 1.R1040 5'-most EST leu701155513.h1

Method BLASTX
NCBI GI g3600054
BLAST score 441
E value 2.0e-43
Match length 179
% identity 42

NCBI Description (AF080120) No definition line found [Arabidopsis thaliana]



Seq. No. 17711

Contig ID 55906\_1.R1040 5'-most EST sat701012165.h1

Method BLASTX
NCBI GI 9464987
BLAST score 758
E value 2.0e-80
Match length 148
% identity 94

NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD 10 (UBIQUITIN-PROTEIN

LIGASE 10) (UBIQUITIN CARRIER PROTEIN 10)

>gi\_421858\_pir\_\_S32672 ubiquitin--protein ligase (EC

6.3.2.19) UBC10 - Arabidopsis thaliana

>gi\_297878\_emb\_CAA78715\_ (Z14991) ubiquitin conjugating
enzyme [Arabidopsis thaliana] >gi\_349213 (L00640) ubiquitin

conjugating enzyme [Arabidopsis thaliana]

Seq. No. 17712

Contig ID 55919 1.R1040

5'-most EST LIB3138-106-Q1-N1-G7

Method BLASTX
NCBI GI g2245066
BLAST score 1038
E value 1.0e-113
Match length 295
% identity 66

NCBI Description (Z97342) Beta-Amylase [Arabidopsis thaliana]

Seq. No. 17713

Contig ID 55925\_1.R1040

5'-most EST LIB3106-099-Q1-K1-G1

Method BLASTX
NCBI GI g3372230
BLAST score 148
E value 2.0e-09
Match length 45
% identity 60

NCBI Description (AF017074) RNA polymerase I, II and III 16.5 kDa subunit

[Arabidopsis thaliana]

Seq. No. 17714

Contig ID 55925 2.R1040 5'-most EST sat701005816.h1

Method BLASTX
NCBI GI g3372230
BLAST score 182
E value 2.0e-13
Match length 64
% identity 50

NCBI Description (AF017074) RNA polymerase I, II and III 16.5 kDa subunit

[Arabidopsis thaliana]

Seq. No. 17715

Contig ID 55930\_1.R1040 5'-most EST leu701150491.h1

Seq. No. 17716

NCBI GI

E value

BLAST score



```
Contig ID
                   55930 2.R1040
 5'-most EST
                   LIB3107-033-01-K1-F10
 Seq. No.
                   17717
 Contig ID
                   55932 1.R1040
 5'-most EST
                   LIB3138-045-Q1-N1-G5
Seq. No.
                   17718
Contig ID
                   55947 1.R1040
5'-most EST
                   epx701103892.h1
Method
                   BLASTX
NCBI GI
                   q2341033
BLAST score
                   219
E value
                   8.0e-18
Match length
                   53
% identity
                   74
NCBI Description
                   (AC000104) Similar to Babesia aldo-keto reductase
                   (gb_M93122). [Arabidopsis thaliana]
Seq. No.
                   17719
Contiq ID
                   55954 1.R1040
5'-most EST
                   LIB3106-099-Q1-K1-E3
Seq. No.
                   17720
Contig ID
                   55957 1.R1040
5'-most EST
                   jC-gmle01810070d11d1
Method
                   BLASTX
NCBI GI
                   q2494280
BLAST score
                   623
E value
                   9.0e-65
Match length
                   244
% identity
                   63
                   ELONGATION FACTOR TS (EF-TS) >gi_1653231_dbj_BAA18146_
NCBI Description
                   (D90912) elongation factor TS [Synechocystis sp.]
Seq. No.
                   17721
                   55958 1.R1040
Contig ID
5'-most EST
                   LIB3106-099-Q1-K1-D2
Seq. No.
                   17722
Contig ID
                   55963 1.R1040
5'-most EST
                   LIB3106-099-Q1-K1-D8
Method
                   BLASTX
NCBI GI
                   g4006891
BLAST score
                   256
E value
                   6.0e-22
Match length
                   77
% identity
                   62
NCBI Description (Z99708) putative protein [Arabidopsis thaliana]
Seq. No.
                   17723
Contig ID
                   55963 2.R1040
5'-most EST
                  pcp700990153.h1
Method
                  BLASTX
```

q4006891

3.0e-20



Match length % identity 61

NCBI Description (Z99708) putative protein [Arabidopsis thaliana]

Seq. No. 17724

55979 1.R1040 Contig ID 5'-most EST wvk700685539.hl

17725 Seq. No.

Contig ID 55995 1.R1040 5'-most EST g4305<del>5</del>03

Seq. No.

Contig ID 56021 1.R1040

5'-most EST LIB3106-098-Q1-K1-B5

17726

Seq. No. 17727

Contig ID 56023 1.R1040

5'-most EST LIB3106-098-Q1-K1-F2

Seq. No. 17728

Contig ID 56024 1.R1040 5'-most EST kl1701207338.h1

Seq. No. 17729

Contig ID 56025 1.R1040 5'-most EST fua701041076.h1

Seq. No. 17730

Contig ID 56028 1.R1040

5'-most EST LIB3106-098-Q1-K1-F8

Seq. No. 17731

Contig ID 56033 1.R1040

5'-most EST LIB3106-098-Q1-K1-D1

Method BLASTX NCBI GI q4558563 BLAST score 304 E value 3.0e-27 Match length 127 % identity 54

NCBI Description (AC007138) putative NifU-like metallocluster assembly

factor [Arabidopsis thaliana]

Seq. No. 17732

Contig ID 56065 1.R1040

5'-most EST LIB3106-098-Q1-K1-C7

Seq. No.

17733

Contig ID 56084 1.R1040 5'-most EST LIB3106-097-Q1-K1-G3

Method BLASTN NCBI GI g3821780 BLAST score 36

E value 1.0e-10 Match length 37 % identity 61



## NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 17734

Contig ID 56090 1.R1040

5'-most EST LIB3106-097-Q1-K1-H1

Method BLASTX
NCBI GI g3980413
BLAST score 1042
E value 1.0e-134
Match length 399
% identity 32

NCBI Description (AC004561) pumilio-like protein [Arabidopsis thaliana]

Seq. No. 17735

Contig ID 56099\_1.R1040 5'-most EST uC-gmronoir065e02b1

Seq. No. 17736

Contig ID 56104 1.R1040

5'-most EST LIB3106-097-Q1-K1-F2

Seq. No. 17737

Contig ID 56110\_1.R1040 5'-most EST sat701008622.h1

Method BLASTX
NCBI GI g2654559
BLAST score 355
E value 3.0e-33
Match length 192
% identity 38

NCBI Description (AF006621) embryonic lung protein [Homo sapiens]

Seq. No.

Contig ID 56120\_1.R1040 5'-most EST hrw701060701.h1

17738

Method BLASTX
NCBI GI g3646375
BLAST score 150
E value 2.0e-09
Match length 41
% identity 66

NCBI Description (AJ011079) RGP2 protein [Oryza sativa]

Seq. No. 17739

Contig ID 56120\_2.R1040 5'-most EST eep700864022.h1

Seq. No. 17740

Contig ID 56122 1.R1040

5'-most EST LIB3106-097-Q1-K1-E1

Seq. No. 17741

Contig ID 56124 1.R1040

5'-most EST ASG3244V4R-02-Q1-E1-B6

Seq. No. 17742

Contig ID 56135\_1.R1040



5'-most EST uC-gmflminsoy021c01b1

Method BLASTN
NCBI GI g3128143
BLAST score 47
E value 9.0e-17
Match length 220
% identity 83

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MTI20, complete sequence [Arabidopsis thaliana]

Seq. No. 17743

Contig ID 56137 1.R1040

5'-most EST LIB3109-002-Q1-K3-B7

Method BLASTX
NCBI GI g4454481
BLAST score 155
E value 3.0e-10
Match length 92
% identity 38

NCBI Description (AC006234) unknown protein [Arabidopsis thaliana]

>gi 4512647 gb AAD21702.1 (AC007048) unknown protein

[Arabidopsis thaliana]

Seq. No. 17744

Contig ID 56137\_2.R1040

5'-most EST LIB3106-097-Q1-K1-C4

Method BLASTX
NCBI GI g4454481
BLAST score 151
E value 7.0e-10
Match length 83
% identity 37

NCBI Description (AC006234) unknown protein [Arabidopsis thaliana]

>gi\_4512647\_gb\_AAD21702.1\_ (AC007048) unknown protein

[Arabidopsis thaliana]

Seq. No. 17745

Contig ID 56137 3.R1040

5'-most EST LIB3109-003-Q1-K1-E8

Seq. No. 17746

Contig ID 56164\_1.R1040

5'-most EST LIB3106-096-Q1-K1-G9

Method BLASTX
NCBI GI g4204812
BLAST score 197
E value 7.0e-15
Match length 85
% identity 49

NCBI Description (U52519) actin [Girardia tigrina]

Seq. No. 17747

Contig ID 56164\_2.R1040

5'-most EST uC-gmflminsoy053a07b1

Method BLASTX NCBI GI g84000 BLAST score 160



```
1.0e-10
E value
Match length
                  60
% identity
                  50
NCBI Description
                  actin 2 - Trypanosoma brucei
                  17748
Seq. No.
Contig ID
                  56170 1.R1040
5'-most EST
                  uC-gmronoir065f01b1
                  BLASTX
Method
NCBI GI
                  g1255951
BLAST score
                  514
E value
                  3.0e-52
Match length
                  130
% identity
                  75
                  (X96932) PS60 [Nicotiana tabacum]
NCBI Description
                  17749
Seq. No.
Contig ID
                  56170 2.R1040
                  fua701038089.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g1255951
BLAST score
                  501
E value
                  7.0e-51
Match length
                  117
% identity
                  81
NCBI Description
                  (X96932) PS60 [Nicotiana tabacum]
                  17750
Seq. No.
Contig ID
                  56170 3.R1040
                  LIB3106-096-Q1-K1-G12
5'-most EST
                  BLASTX
Method
                  g1255951
NCBI GI
BLAST score
                  345
E value
                  2.0e-32
Match length
                  70
% identity
                  89
                  (X96932) PS60 [Nicotiana tabacum]
NCBI Description
                  17751
Seq. No.
                  56170 4.R1040
Contig ID
5'-most EST
                  q4302107
Method
                  BLASTX
                  g4539350
NCBI GI
BLAST score
                  130
                  3.0e-11
E value
                  72
Match length
% identity
                  65
                  (AL035539) putative pectinesterase [Arabidopsis thaliana]
NCBI Description
```

17752 Seq. No.

56170 5.R1040 Contig ID vzy700751457.hl 5'-most EST

BLASTX Method g128592 NCBI GI BLAST score 143 3.0e-09 E value Match length 55



```
% identity
NCBI Description
                   POLLEN-SPECIFIC PROTEIN NTP303 PRECURSOR
                   >gi_82190_pir__S22495 pollen-specific protein precursor -
                   common tobacco >gi_19902_emb_CAA43454_ (X61146) pollen
                   specific protein [Nicotiana tabacum]
Seq. No.
                   17753
Contig ID
                   56181 1.R1040
5'-most EST
                  LIB3106-096-Q1-K1-F3
Seq. No.
                   17754
Contig ID
                   56194 1.R1040
5'-most EST
                   LIB3106-096-Q1-K1-D10
Seq. No.
                   17755
Contig ID
                   56234 1.R1040
5'-most EST
                   LIB3106-095-Q1-K1-F9
Seq. No.
                   17756
Contig ID
                   56241 1.R1040
5'-most EST
                   jC-gmst02400036c11d2
                   17757
Seq. No.
Contig ID
                   56256_1.R1040
                   LIB31\overline{0}9-050-Q1-K1-G1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3036816
BLAST score
                   224
E value
                   4.0e-18
                   106
Match length
% identity
                   47
NCBI Description
                   (AL022373) myosin-like protein [Arabidopsis thaliana]
Seq. No.
                   17758
Contig ID
                   56261 1.R1040
5'-most EST
                   seb700651453.h1
                   17759
Seq. No.
Contig ID
                   56269 1.R1040
5'-most EST
                   q5752727
Method
                   BLASTN
NCBI GI
                   q438216
BLAST score
                   191
E value
                   1.0e-103
Match length
                   375
% identity
                   88
```

NCBI Description

P.sativum mRNA for T subunit of glycine decarboxylase

multi-enzyme complex

Seq. No. 17760 56269 2.R1040 Contig ID 5'-most EST q4277008 Method BLASTX NCBI GI g3915699 BLAST score 383 1.0e-36 E value Match length 148



% identity NCBI Description

AMINOMETHYLTRANSFERASE PRECURSOR (GLYCINE CLEAVAGE SYSTEM T

PROTEIN) >gi\_541970\_pir\_\_S40260 T-protein - garden pea >gi\_1362061\_pir\_\_S56661 glycine decarboxylase T protein precursor - garden pea >gi\_438217\_emb\_CAA81080\_(Z25861) T-protein [Pisum sativum] >gi\_3021553\_emb\_CAA10976

(AJ222771) T protein [Pisum sativum]

Seq. No. 17761

Contig ID 56281 1.R1040

5'-most EST LIB3106-095-Q1-K1-A3

Method BLASTX
NCBI GI g732189
BLAST score 351
E value 4.0e-33
Match length 141
% identity 50

NCBI Description HYPOTHETICAL 49.1 KD PROTEIN IN SSB2-SPX18 INTERGENIC

REGION >gi\_2131922\_pir\_\_S50724 hypothetical protein YNL207w - yeast (Saccharomyces cerevisiae) >gi 600058 emb CAA55501

(X78898) N1342 [Saccharomyces cerevisiae]

>gi\_1302211\_emb\_CAA96109\_ (Z71483) ORF YNL207w

[Saccharomyces cerevisiae]

Seq. No. 17762

Contig ID 56287 1.R1040

5'-most EST LIB3106-095-Q1-K1-B10

Method BLASTX
NCBI GI g4063751
BLAST score 235
E value 2.0e-19
Match length 173
% identity 31

NCBI Description (AC005851) putative white protein [Arabidopsis thaliana]

>gi 4510409 gb AAD21495.1 (AC006929) putative white

protein [Arabidopsis thaliana]

Seq. No. 17763

Contig ID 56297 1.R1040

5'-most EST LIB3106-094-Q1-K1-G8

Method BLASTX
NCBI GI g3482967
BLAST score 754
E value 2.0e-80
Match length 168
% identity 80

NCBI Description (AL031369) Protein phosphatase 2C-like protein [Arabidopsis

thaliana] >gi\_4559345 gb AAD23006.1 AC006585 1 (AC006585)

protein phosphatase 2C [Arabidopsis thaliana]

Seq. No. 17764

Contig ID 56301\_1.R1040

5'-most EST LIB3106-094-Q1-K1-H12

Seq. No. 17765

Contig ID 56321\_1.R1040 5'-most EST epx701104557.h1



Method BLASTX
NCBI GI g953179
BLAST score 166
E value 2.0e-11
Match length 49
% identity 63

NCBI Description (Z37980) ORF14 [Escherichia coli]

Seq. No. 17766

Contig ID 56327\_1.R1040

5'-most EST LIB3106-094-Q1-K1-G5

Method BLASTX
NCBI GI g1708972
BLAST score 222
E value 2.0e-21
Match length 119
% identity 41

NCBI Description (R)-MANDELONITRILE LYASE ISOFORM 3 PRECURSOR

(HYDROXYNITRILE LYASE 3) ((R)-OXYNITRILASE 3) >gi\_1262279

(U51562) (R)-(+)-mandelonitrile lyase isoform MDL $\overline{3}$  precursor [Prunus serotina] >qi 2343181 (AF013161)

(R)-(+)-mandelonitrile lyase isoform MDL3 precursor [Prunus

serotina]

Seq. No. 17767

Contig ID 56340 1.R1040

5'-most EST LIB3109-038-Q1-K1-G7

Method BLASTX
NCBI GI g1652591
BLAST score 151
E value 2.0e-09
Match length 127
% identity 37

NCBI Description (D90906) chloroplast import-associated channel IAP75

[Synechocystis sp.]

Seq. No. 17768

Contig ID 56340\_2.R1040 5'-most EST kmv700739033.h1

Seq. No. 17769

Contig ID 56342\_1.R1040
5'-most EST g5509044
Method BLASTX
NCBI GI g4262181
BLAST score 234

E value 3.0e-19
Match length 170
% identity 42

NCBI Description (AC005508) 37496 [Arabidopsis thaliana]

Seq. No. 17770

Contig ID 56342 2.R1040 5'-most EST xpa700792368.h1

Seq. No. 17771

Contig ID 56355 1.R1040



5'-most EST taw700657264.h1

Seq. No. 17772

Contig ID 56358 1.R1040

5'-most EST LIB3107-055-Q1-K1-E2

Seq. No. 17773

Contig ID 56401\_1.R1040

5'-most EST LIB3106-079-P1-K1-F10

Method BLASTX
NCBI GI g1703088
BLAST score 340
E value 1.0e-31
Match length 112

% identity 66

NCBI Description ACYL CARRIER PROTEIN 4 PRECURSOR (ACP)

>gi 1166431 emb CAA64542 (X95253) acyl carrier protein

[Cuphea lanceolata]

Seq. No. 17774

Contig ID 56402 1.R1040

5'-most EST LIB3106-093-Q1-K1-G6

Seq. No. 17775

Contig ID 56420\_1.R1040 5'-most EST kmv700741892.h1

Method BLASTX
NCBI GI g115766
BLAST score 245
E value 8.0e-21
Match length 63
% identity 71

NCBI Description

CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE II PRECURSOR (CAB) >gi\_82243\_pir\_\_S00442 chlorophyll a/b-binding protein

precursor - garden petunia >gi\_169214 (M21317) chlorophyll

binding protein precursor [Petunia hybrida]

>gi\_226259 prf 1503272A chlorophyll binding protein

[Petunia sp.]

Seq. No. 17776

Contig ID 56434 1.R1040

5'-most EST LIB3106-093-Q1-K1-D6

Method BLASTX
NCBI GI g4567319
BLAST score 469
E value 3.0e-95
Match length 214
% identity 78

NCBI Description (AC005956) putative copper amine oxidase [Arabidopsis

thaliana]

Seq. No. 17777

Contig ID 56465\_1.R1040

5'-most EST LIB3106-092-Q1-K1-G7

Seq. No. 17778

Contig ID 56471 1.R1040



5'-most EST ncj700980958.h1 Method BLASTX NCBI GI q2696611 BLAST score 160 5.0e-11 E value Match length 68 % identity 50 NCBI Description (D78303) RNA splicing-related protein [Rattus norvegicus] Seq. No. 17779 Contig ID 56486 1.R1040 5'-most EST sat701012915.h1 Method BLASTX g4056507 NCBI GI BLAST score 281 E value 4.0e-25 Match length 98 % identity 62 NCBI Description (AC005896) putative RNA binding protein [Arabidopsis thaliana] Seq. No. 17780 Contig ID 56489 1.R1040 5'-most EST LIB3106-092-Q1-K1-G6 Seq. No. 17781 Contig ID 56490 1.R1040 5'-most EST fua701040309.h1 Method BLASTX g1076748 NCBI GI BLAST score 506 E value 1.0e-53 Match length 208 % identity 50 NCBI Description major intrinsic protein - rice >gi 440869 dbj BAA04257 (D17443) major intrinsic protein [Oryza sativa] Seq. No. 17782 Contig ID 56505 1.R1040 5'-most EST LIB3106-092-01-K1-E4 Method BLASTX NCBI GI g4512698 BLAST score 417 E value 1.0e-50 Match length 124 % identity 82 NCBI Description (AC006569) hypothetical protein [Arabidopsis thaliana] Seq. No. 17783 56516 1.R1040 Contig ID 5'-most EST bnu700967675.h1 BLASTN Method

Contig ID 56516\_1.R10
5'-most EST bnu70096767
Method BLASTN
NCBI GI g703235
BLAST score 43
E value 8.0e-15
Match length 87
% identity 87



NCBI Description Pisum sativum outer membrane protein (OM14) mRNA, complete

17784 Seq. No.

Contig ID 56516 2.R1040 5'-most EST g5752759 Method BLASTN NCBI GI g703235 BLAST score 47 E value 2.0e-17 Match length 123

% identity NCBI Description Pisum sativum outer membrane protein (OM14) mRNA, complete

85

Seq. No. 17785

Contig ID 56520 3.R1040 5'-most EST hyd700727804.h1

Seq. No. 17786

Contig ID 56522 1.R1040 5'-most EST zpv700759163.h1

Method BLASTX NCBI GI g3157938 BLAST score 270 E value 9.0e-24 Match length 121 % identity 54

NCBI Description (AC002131) Similar to seryl-tRNA synthetase gb\_U10400 from

S cerevisiae. EST gb N96627 comes from this gene.

[Arabidopsis thaliana]

Seq. No. 17787

Contig ID 56546 1.R1040

5'-most EST LIB3106-091-Q1-K1-G3

Seq. No. 17788

Contig ID 56554 1.R1040

5'-most EST jC-gmfl02220115f07a1

Seq. No. 17789

Contig ID 56554 2.R1040 5'-most EST asn701135932.h1

Seq. No. 17790

Contig ID 56561 1.R1040

5'-most EST LIB3106-091-Q1-K1-E2

Method BLASTX NCBI GI g3395427 BLAST score 105 E value 2.0e-10 Match length 47 % identity 61

NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]

Seq. No. 17791

56562\_1.R1040 Contig ID



```
5'-most EST
                   wrg700787762.h2
Method
                   BLASTX
NCBI GI
                   q4151066
BLAST score
                   760
E value
                   1.0e-101
Match length
                   207
% identity
                   87
                  (Y10861) ribonucleotide reductase [Nicotiana tabacum]
NCBI Description
Seq. No.
                   17792
Contig ID
                   56563 1.R1040
5'-most EST
                   eep700864880.hl
Method
                  BLASTX
NCBI GI
                  q1871187
BLAST score
                   170
E value
                   8.0e-12
Match length
                  72
% identity
                   57
NCBI Description
                  (U90439) unknown protein [Arabidopsis thaliana]
Seq. No.
                  17793
Contig ID
                  56570 1.R1040
5'-most EST
                  LIB3106-005-Q1-K1-H2
Method
                  BLASTX
NCBI GI
                  q2293360
BLAST score
                  166
E value
                  2.0e-11
Match length
                  76
% identity
                  47
NCBI Description
                  (D87670) polyphenol oxidase [Malus domestica]
Seq. No.
                  17794
Contig ID
                  56582 1.R1040
5'-most EST
                  sat701005906.h1
Seq. No.
                  17795
                  56582 2.R1040
Contig ID
5'-most EST
                  jC-gmf102220063d03a1
Seq. No.
                  17796
Contig ID
                  56584 1.R1040
5'-most EST
                  LIB3106-091-Q1-K1-C9
Method
                  BLASTN
NCBI GI
                  g2760170
BLAST score
                  35
                  5.0e-10
                  87
                  85
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MIO24, complete sequence [Arabidopsis thaliana]
```

E value Match length % identity

Seq. No. 17797

Contig ID 56596 1.R1040 5'-most EST trc700566783.h1

Seq. No. 17798

Contig ID 56623 1.R1040

Match length

NCBI Description

% identity

160

40



```
5'-most EST
                   LIB3106-090-01-K1-F8
Method
                   BLASTX
NCBI GI
                   q547199
BLAST score
                   207
E value
                   7.0e-16
Match length
                   172
% identity
                   33
NCBI Description
                  BPI=bactericidal/permeability-increasing protein [human,
                   HL-60 cells, Peptide, 487 aa]
Seq. No.
                   17799
Contig ID
                   56629 1.R1040
5'-most EST
                   LIB3106-090-Q1-K1-G2
Seq. No.
                   17800
Contig ID
                   56630 1.R1040
5'-most EST
                   LIB3106-090-Q1-K1-F11
Method
                   BLASTX
NCBI GI
                   g3850072
BLAST score
                   248
                   5.0e-21
E value
Match length
                   114
% identity
                   44
                   (AL033385) dna-directed rna polymerase iii subunit
NCBI Description
                   [Schizosaccharomyces pombe]
Seq. No.
                   17801
Contig ID
                   56632 1.R1040
5'-most EST
                  ncj700975505.h1
Method
                  BLASTX
NCBI GI
                   q4490733
BLAST score
                   237
E value
                  8.0e-20
Match length
                  97
% identity
                  51
                  (AL035709) putative protein [Arabidopsis thaliana]
NCBI Description
                  17802
Seq. No.
                  56635 1.R1040
Contig ID
5'-most EST
                  LIB3109-021-Q1-K1-D9
Seq. No.
                  17803
Contig ID
                  56635 3.R1040
5'-most EST
                  g4303451
Seq. No.
                  17804
                  56644 1.R1040
Contig ID
5'-most EST
                  zhf700951746.h1
Method
                  BLASTX
NCBI GI
                  g1109830
BLAST score
                  272
E value
                  9.0e-24
```

(U41534) coded for by C. elegans cDNA CEESI42F; Similar to helicases of SNF2/RAD54 family. [Caenorhabditis elegans]



```
17805
Seq. No.
Contig ID
                  56647 1.R1040
5'-most EST
                  LIB3106-090-Q1-K1-D8
Seq. No.
                  17806
Contig ID
                  56655 1.R1040
5'-most EST
                  LIB3106-010-Q1-K1-A3
Seq. No.
                  17807
Contig ID
                  56666_1.R1040
5'-most EST
                  uC-gmrominsoy229d10b1
Method
                  BLASTX
NCBI GI
                  q1935019
BLAST score
                  512
E value
                  3.0e-52
Match length
                  110
% identity
                  91
NCBI Description (Z93774) sucrose transport protein [Vicia faba]
Seq. No.
                  17808
                  56675 1.R1040
Contig ID
5'-most EST
                  pmv700891208.h1
Method
                  BLASTX
NCBI GI
                  g1771158
BLAST score
                  348
E value
                  7.0e-33
Match length
                  138
% identity
                  27
NCBI Description (Y07861) MFP1 protein [Lycopersicon esculentum]
                  17809
Seq. No.
Contig ID
                  56677 1.R1040
5'-most EST
                  LIB3106-089-Q1-K1-H2
Seq. No.
                  17810
Contig ID
                  56684 1.R1040
5'-most EST
                  LIB3170-041-Q1-K1-C7
Method
                  BLASTX
NCBI GI
                  g549725
BLAST score
                  161
E value
                  9.0e-11
Match length
                  74
% identity
                  42
NCBI Description
                  NADH-CYTOCHROME B5 REDUCTASE PRECURSOR (P34/P32)
                  >gi_481119 pir S37800 cytochrome-b5 reductase (EC
                  1.6.2.2), mitochondrial outer membrane form - yeast
                  (Saccharomyces cerevisiae) >gi_407497_emb_CAA81503_
                  (Z26877) unknown [Saccharomyces cerevisiae]
```

(X81474) NADH-cytochrome b5 reductase [Saccharomyces cerevisiae] >gi\_1582554 prf 2118404Q ORF [Saccharomyces cerevisiae] Seq. No. 17811

56691 1.R1040 Contig ID 5'-most EST zhf700957571.h1

>gi\_486258\_emb\_CAA81991\_ (Z28150) ORF YKL150w

[Saccharomyces cerevisiae] >gi\_1490392\_emb\_CAA57227



```
Method
                   BLASTX
NCBI GI
                   g1071913
BLAST score
                   1368
E value
                   1.0e-152
                   368
Match length
                   74
% identity
```

NCBI Description cysteine synthase (EC 4.2.99.8) C precursor, mitochondrial - spinach >qi 1066153 dbj BAA07177 (D37963) cysteine

synthase [Spinacia oleracea]

17812 Seq. No.

56714 1.R1040 Contig ID

5'-most EST LIB3106-089-Q1-K1-E6

Seq. No. 17813

56726 1.R1040 Contig ID 5'-most EST g5057842

Seq. No.

17814 56751 1.R1040 Contig ID

5'-most EST LIB3139-014-P1-N1-H5

17815 Seq. No.

Contig ID 56756\_1.R1040

5'-most EST LIB3106-088-Q1-K1-G7

Method BLASTX g4580398 NCBI GI BLAST score 268 E value 2.0e-23 Match length 117 52 % identity

(AC007171) putative protein kinase APK1A [Arabidopsis NCBI Description

thaliana]

Seq. No.

17816 Contig ID 56760 1.R1040

5'-most EST LIB3106-088-Q1-K1-H2

Seq. No.

17817

56768 1.R1040 Contig ID 5'-most EST q5607053 Method BLASTN NCBI GI g1087110 BLAST score 190 E value 1.0e-102

Match length 538 % identity

NCBI Description Rac13=21.8 kda GTP-binding protein [Gossypium

hirsutum=cotton plants, cv. Acala SJ-2, boll fibers, mRNA

Partial, 913 nt]

Seq. No.

17818

Contig ID

56776 1.R1040

5'-most EST

LIB3106-088-Q1-K1-F4

Seq. No.

17819

Contig ID

56805 1.R1040



5'-most EST LIB3107-065-Q1-K1-A10

Method BLASTN
NCBI GI g1305530
BLAST score 37
E value 3.0e-11
Match length 85
% identity 86

NCBI Description Solanum lycopersicum defective chloroplasts and leaves

(DCL) mRNA, complete cds

Seq. No. 17820

Contig ID 56810\_1.R1040

5'-most EST uC-gmrominsoy320a12b1

Method BLASTX
NCBI GI 9464846
BLAST score 572
E value 3.0e-68
Match length 135
% identity 92

NCBI Description TUBULIN ALPHA-6 CHAIN >gi 322880 pir S28983 tubulin

alpha-6 chain - maize >gi 22158 emb CAA44863 (X63178)

alpha-tubulin #6 [Zea mays]

Seq. No. 17821

Contig ID 56810 2.R1040 5'-most EST kmv700738679.h1

Method BLASTX
NCBI GI g464846
BLAST score 265
E value 2.0e-23
Match length 68
% identity 72

NCBI Description TUBULIN ALPHA-6 CHAIN >gi\_322880\_pir\_\_S28983 tubulin

alpha-6 chain - maize >gi\_22158\_emb\_CAA44863\_ (X63178)

alpha-tubulin #6 [Zea mays]

Seq. No. 17822

Contig ID 56813\_1.R1040 5'-most EST ncj700984326.h1

Method BLASTX
NCBI GI g4220445
BLAST score 182
E value 3.0e-13
Match length 169
% identity 4

NCBI Description (AC006216) Similar to gi\_3004555 F19F24.14 salt inducible

protein homolog from Arabidopsis thaliana BAC gb AC003673.

[Arabidopsis thaliana]

Seq. No. 17823

Contig ID 56819\_1.R1040 5'-most EST leu701156633.h1

Method BLASTX
NCBI GI g2275202
BLAST score 450
E value 2.0e-44
Match length 217



% identity (AC002337) acyl-CoA synthetase isolog [Arabidopsis NCBI Description

thaliana]

Seq. No. 17824 56821 1.R1040 Contiq ID

5'-most EST jC-qmf102220051b08a1

Method BLASTX q3461814 NCBI GI BLAST score 295 2.0e-26 E value

Match length 84 % identity

(AC004138) hypothetical protein [Arabidopsis thaliana] NCBI Description

Seq. No. 17825

56844 1.R1040 Contig ID vwf700673822.h1 5'-most EST

Seq. No. 17826

Contig ID 56846 1.R1040

LIB3106-087-Q1-K1-F9 5'-most EST

Seq. No. 17827

56854 1.R1040 Contig ID 5'-most EST pcp700994208.h1

BLASTX Method q1498229 NCBI GI 208 BLAST score 4.0e-16 E value Match length 73

52 % identity

NCBI Description (X98743) RNA helicase [Homo sapiens]

Seq. No.

Contig ID 56854 2.R1040

5'-most EST jC-gmro02910027g12a1

17828

Method BLASTX NCBI GI g2827700 BLAST score 612 9.0e-64 E value Match length 160 % identity 74

(AL021684) DEAD box ATP dependent helicase protein NCBI Description

[Arabidopsis thaliana]

Seq. No.

Contig ID 56854 3.R1040 5'-most EST uC-gmropic091f08b1

17829

Seq. No.

17830

56854 5.R1040 Contig ID 5'-most EST uC-gmropic017g03b1

Seq. No.

17831

56862 1.R1040 Contig ID 5'-most EST kl1701206459.h1



Method BLASTX
NCBI GI g1723490
BLAST score 206
E value 4.0e-16
Match length 132
% identity 37

NCBI Description HYPOTHETICAL 32.6 KD PROTEIN C1F3.04C IN CHROMOSOME I

>gi 1256515 emb CAA94622 (Z70690) unknown

[Schizosaccharomyces pombe]

Seq. No. 17832

Contig ID 56866\_1.R1040 5'-most EST gsv701045355.h1

Method BLASTX
NCBI GI g3822036
BLAST score 349
E value 1.0e-32
Match length 183
% identity 44

NCBI Description (AF072326) endo-1,3-1,4-beta-D-glucanase [Zea mays]

Seq. No. 17833

Contig ID 56873\_1.R1040 5'-most EST fua701041385.h1

Method BLASTN
NCBI GI g3449325
BLAST score 35
E value 6.0e-10
Match length 51
% identity 92

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K16H17, complete sequence [Arabidopsis thaliana]

Seq. No. 17834

Contig ID 56875\_1.R1040 5'-most EST zhf700954808.h1

Seq. No. 17835

Contig ID 56881\_1.R1040 5'-most EST xpa700797494.h1

Method BLASTX
NCBI GI g2702273
BLAST score 196
E value 4.0e-15
Match length 138
% identity 46

NCBI Description (AC003033) carrot B2 protein-like [Arabidopsis thaliana]

Seq. No.

17836

Contig ID 56882\_1.R1040

5'-most EST LIB3106-047-Q1-K1-D8

Seq. No.

17837

Contig ID 56885 1.R1040 5'-most EST vzy700756185.h1

Method BLASTX NCBI GI g4335724



```
BLAST score
                   157
E value
                   2.0e-10
Match length
                   73
% identity
                   58
NCBI Description
                    (ACO06248) putative RING-H2 finger protein [Arabidopsis
Seq. No.
                   17838
                   56885 2.R1040
Contig ID
5'-most EST
                   rca700998633.h1
Seq. No.
                   17839
Contig ID
                   56899 1.R1040
5'-most EST
                   kl1701207127.h1
Method
                   BLASTX
                   g1173194
NCBI GI
BLAST score
                   173
E value
                   1.0e-16
Match length
                   94
% identity
                   49
NCBI Description
                   30S RIBOSOMAL PROTEIN S13, CHLOROPLAST PRECURSOR (CS13)
                   >gi 2119093 pir S59594 ribosomal protein S13 precursor,
                   chloroplast - Arabidopsis thaliana >gi 16767 emb CAA79013
                    (Z17611) chloroplast 30S ribosomal protein S13 [Arabidopsis
                   thaliana] >gi_662869_emb_CAA88028_ (Z47986) chloroplast ribosomal protein S13 [Arabidopsis thaliana]
                   >gi_1107483_emb_CAA63021_ (X91955) 30S ribosomal protein
                   S13 [Arabidopsis thaliana] >gi 1515107 emb CAA60413
                    (X86734) plastid ribosomal protein S13 [Arabidopsis
                   thaliana]
Seq. No.
                   17840
Contig ID
                   56904 1.R1040
5'-most EST
                   uxk70\overline{0}669956.h1
Seq. No.
                   17841
Contig ID
                   56906 1.R1040
5'-most EST
                   LIB3106-087-Q1-K1-A6
Method
                   BLASTX
NCBI GI
                   g3549291
BLAST score
                   493
E value
                   1.0e-49
Match length
                   107
% identity
                   85
NCBI Description
                   (AF074923) endo-1,4-beta-glucanase precursor [Fragaria x
                   ananassa]
```

Seq. No. 17842

Contig ID 56913 1.R1040 5'-most EST zzp700834609.h1

Method BLASTX NCBI GI q2275199 BLAST score 416 E value 2.0e-40 Match length 129 % identity 72

NCBI Description (AC002337) hypothetical protein [Arabidopsis thaliana]



```
17843
Seq. No.
Contig ID
                   56918 1.R1040
5'-most EST
                  LIB31\overline{0}6-086-Q1-K1-G9
Method
                  BLASTX
NCBI GI
                   q4099092
BLAST score
                   404
E value
                   2.0e-39
                   103
Match length
% identity
                   69
                  (U83179) unknown [Arabidopsis thaliana]
NCBI Description
                   17844
Seq. No.
                   56921 1.R1040
Contig ID
5'-most EST
                  LIB3106-086-Q1-K1-H11
Method
                  BLASTX
NCBI GI
                   g3450842
BLAST score
                   329
E value
                   1.0e-30
Match length
                   103
% identity
                   62
                  (AF080436) mitogen activated protein kinase kinase [Oryza
NCBI Description
                   sativa]
Seq. No.
                   17845
                   56923 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220070g04a1
                   17846
Seq. No.
Contig ID
                   56925 1.R1040
5'-most EST
                  LIB3106-086-Q1-K1-E4
Seq. No.
                   17847
Contig ID
                   56927 1.R1040
5'-most EST
                   uC-gmropic026f07b1
Method
                   BLASTX
NCBI GI
                   g4325372
                   197
BLAST score
E value
                   5.0e-15
Match length
                   77
% identity
                   44
NCBI Description
                  (AF128396) contains similarity to protein disulfide
                   isomerases [Arabidopsis thaliana]
Seq. No.
                   17848
Contig ID
                   56931 1.R1040
5'-most EST
                   LIB3139-101-P1-N1-H5
Method
                   BLASTX
NCBI GI
                   g2827642
BLAST score
                   204
E value
                   6.0e-16
Match length
                   108
```

Seq. No. 17849

% identity

NCBI Description

Contig ID 56934 1.R1040

(AL021636) hypothetical protein [Arabidopsis thaliana]



5'-most EST LIB3106-086-Q1-K1-F3 Method BLASTX NCBI GI g3068705 BLAST score 212 9.0e-17 E value 96 Match length % identity 44 (AF049236) unknown [Arabidopsis thaliana] NCBI Description Seq. No. 17850 56934 2.R1040 Contig ID uaw700661809.hl 5'-most EST 17851 Seq. No. Contig ID 56951 1.R1040 vwf700678620.h1 5'-most EST 17852 Seq. No. 56964 1.R1040 Contig ID  $seb70\overline{0}649881.h1$ 5'-most EST Method BLASTX q4220480 NCBI GI 708 BLAST score 2.0e-74 E value 408 Match length % identity 40 NCBI Description (AC006069) unknown protein [Arabidopsis thaliana] Seq. No. 17853 56968 1.R1040 Contig ID 5'-most EST LIB3107-009-Q1-K1-F12 Method BLASTX g3193330 NCBI GI BLAST score 503 E value 8.0e-51 Match length 157 % identity 65 NCBI Description (AF069299) contains similarity to Medicago sativa corC (GB:L22305) [Arabidopsis thaliana] Seq. No. 17854 56968 2.R1040 Contig ID 5'-most EST uC-gmflminsoy118c08b1 Method BLASTX NCBI GI g3738316 BLAST score 150 1.0e-13 E value Match length 59 % identity 67 NCBI Description (AC005170) unknown protein [Arabidopsis thaliana] Seq. No. 17855

56980 1.R1040 Contig ID 5'-most EST kl1701213465.h1

Method BLASTX NCBI GI g2809245 BLAST score 440



E value 2.0e-43
Match length 130
% identity 68

NCBI Description (AC002560) F21B7.14 [Arabidopsis thaliana]

Seq. No. 17856

Contig ID 56980 2.R1040

5'-most EST LIB3106-014-Q1-K1-A6

Method BLASTX
NCBI GI g2809245
BLAST score 250
E value 2.0e-22
Match length 99
% identity 58

NCBI Description (AC002560) F21B7.14 [Arabidopsis thaliana]

Seq. No. 17857

Contig ID 56982 1.R1040

5'-most EST LIB3106-086-Q1-K1-A10

Method BLASTX
NCBI GI g3128185
BLAST score 200
E value 1.0e-15
Match length 61
% identity 64

NCBI Description (AC004521) unknown protein [Arabidopsis thaliana]

Seq. No. 17858

Contig ID 56983 1.R1040

5'-most EST LIB3106-011-Q1-K1-D3

Method BLASTX
NCBI GI g3785988
BLAST score 218
E value 2.0e-17
Match length 84
% identity 52

NCBI Description (AC005560) unknown protein [Arabidopsis thaliana]

Seq. No. 17859

Contig ID 56983\_2.R1040

5'-most EST LIB3106-086-Q1-K1-A9

Seq. No. 17860

Contig ID 56986 1.R1040

5'-most EST LIB3107-003-Q1-K1-D1

Method BLASTX
NCBI GI g1762309
BLAST score 617
E value 4.0e-64
Match length 131
% identity 91

NCBI Description (U53345) AP-1 Golgi-related complex component; clathrin

coated vesicles; clathrin assembly protein [Camptotheca

acuminata]

Seq. No. 17861

Contig ID 56986\_2.R1040



5'-most EST leu701147847.h1

Method BLASTX
NCBI GI g2231702
BLAST score 425
E value 5.0e-42
Match length 88
% identity 88

NCBI Description (U92086) clathrin assembly protein AP19 homolog

[Arabidopsis thaliana] >gi\_3080409 emb\_CAA18728\_ (AL022604)

clathrin assembly protein AP19 homolog [Arabidopsis

thaliana]

Seq. No. 17862

Contig ID 56995\_1.R1040 5'-most EST jsh701065230.h1

Method BLASTX
NCBI GI g2660677
BLAST score 513
E value 4.0e-52
Match length 150
% identity 63

NCBI Description (AC002342) unknown protein [Arabidopsis thaliana]

Seq. No. 17863

Contig ID 57000\_1.R1040

5'-most EST LIB3106-085-Q1-K1-G6

Method BLASTX
NCBI GI g1143711
BLAST score 207
E value 3.0e-16
Match length 110
% identity 45

NCBI Description (U13631) non-green plastid inner envelope membrane protein

precursor [Brassica oleracea]

Seq. No. 17864

Contig ID 57001\_1.R1040

5'-most EST LIB3106-085-Q1-K1-G7

Seq. No. 17865

Contig ID 57011\_1.R1040 5'-most EST crh700854461.h1

Method BLASTX
NCBI GI g1101770
BLAST score 408
E value 7.0e-40
Match length 97
% identity 72

NCBI Description (U39448) MYB-like transcriptional factor MBF1 [Picea

mariana]

Seq. No. 17866

Contig ID 57021\_1.R1040 5'-most EST leu701145671.h1

Seq. No. 17867

Contig ID 57030\_1.R1040



5'-most EST fC-gmst700888668f5

Method BLASTX
NCBI GI g1142619
BLAST score 1749
E value 0.0e+00
Match length 545
% identity 75

NCBI Description (U18348) phaseolin G-box binding protein PG1 [Phaseolus

vulgaris]

Seq. No. 17868

Contig ID 57034\_1.R1040 5'-most EST epx701110485.h1

Method BLASTX
NCBI GI g927428
BLAST score 571
E value 6.0e-59
Match length 135
% identity 79

NCBI Description (X86733) fis1 [Linum usitatissimum]

Seq. No. 17869

Contig ID 57034\_2.R1040 5'-most EST trc700562333.h1

Method BLASTX
NCBI GI g927428
BLAST score 491
E value 1.0e-58
Match length 144
% identity 81

NCBI Description (X86733) fis1 [Linum usitatissimum]

Seq. No. 17870

Contig ID 57037\_1.R1040 5'-most EST pmv700893176.h1

Seq. No. 17871

Contig ID 57050\_1.R1040

5'-most EST LIB3138-047-Q1-N1-G5

Seq. No. 17872

Contig ID 57058\_1.R1040

5'-most EST jC-gmle01810020a05a1

Method BLASTN
NCBI GI g176224
BLAST score 55
E value 7.0e-22
Match length 55
% identity 100

NCBI Description Tobacco chloroplast 5S large rRNA

Seq. No. 17873

Contig ID 57092\_1.R1040 5'-most EST wvk700683186.h1

Seq. No. 17874

Contig ID 57093 1.R1040



```
5'-most EST
                   LIB3106-079-P1-K1-G9
Method
                   BLASTX
NCBI GI
                   a3687239
                   648
BLAST score
                   6.0e-68
E value
                   127
Match length
% identity
                   96
                   (AC005169) putative clathrin coat assembly protein
NCBI Description
                   [Arabidopsis thaliana]
                   17875
Seq. No.
Contig ID
                   57095 1.R1040
5'-most EST
                   leu70\overline{1}149041.h1
Method
                   BLASTX
NCBI GI
                   q3150403
BLAST score
                   693
                   7.0e-73
E value
Match length
                   273
% identity
                   55
NCBI Description (AC004165) hypothetical protein [Arabidopsis thaliana]
                   17876
Seq. No.
Contig ID
                   57095 2.R1040
5'-most EST
                   LIB3109-006-Q1-K1-C7
                   17877
Seq. No.
                   57098 1.R1040
Contig ID
                   uC-gmrominsoy317d11b1
5'-most EST
                   17878
Seq. No.
                   57113 1.R1040
Contig ID
                   LIB3106-079-P1-K1-C3
5'-most EST
                   BLASTX
Method
NCBI GI
                   q2827514
BLAST score
                   419
E value
                   3.0e-41
Match length
                   122
                   63
% identity
NCBI Description (AL021633) predicted protein [Arabidopsis thaliana]
Seq. No.
                   17879
                   57147 1.R1040
Contig ID
                   LIB3106-078-P1-K1-H5
5'-most EST
                   17880
Seq. No.
                   57154 1.R1040
Contig ID
5'-most EST
                   LIB3106-078-P1-K1-E6
Method
                   BLASTX
                   g3915189
NCBI GI
BLAST score
                   332
                   7.0e-31
E value
                   91
Match length
% identity
                   68
                   UBIQUITIN-CONJUGATING ENZYME X (UBIQUITIN-PROTEIN LIGASE)
```

Seq. No. 17881

NCBI Description

(UBIQUITIN CARRIER PROTEIN)



Contig ID 57166 1.R1040 5'-most EST g5666923 Method BLASTX NCBI GI g1928886 BLAST score 212 1.0e-16 E value 106 Match length % identity 42

NCBI Description (U92010) lin-10 protein homolog [Rattus norvegicus]

Seq. No.

17882

Contig ID 57169 1.R1040

5'-most EST LIB3106-078-P1-K1-D11

Seq. No.

17883

Contig ID 57174\_1.R1040

5'-most EST jC-gmfl02220057b10a1

Method BLASTX
NCBI GI g4522009
BLAST score 493
E value 4.0e-98
Match length 303
% identity 65

NCBI Description (AC007069) unknown protein [Arabidopsis thaliana]

Seq. No. 17884

Contig ID 57180 1.R1040 5'-most EST jex700904691.h1

Method BLASTX
NCBI GI g960289
BLAST score 560
E value 2.0e-57
Match length 157
% identity 72

NCBI Description (L34343) anthranilate synthase alpha subunit [Ruta

graveolens]

Seq. No. 17885

Contig ID 57180\_2.R1040

5'-most EST uC-gmronoir036h06b1

Seq. No. 17886

Contig ID 57187\_1.R1040 5'-most EST zzp700830742.h1

Method BLASTX
NCBI GI g2804453
BLAST score 210
E value 2.0e-16
Match length 93
% identity 44

NCBI Description (AF043699) contains similarity to the prolyl oligopeptidase

family [Caenorhabditis elegans]

Seq. No. 17887

Contig ID 57187\_2.R1040

5'-most EST LIB3170-062-Q1-J1-G1

Method BLASTX



NCBI GI g2804453 BLAST score 235 E value 1.0e-19 Match length 103 % identity 45

NCBI Description (AF043699) contains similarity to the prolyl oligopeptidase

family [Caenorhabditis elegans]

Seq. No. 17888

Contig ID 57190 1.R1040

5'-most EST LIB3106-078-P1-K1-B6

Seq. No. 17889

Contig ID 57191 1.R1040

5'-most EST LIB3106-078-P1-K1-C1

Seq. No. 17890

Contig ID 57206 1.R1040

5'-most EST LIB3106-078-P1-K1-A1

Seq. No. 17891

Contig ID 57207\_1.R1040 5'-most EST seb700650319.h1

Method BLASTX
NCBI GI g3548808
BLAST score 229
E value 2.0e-20
Match length 90
% identity 57

NCBI Description (AC005313) unknown protein [Arabidopsis thaliana]

Seq. No. 17892

Contig ID 57209 1.R1040

5'-most EST LIB3170-076-Q1-K1-B5

Seq. No. 17893

Contig ID 57209 2.R1040 5'-most EST wvk700684856.h1

Seq. No. 17894

Contig ID 57215 1.R1040

5'-most EST LIB3106-077-P1-K1-F3

Seq. No. 17895

Contig ID 57217\_1.R1040 5'-most EST fde700871973.h1

Seq. No. 17896

Contig ID 57232\_1.R1040 5'-most EST zvj700605207.h2

Method BLASTX
NCBI GI g3927835
BLAST score 336
E value 2.0e-31
Match length 138
% identity 55

NCBI Description (AC005727) similar to Streptomyces PapA [Arabidopsis



## thaliana]

17897 Seq. No.

Contig ID 57246 1.R1040 5'-most EST pxt700943073.hl

Seq. No. 17898

Contig ID 57260 1.R1040

5'-most EST LIB3106-076-Q1-K1-G2

Seq. No. 17899

Contig ID 57266 1.R1040

5'-most EST uC-gmflminsoy045g05b1

Method BLASTX g1086833 NCBI GI BLAST score 421 3.0e-41E value Match length 184 % identity 43

NCBI Description (U41264) coded for by C. elegans cDNA CEESN26F; coded for

by C. elegans cDNA CEESI89F; similar to 60S acidic

ribosomal protein Po (L10) [Caenorhabditis elegans]

Seq. No. 17900

Contig ID 57272 1.R1040 5'-most EST pxt700945928.hl

Method BLASTX NCBI GI g2499115 BLAST score 1243 E value 1.0e-137 Match length 299 % identity 78

NCBI Description VACUOLAR ASSEMBLY PROTEIN VPS41 HOMOLOG >gi 1835788

(U86662) VPS41 [Lycopersicon esculentum]

17901 Seq. No.

57274 1.R1040 Contig ID

5'-most EST LIB3106-076-Q1-K1-H11

Seq. No. 17902

57313 1.R1040 Contig ID

5'-most EST LIB3106-076-Q1-K1-C9

Seq. No. 17903

57314 1.R1040 Contig ID

5'-most EST LIB3170-086-Q1-K1-A6

Seq. No. 17904

57314 2.R1040 Contig ID 5'-most EST seb700654154.h1

17905 Seq. No.

Contig ID 57314 3.R1040 5'-most EST hyd700726171.hl

Seq. No. 17906

Contig ID 57323 1.R1040



```
5'-most EST
                  LIB3170-029-Q1-J1-G10
Seq. No.
                   17907
Contig ID
                   57339 1.R1040
5'-most EST
                  LIB3106-075-Q1-K2-H1
                   17908
Seq. No.
Contig ID
                   57340 1.R1040
5'-most EST
                  LIB3106-075-Q1-K1-H11
                  BLASTX
Method
                   g3790743
NCBI GI
                   178
BLAST score
E value
                   6.0e-13
Match length
                   51
% identity
                   61
                  (AF099919) contains similarity to cytochrome C oxidase
NCBI Description
                   assembly protein COX17 homologues [Caenorhabditis elegans]
                   17909
Seq. No.
Contig ID
                  57357 1.R1040
5'-most EST
                  LIB3170-088-Q1-J1-G1
Method
                  BLASTX
                  g2500435
NCBI GI
BLAST score
                   283
E value
                   3.0e-25
Match length
                   71
                   70
% identity
                  30S RIBOSOMAL PROTEIN S10 >gi 1653406 dbj BAA18320
NCBI Description
                   (D90913) 30S ribosomal protein S10 [Synechocystis sp.]
                   17910
Seq. No.
                   57357 2.R1040
Contig ID
5'-most EST
                   ssr70\overline{0}557433.h1
Seq. No.
                   17911
Contig ID
                   57367 1.R1040
5'-most EST
                   LIB3106-075-Q1-K2-D7
                   BLASTN
Method
NCBI GI
                   q4218188
BLAST score
                   49
E value
                   2.0e-18
Match length
                   128
% identity
NCBI Description
                  Glycine max cytosolic glutamine synthetase (gs15) gene
                  promoter
Seq. No.
                   17912
                   57371 1.R1040
Contig ID
5'-most EST
                   kmv700743182.h1
```

Seq. No. 17913

Contig ID 57378 1.R1040 5'-most EST zzp700830301.h1

Method BLASTX
NCBI GI g2245064
BLAST score 501
E value 1.0e-50



Match length 150 % identity 62

NCBI Description (Z97342) hypothetical protein [Arabidopsis thaliana]

Seq. No. 17914

Contig ID 57386\_1.R1040 5'-most EST ncj700988288.h1

Method BLASTX
NCBI GI g1783312
BLAST score 823
E value 5.0e-88
Match length 322
% identity 53

NCBI Description (X98520) receptor-like kinase [Brassica oleracea]

Seq. No. 17915

Contig ID 57388\_1.R1040 5'-most EST fde700875802.h1

Method BLASTX
NCBI GI g4512664
BLAST score 905
E value 8.0e-98
Match length 208
% identity 80

NCBI Description (AC006931) putative ribose phosphate pyrophosphokinase

[Arabidopsis thaliana]

>gi\_4544471\_gb\_AAD22378.1\_AC006580\_10 (AC006580) putative ribose phosphate pyrophosphokinase [Arabidopsis thaliana]

Seq. No. 17916

Contig ID 57398\_1.R1040

5'-most EST LIB3106-075-Q1-K2-A11

Seq. No. 17917

Contig ID 57398\_2.R1040

5'-most EST jC-gmst02400074b12a1

Method BLASTX
NCBI GI g1532168
BLAST score 259
E value 2.0e-22
Match length 67
% identity 75

NCBI Description (U63815) localized according to blastn similarity to EST

sequences; therefore, the coding span corresponds only to an area of similarity since the initation codon and stop codon could not be precisely determined [Arabidopsis

thaliana]

Seq. No. 17918

Contig ID 57400\_1.R1040

5'-most EST LIB3106-075-Q1-K2-A2

Seq. No. 17919

Contig ID 57403\_1.R1040

5'-most EST LIB3106-075-Q1-K1-A7

Seq. No. 17920



Contig ID 57403\_2.R1040 5'-most EST LIB3170-083-Q1-J1-H1

Seq. No. 17921

Contig ID 57404 1.R1040 5'-most EST ncj700980729.h1

Method BLASTX
NCBI GI g4263820
BLAST score 321
E value 7.0e-35
Match length 141
% identity 57

NCBI Description (AC006067) hypothetical protein [Arabidopsis thaliana]

Seq. No. 17922

Contig ID 57409\_1.R1040 5'-most EST gsv701054654.h1

Seq. No. 17923

Contig ID 57427\_1.R1040 5'-most EST smw700646279.h1

Seq. No. 17924

Contig ID 57427\_2.R1040

5'-most EST jC-gmf102220056d06a1

Seq. No. 17925

Contig ID 57427\_3.R1040 5'-most EST jsh701066180.h1

Seq. No. 17926

Contig ID 57427\_4.R1040 5'-most EST wrg700792223.h1

Seq. No. 17927

Contig ID 57432 1.R1040

5'-most EST LIB3106-074-Q1-K1-G8

Seq. No. 17928

Contig ID 57439\_1.R1040 5'-most EST zhf700956064.h1

Method BLASTX
NCBI GI g2245095
BLAST score 357
E value 1.0e-33
Match length 87
% identity 74

NCBI Description (Z97343) formyltransferase purU homolog [Arabidopsis

thaliana]

Seq. No. 17929

Contig ID 57441\_1.R1040

5'-most EST LIB3106-074-Q1-K1-H7

Seq. No. 17930

Contig ID 57452 1.R1040 5'-most EST ncj700981120.h1



BLASTN Method g2924257 NCBI GI BLAST score 60 5.0e-25 E value Match length 298 % identity 69 Tobacco chloroplast genome DNA NCBI Description Seq. No. 17931 Contig ID 57456 1.R1040 5'-most EST uC-gmropic067e08b1 Method BLASTX NCBI GI g4063749 BLAST score 344 E value 5.0e-32 Match length 178

% identity 30

(AC005851) hypothetical protein [Arabidopsis thaliana] NCBI Description

17932 Seq. No.

57456 5.R1040 Contig ID 5'-most EST eep700866424.h1

17933 Seq. No.

57466 1.R1040 Contig ID 5'-most EST kl1701202945.h1

BLASTX Method g2979556 NCBI GI BLAST score 283 6.0e-25 E value Match length 196 % identity 35

(AC003680) unknown protein [Arabidopsis thaliana] NCBI Description

Seq. No.

57471\_1.R1040 Contig ID

5'-most EST LIB3106-074-Q1-K1-E3

17934

Seq. No. 17935

Contig ID 57472 1.R1040

LIB3106-074-Q1-K1-E4 5'-most EST

BLASTN Method NCBI GI g3821780 BLAST score 36 E value 1.0e-10 Match length 37 % identity 61

NCBI Description Xenopus laevis cDNA clone 27A6-1

17936 Seq. No.

57473 1.R1040 Contiq ID

5'-most EST LIB3106-074-Q1-K1-E5

Method BLASTX g2245096 NCBI GI BLAST score 544 8.0e-56 E value Match length 131



```
% identity
                   (Z97343) inositol 2-dehydrogenase homolog [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  17937
                  57479 1.R1040
Contig ID
                  kmv700739923.h1
5'-most EST
                  17938
Seq. No.
                  57489 1.R1040
Contig ID
                  uC-gmflminsoy115a10b1
5'-most EST
                  BLASTX
Method
                   g282430
NCBI GI
                   707
BLAST score
E value
                   2.0e-74
Match length
                   306
% identity
                   58
                  leucine--tRNA ligase (EC 6.1.1.4) - Bacillus subtilis
NCBI Description
                   >gi 143148 (M88581) transfer RNA-Leu synthetase [Bacillus
                   subtilis]
                   17939
Seq. No.
                   57490 1.R1040
Contig ID
                   ncj700983045.hl
5'-most EST
Method
                  BLASTX
NCBI GI
                   g807698
BLAST score
                   341
                   7.0e-32
E value
Match length
                   132
                   51
% identity
                  (D32206) prepro-cucumisin [Cucumis melo]
NCBI Description
                   17940
Seq. No.
                   57512_1.R1040
Contig ID
5'-most EST
                   LIB3106-073-Q1-K1-H4
Method
                   BLASTX
                   g4538965
NCBI GI
BLAST score
                   202
                   7.0e-16
E value
Match length
                   119
% identity
                   36
                  (AL049488) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   17941
Seq. No.
Contig ID
                   57515 1.R1040
5'-most EST
                   LIB3106-073-Q1-K1-H7
                   17942
Seq. No.
Contig ID
                   57528 1.R1040
5'-most EST
                   LIB3109-045-Q1-K1-D11
Method
                   BLASTX
```

NCBI GI g2462733 BLAST score 498 3.0e-50 E value Match length 164 % identity 61

NCBI Description (AC002292) Putative enoyl-CoA hydratase/isomerase



## [Arabidopsis thaliana]

Seq. No. 17943 Contig ID 57531 1.R1040

5'-most EST jC-gmst02400044e08a1

Seq. No. 17944

Contig ID 57535\_1.R1040 5'-most EST zhf700961962.h1

Seq. No. 17945

Contig ID 57556\_1.R1040 5'-most EST ssr700560390.h1

Method BLASTX
NCBI GI g2706455
BLAST score 412
E value 5.0e-40
Match length 188
% identity 42

NCBI Description (AL021046) probable involvement in transcription initiation

[Schizosaccharomyces pombe]

Seq. No. 17946

Contig ID 57562 1.R1040

5'-most EST LIB3106-073-Q1-K1-C2

Method BLASTX
NCBI GI g3193328
BLAST score 309
E value 3.0e-28
Match length 130
% identity 52

NCBI Description (AF069299) No definition line found [Arabidopsis thaliana]

Seq. No. 17947

Contig ID 57563\_1.R1040 5'-most EST rca701002452.h1

Method BLASTX
NCBI GI g2088647
BLAST score 449
E value 1.0e-44
Match length 127
% identity 68

NCBI Description (AF002109) hypothetical protein [Arabidopsis thaliana]

>gi\_3158394 (AF036340) LRR-containing F-box protein

[Arabidopsis thaliana]

Seq. No. 17948

Contig ID 57589 1.R1040

5'-most EST LIB3106-072-P1-K1-F8

Seq. No. 17949

Contig ID 57597 1.R1040 5'-most EST asn701142388.h1

Method BLASTX
NCBI GI g1255951
BLAST score 428
E value 4.0e-42



Match length 90 % identity 86

NCBI Description (X96932) PS60 [Nicotiana tabacum]

Seq. No.

17950

BLASTX

Contig ID 5'-most EST 57603\_1.R1040 sat701003416.h1

Method NCBI GI BLAST score

g2828296 273

E value Match length % identity 8.0e-24 60

87

NCBI Description

(AL021687) RNase L inhibitor [Arabidopsis thaliana]

Seq. No.

17951

Contig ID 5'-most EST

57605\_1.R1040

T jsh701069638.h1

Seq. No.

Seq. No.

17952

Contig ID 5'-most EST

57606\_1.R1040 jsh701070051.h2

J MOSC EST

17953

887

Contig ID 5'-most EST 57609\_1.R1040 eep700868526.h1

Method NCBI GI

BLASTX g1173104

BLAST score E value Match length

1.0e-95 216

% identity NCBI Description 69
RIBONUCLEASE 2 PRECURSOR >gi\_289210 (M98336) ribonuclease
[Arabidopsis thaliana] >gi\_2642160 (AC003000) ribonuclease,

RNS2 [Arabidopsis thaliana]

Seq. No.

17954

Contig ID 5'-most EST

57611\_1.R1040 leu701153126.h1

Seq. No.

17955

Contig ID 5'-most EST 57615\_1.R1040 zzp700831178.h1

Method NCBI GI

BLASTX g3549666

BLAST score E value 325 5.0e-30

Match length % identity

78 79

NCBI Description

(AL031394) putative protein [Arabidopsis thaliana]

Seq. No.

17956

Contig ID

57622 1.R1040

5'-most EST Method NCBI GI g4306218 BLASTX g4105190

BLAST score 446



E value 7.0e-44
Match length 243
% identity 40

NCBI Description (AF044127) peroxisomal short-chain alcohol dehydrogenase

[Homo sapiens]

Seq. No. 17957

Contig ID 57626\_1.R1040 5'-most EST jsh701065533.h1

Seq. No. 17958

Contig ID 57633\_1.R1040 5'-most EST ncj700987063.h1

Method BLASTX
NCBI GI g3080428
BLAST score 440
E value 1.0e-43
Match length 100
% identity 78

NCBI Description (AL022604) putative protein [Arabidopsis thaliana]

Seq. No. 17959

Contig ID 57640\_1.R1040 5'-most EST sat701014115.h1

Method BLASTX
NCBI GI g2499535
BLAST score 583
E value 3.0e-60
Match length 202
% identity 64

NCBI Description 2-OXOGLUTARATE/MALATE TRANSLOCATOR PRECURSOR >gi\_595681

(U13238) 2-oxoglutarate/malate translocator [Spinacia

oleracea]

Seq. No. 17960

Contig ID 57640 4.R1040 5'-most EST gsv701055011.h1

Method BLASTX
NCBI GI g2499535
BLAST score 182
E value 9.0e-14
Match length 78
% identity 82

NCBI Description 2-0XOGLUTARATE/MALATE TRANSLOCATOR PRECURSOR >gi 595681

(U13238) 2-oxoglutarate/malate translocator [Spinacia

oleracea]

Seq. No. 17961

Contig ID 57642 1.R1040 5'-most EST pxt700943553.h1

Method BLASTX
NCBI GI 94559333
BLAST score 277
E value 6.0e-25
Match length 82
% identity 45

NCBI Description (AC007087) unknown protein [Arabidopsis thaliana]

NCBI GI

E value

BLAST score

Match length % identity

g2062172

3.0e-34 85

361

80



17962 Seq. No. 57643 1.R1040 Contig ID pmv700892843.hl 5'-most EST BLASTX Method g2864613 NCBI GI BLAST score 222 E value 2.0e-19 Match length 79 65 % identity NCBI Description (AL021811) S-receptor kinase -like protein [Arabidopsis thaliana] >gi\_4049333\_emb\_CAA22558\_ (AL034567) S-receptor kinase-like protein [Arabidopsis thaliana] 17963 Seq. No. Contig ID 57646 1.R1040 5'-most EST gsv701045325.h1 Method BLASTX NCBI GI q4200249 BLAST score 143 1.0e-08 E value Match length 63 46 % identity NCBI Description (AL035297) hypothetical protein [Homo sapiens] Seq. No. 17964 Contig ID 57653 1.R1040 5'-most EST LIB3106-071-P1-K1-G6 17965 Seq. No. 57659 1.R1040 Contig ID 5'-most EST gsv701053064.h1 BLASTX Method NCBI GI q2444178 BLAST score 723 E value 1.0e-76 Match length 163 % identity 83 NCBI Description (U94784) unconventional myosin [Helianthus annuus] Seq. No. 17966 57671 1.R1040 Contig ID 5'-most EST LIB3106-071-P1-K1-F4 Seq. No. 17967 Contig ID 57676 1.R1040 5'-most EST LIB3106-071-P1-K1-C8 17968 Seq. No. 57677 1.R1040 Contig ID 5'-most EST LIB3106-071-P1-K1-D10 Method BLASTX





```
(AC001645) unknown protein [Arabidopsis thaliana]
NCBI Description
```

Seq. No. 17969

Contig ID 57683 1.R1040

5'-most EST LIB3106-071-P1-K1-D6

17970 Seq. No.

Contig ID 57698 1.R1040 5'-most EST eep700864772.hl

Method BLASTX NCBI GI g1181615 BLAST score 762 E value 3.0e-81Match length 166 % identity 87

NCBI Description (D83078) nitrilase [Nicotiana tabacum]

17971 Seq. No.

57700 1.R1040 Contig ID

5'-most EST LIB3106-071-P1-K1-C1

Method BLASTN NCBI GI q3821780 BLAST score 36 1.0e-10 E value Match length 48 % identity 67

Xenopus laevis cDNA clone 27A6-1 NCBI Description

Seq. No.

17972 57715 1.R1040 Contig ID  $kmv70\overline{0}737715.h1$ 5'-most EST

Seq. No.

Contig ID 57749 1.R1040

5'-most EST LIB3106-070-P1-K1-E4

17973

Method BLASTX g2956707 NCBI GI BLAST score 477 E value 4.0e-48 Match length 112 % identity 78

NCBI Description (Y16778) peroxidase [Spinacia oleracea]

17974 Seq. No.

Contig ID 57752 2.R1040 5'-most EST  $jsh70\overline{1}065380.h1$ 

Method BLASTX NCBI GI g2773184 BLAST score 253 8.0e-22 E value Match length 108 % identity 46

NCBI Description (AF039720) similar to the "DEAD" box family of helicases;

most similar to eukaryotic initiation factor 4A

[Caenorhabditis elegans]

Seq. No. 17975



```
Contig ID
                  57786 1.R1040
                  pcp700994056.h1
5'-most EST
                  17976
Seq. No.
                  57798 1.R1040
Contig ID
                  awf700843419.h1
5'-most EST
                  BLASTX
Method
                  q4559387
NCBI GI
BLAST score
                  259
                  2.0e-22
E value
                  76
Match length
                  62
% identity
                  (AC006526) putative oxal protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  17977
                  57812 1.R1040
Contig ID
5'-most EST
                  pcp700995557.h1
Method
                  BLASTX
                  g4101707
NCBI GI
BLAST score
                   437
                  8.0e-43
E value
                  230
Match length
                  39
% identity
                  (AF006080) glucose acyltransferase [Solanum berthaultii]
NCBI Description
                  17978
Seq. No.
Contig ID
                   57828 1.R1040
                  LIB3106-069-P1-K1-D4
5'-most EST
                   17979
Seq. No.
                   57836 1.R1040
Contig ID
                   2DC-01-Q1-E1-G8
5'-most EST
                   17980
Seq. No.
Contig ID
                   57853 1.R1040
5'-most EST
                  LIB3106-068-P1-K1-H1
                   17981
Seq. No.
                   57858 1.R1040
Contig ID
5'-most EST
                   sat701004649.h1
                   BLASTX
Method
                   q3212854
NCBI GI
BLAST score
                   532
                   2.0e-54
E value
Match length
                   144
                   74
% identity
NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]
Seq. No.
                   17982
                   57858 2.R1040
Contig ID
```

vzy700755387.h1 5'-most EST

Method BLASTX g3212854 NCBI GI BLAST score 234 E value 4.0e-19 Match length 199 % identity 43



NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]

Seq. No. 17983

Contig ID 57858 3.R1040 5'-most EST g5677759 Method BLASTX NCBI GI g3212854 BLAST score 182 3.0e-13 E value Match length 56 % identity 64

NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]

Seq. No. 17984

Contig ID 57858 5.R1040

5'-most EST LIB3109-021-Q1-K1-F12

Seq. No. 17985

Contig ID 57858\_6.R1040 5'-most EST uaw700661056.h1

Seq. No. 17986

Contig ID 57860 1.R1040

5'-most EST jC-gmfl02220084a03a1

Seq. No. 17987

Contig ID 57860\_2.R1040 5'-most EST ssr700560438.h1

Seq. No. 17988

Contig ID 57867\_1.R1040 5'-most EST bth700845580.h1

Seq. No. 17989

Contig ID 57869\_1.R1040 5'-most EST zzp700832032.h1

Method BLASTX
NCBI GI g267453
BLAST score 230
E value 6.0e-19
Match length 77
% identity 56

NCBI Description HYPOTHETICAL 37.5 KD PROTEIN ZK637.5 IN CHROMOSOME III >gi\_102496\_pir\_\_S15791 arsenical pump-driving ATPase

homolog - Caenorhabditis elegans >gi\_3881667\_emb\_CAA77452\_(Z11115) predicted using Genefinder; ArsA homologue; cDNA EST EMBL:D73741 comes from this gene; cDNA EST EMBL:D71137 comes from this gene; cDNA EST EMBL:C08164 comes from this

gene; cDNA EST EMBL: C09807 comes from this gene; cD

Seq. No. 17990

Contig ID 57869 2.R1040

5'-most EST uC-qmflminsoy065e09b1

Method BLASTX
NCBI GI g267453
BLAST score 259
E value 3.0e-22



Match length % identity NCBI Description

84 58

ion HYPOTHETICAL 37.5 KD PROTEIN ZK637.5 IN CHROMOSOME III >gi\_102496\_pir\_\_S15791 arsenical pump-driving ATPase homolog - Caenorhabditis elegans >gi\_3881667\_emb\_CAA77452

(Z11115) predicted using Genefinder; ArsA homologue; cDNA EST EMBL:D73741 comes from this gene; cDNA EST EMBL:D71137 comes from this gene; cDNA EST EMBL:D71137

gene; cDNA EST EMBL: C09807 comes from this gene; cD

Seq. No. 17991

Contig ID 57876\_1.R1040 5'-most EST dpv701101078.h1

Method BLASTN
NCBI GI g1177368
BLAST score 78
E value 1.0e-35
Match length 150
% identity 88

NCBI Description Z.mays mRNA for ribosomal protein L39

Seq. No. 17992

Contig ID 57876\_2.R1040
5'-most EST g4397604
Method BLASTN
NCBI GI g1177368
BLAST score 79
E value 2.0e-36

E value 2.0eMatch length 147
% identity 88

NCBI Description Z.mays mRNA for ribosomal protein L39

Seq. No.

Contig ID 57886\_1.R1040

5'-most EST LIB3106-068-P1-K1-G4

17993

Method BLASTX
NCBI GI g3747026
BLAST score 217
E value 2.0e-17
Match length 78
% identity 47

NCBI Description (AF093244) import protein Tim9p [Saccharomyces cerevisiae]

Seq. No.

\*3

17994

Contig ID 57890\_1.R1040 5'-most EST zhf700963567.h1

Seq. No. 17995

Contig ID 57904 1.R1040 5'-most EST leu701148801.h1

Seq. No. 17996

Contig ID 57906\_1.R1040

5'-most EST LIB3106-068-P1-K1-A12

Method BLASTX
NCBI GI g1362016
BLAST score 199



E value 2.0e-15
Match length 90
% identity 50

NCBI Description zinc finger protein 3 - Arabidopsis thaliana >gi\_790677

(L39646) zinc finger protein [Arabidopsis thaliana] >gi 4063732 (AC006259) ZFP3 zinc finger protein

[Arabidopsis thaliana]

Seq. No. 17997

Contig ID 57913\_1.R1040

5'-most EST uC-gmflminsoy045b04b1

Method BLASTX
NCBI GI g1737222
BLAST score 907
E value 4.0e-98
Match length 211
% identity 82

NCBI Description (U79958) BP-80 vacuolar sorting receptor [Pisum sativum]

Seq. No. 17998

Contig ID 57916\_1.R1040 5'-most EST fde700874549.h1

Seq. No. 17999

Contig ID 57921\_1.R1040 5'-most EST seb700654158.h1

Method BLASTX
NCBI GI g3894168
BLAST score 161
E value 3.0e-11
Match length 78
% identity 41

NCBI Description (AC005312) similar to phloem-specific lectin [Arabidopsis

thaliana]

Seq. No. 18000

Contig ID 57927 1.R1040

5'-most EST jC-gmst02400050b05a1

Seq. No. 18001

Contig ID 57932\_1.R1040 5'-most EST zhf700957206.h1

Seq. No. 18002

Contig ID 57938\_1.R1040

5'-most EST LIB3106-067-P1-K1-H2

Seq. No. 18003

Contig ID 57958 1.R1040

5'-most EST LIB3106-067-P1-K1-C10

Seq. No. 18004

Contig ID 57966\_1.R1040

5'-most EST LIB3138-003-Q1-N1-E4

Method BLASTX NCBI GI g2982459 BLAST score 330



E value 2.0e-30 Match length 84 % identity 85

NCBI Description (AL022223) putative protein [Arabidopsis thaliana]

Seq. No. 18005

Contig ID 57988\_1.R1040

5'-most EST LIB3107-002-Q1-K1-E12

Method BLASTN
NCBI GI g4336435
BLAST score 113
E value 1.0e-56
Match length 271
% identity 86

NCBI Description Lotus japonicus protein phosphatase type 2C (PP2C2) mRNA,

complete cds

Seq. No. 18006

Contig ID 57990\_1.R1040 5'-most EST jsh701064361.h1

Method BLASTX
NCBI GI g974782
BLAST score 1085
E value 1.0e-119
Match length 218
% identity 94

NCBI Description (Z49150) cobalamine-independent methionine synthase

[Solenostemon scutellarioides]

Seq. No. 18007

Contig ID 57996\_1.R1040

5'-most EST LIB3106-066-P1-K1-G7

Seq. No. 18008

Contig ID 58014 1.R1040 5'-most EST epx701105705.h1

Method BLASTX
NCBI GI g4455182
BLAST score 1291
E value 1.0e-143
Match length 307
% identity 72

NCBI Description (AL035521) putative protein [Arabidopsis thaliana]

Seq. No. 18009

Contig ID 58038 1.R1040

5'-most EST uC-qmflminsoy075f04b1

Seq. No. 18010

Contig ID 58039\_1.R1040

5'-most EST LIB3106-032-Q1-K1-A12

Seq. No. 18011

Contig ID 58056 1.R1040

5'-most EST LIB3106-066-P1-K1-C10

Seq. No. 18012



Contig ID 58062\_1.R1040

5'-most EST LIB3106-065-P1-K1-H12

Seq. No. 18013

Contig ID 58080 1.R1040

5'-most EST LIB3106-065-P1-K1-F5

Seq. No. 18014

Contig ID 58082 1.R1040

5'-most EST LIB3106-065-P1-K1-F7

Seq. No. 18015

Contig ID 58083\_1.R1040 5'-most EST fua701041574.h1

Method BLASTX
NCBI GI g3080439
BLAST score 155
E value 5.0e-10
Match length 68
% identity 41

NCBI Description (AL022605) putative protein [Arabidopsis thaliana]

Seq. No. 18016

Contig ID 58085\_1.R1040 5'-most EST wvk700686058.h1

Seq. No. 18017

Contig ID 58088\_1.R1040

5'-most EST LIB3106-065-P1-K1-G4

Seq. No. 18018

Contig ID 58097\_1.R1040

5'-most EST LIB3109-010-Q1-K1-F12

Method BLASTX
NCBI GI g3522949
BLAST score 725
E value 8.0e-77
Match length 212
% identity 57

NCBI Description (AC004411) hypothetical protein [Arabidopsis thaliana]

Seq. No. 18019

Contig ID 58115 1.R1040

5'-most EST LIB3106-065-P1-K1-C5

Seq. No. 18020

Contig ID 58127\_1.R1040

5'-most EST LIB3138-103-Q1-N1-E9

Method BLASTN
NCBI GI g20993
BLAST score 163
E value 3.0e-86
Match length 374
% identity 86

NCBI Description P.vulgaris gene for endopeptidase

Seq. No. 18021



```
58129 1.R1040
Contig ID
                  LIB3106-065-P1-K1-A5
5'-most EST
Method
                  BLASTX
                  q3687240
NCBI GI
                  293
BLAST score
                  2.0e-26
E value
                  94
Match length
% identity
                  59
                  (AC005169) extensin-like protein [Arabidopsis thaliana]
NCBI Description
                  18022
Seq. No.
                  58134 1.R1040
Contig ID
                  LIB3106-064-Q1-K1-F8
5'-most EST
Method
                  BLASTX
NCBI GI
                  g1351945
                  386
BLAST score
                  2.0e-37
E value
                  93
Match length
                   48
% identity
                  FLORAL HOMEOTIC PROTEIN APETALA2 >gi 533709 (U12546)
NCBI Description
                  APETALA2 protein [Arabidopsis thaliana]
                  >gi 2464888 emb CAB16765_ (Z99707) APETALA2 protein
                   [Arabidopsis thaliana]
                   18023
Seq. No.
                   58149 1.R1040
Contig ID
                  vzy700751206.h1
5'-most EST
                  BLASTX
Method
                   g4455202
NCBI GI
BLAST score
                   540
                   6.0e-55
E value
                   203
Match length
% identity
                   48
                  (AL035440) putative APG protein [Arabidopsis thaliana]
NCBI Description
                   18024
Seq. No.
                   58149 2.R1040
Contig ID
5'-most EST
                   jC-gmst02400011e08a1
                   18025
Seq. No.
                   58153 1.R1040
Contig ID
                   LIB3106-064-Q1-K1-F10
5'-most EST
                   BLASTX
Method
NCBI GI
                   g4455169
BLAST score
                   279
                   2.0e-39
E value
                   167
Match length
                   56
% identity
                   (AL035521) putative aldehyde dehydrogenase [Arabidopsis
NCBI Description
```

18026 Seq. No.

58157 1.R1040 Contig ID

LIB3106-064-Q1-K1-F4 5'-most EST

thaliana]

18027 Seq. No.

58167 1.R1040 Contig ID

Seq. No.

Contig ID

5'-most EST

18034

58204 1.R1040

 $LIB31\overline{0}6-063-Q1-K1-G6$ 



```
LIB3106-064-Q1-K1-D5
5'-most EST
                  18028
Seq. No.
                  58169 1.R1040
Contig ID
                  ssr700558932.hl
5'-most EST
                  18029
Seq. No.
                  58171 1.R1040
Contig ID
5'-most EST
                  jsh701066061.hl
Method
                  BLASTX
                  g3402673
NCBI GI
BLAST score
                  269
                   2.0e-23
E value
Match length
                  79
% identity
                   67
NCBI Description (AC004697) unknown protein [Arabidopsis thaliana]
                   18030
Seq. No.
                   58190 1.R1040
Contig ID
                   awf70\overline{0}837461.h1
5'-most EST
                  BLASTN
Method
                   g1335861
NCBI GI
BLAST score
                   113
                   2.0e-56
E value
Match length
                   280
                   90
% identity
NCBI Description Glycine max clathrin heavy chain mRNA, complete cds
                   18031
Seq. No.
                   58190 2.R1040
Contig ID
                   awf70\overline{0}837453.h1
5'-most EST
                   BLASTN
Method
                   g1335861
NCBI GI
BLAST score
                   152
                   5.0e-80
E value
Match length
                   272
% identity
                   89
NCBI Description Glycine max clathrin heavy chain mRNA, complete cds
Seq. No.
                   18032
                   58193 1.R1040
Contig ID
5'-most EST
                   LIB3106-064-Q1-K1-A4
                   BLASTX
Method
NCBI GI
                   g4164576
BLAST score
                   508
E value
                   1.0e-51
Match length
                   155
                   68
% identity
                  (AF098946) CTF2A [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   18033
                   58195 1.R1040
Contig ID
5'-most EST
                   jsh701066983.h1
```



Method BLASTX

NCBI GI g3023961

BLAST score 162

E value 5.0e-11

Match length 67

% identity 58

NCBI Description HOMEOBOX PROTEIN KNOTTED-1-LIKE >gi\_1946222\_emb\_CAA96512\_(Z71980) knotted1-like homeobox protein [Malus domestica]

Seq. No. 18035

Contig ID 58208 1.R1040

5'-most EST LIB3138-079-P1-N1-A2

Seq. No. 18036

Contig ID 58212\_1.R1040 5'-most EST sat701006874.h1

Seq. No. 18037

Contig ID 58221\_1.R1040

5'-most EST LIB3106-063-Q1-K1-F11

Method BLASTX
NCBI GI g4006902
BLAST score 197
E value 5.0e-15
Match length 156
% identity 30

NCBI Description (Z99708) putative protein [Arabidopsis thaliana]

Seq. No. 18038

Contig ID 58228 1.R1040

5'-most EST LIB3170-088-Q1-K1-G4

Method BLASTX
NCBI GI g4567311
BLAST score 462
E value 2.0e-45
Match length 122
% identity 69

NCBI Description (AC005956) putative protein kinase [Arabidopsis thaliana]

Seq. No. 18039

Contig ID 58228\_2.R1040 5'-most EST zsq701128272.h1

Seq. No. 18040

Contig ID 58228\_3.R1040

5'-most EST jC-gmst02400004e11a1

Seq. No. 18041

Contig ID 58228\_5.R1040 5'-most EST pxt700942903.h1

Seq. No. 18042

Contig ID 58228\_6.R1040 5'-most EST asn701138349.h1

Method BLASTX
NCBI GI g4567311
BLAST score 300



E value 2.0e-27
Match length 68
% identity 75

NCBI Description (AC005956) putative protein kinase [Arabidopsis thaliana]

Seq. No. 18043

Contig ID 58232\_1.R1040 5'-most EST leu701149993.h1

Seq. No. 18044

Contig ID 58235\_1.R1040 5'-most EST fC-gmf1700906134a1

Method BLASTX
NCBI GI g2982444
BLAST score 2732
E value 0.0e+00
Match length 796
% identity 42

NCBI Description (AL022224) CLV1 receptor kinase like protein [Arabidopsis

thaliana]

Seq. No. 18045

Contig ID 58262\_1.R1040 5'-most EST uaw700666489.h1

Method BLASTX
NCBI GI g2252860
BLAST score 179
E value 4.0e-25
Match length 97
% identity 66

NCBI Description (AF013294) No definition line found [Arabidopsis thaliana]

Seq. No. 18046

Contig ID 58276 1.R1040

5'-most EST LIB3106-063-Q1-K1-B3

Method BLASTX
NCBI GI g1888357
BLAST score 735
E value 1.0e-146
Match length 501
% identity 54

NCBI Description (X98130) alpha-mannosidase [Arabidopsis thaliana] >gi\_1890154 emb CAA72432\_ (Y11767) alpha-mannosidase

precursor [Arabidopsis thaliana]

Seq. No. 18047

Contig ID 58276 2.R1040

5'-most EST LIB3107-034-Q1-K1-A5

Method BLASTX
NCBI GI g1888357
BLAST score 720
E value 3.0e-76
Match length 195
% identity 66

NCBI Description (X98130) alpha-mannosidase [Arabidopsis thaliana]

>gi 1890154 emb CAA72432 (Y11767) alpha-mannosidase

precursor [Arabidopsis thaliana]



18048 Seq. No.

58276 3.R1040 Contig ID 5'-most EST fC-gmst700651561r8

BLASTX Method q1888357 NCBI GI BLAST score 268 2.0e-23 E value 93 Match length 59 % identity

(X98130) alpha-mannosidase [Arabidopsis thaliana] NCBI Description

>qi 1890154 emb CAA72432 (Y11767) alpha-mannosidase

precursor [Arabidopsis thaliana]

Seq. No. 18049

Contig ID 58279 1.R1040 vzy700753286.h1 5'-most EST

BLASTX Method q3335366 NCBI GI BLAST score 397 4.0e-38 E value 223 Match length % identity 35

(AC003028) unknown protein [Arabidopsis thaliana] NCBI Description

18050 Seq. No.

58281 1.R1040 Contig ID zsg701123884.h1 5'-most EST

BLASTX Method q2583110 NCBI GI 150 BLAST score 1.0e-09 E value 57 Match length

58 % identity

(AC002387) unknown protein [Arabidopsis thaliana] NCBI Description

18051 Seq. No.

58302 1.R1040 Contig ID rlr700901107.hl 5'-most EST

Method BLASTX q3482921 NCBI GI BLAST score 144 5.0e-09 E value 58 Match length % identity 45

(AC003970) Unknown protein [Arabidopsis thaliana] NCBI Description

18052 Seq. No.

58306 1.R1040 Contig ID

5'-most EST LIB3106-062-Q1-K1-F11

Method BLASTX g4033763 NCBI GI BLAST score 346 3.0e-32 E value Match length 280 29 % identity

NCBI Description IMPORTIN BETA-3 SUBUNIT (KARYOPHERIN BETA-3 SUBUNIT)



(RAN-BINDING PROTEIN 5) >gi\_2253156\_emb\_CAA70103\_ (Y08890) Ran GTP binding protein 5 [Homo sapiens]

Seq. No. 18053

Contig ID 58308 1.R1040

5'-most EST LIB3106-062-Q1-K1-F2

Seq. No. 18054

Contig ID 58312\_1.R1040 5'-most EST uC-gmropic019b02b1

Method BLASTX
NCBI GI g1843628
BLAST score 560
E value 1.0e-57
Match length 126
% identity 55

NCBI Description (U88061) SNF5 homolog BSH [Arabidopsis thaliana]

Seq. No. 18055

Contig ID 58313 1.R1040 5'-most EST q5753123 Method BLASTX NCBI GI g2654226 BLAST score 175 E value 1.0e-12 Match length 45 % identity 71

NCBI Description (AJ003069) aminoacyl-t-RNA synthetase [Arabidopsis

thaliana]

Seq. No. 18056

Contig ID 58314 1.R1040

5'-most EST LIB3138-091-Q1-N1-E10

Seq. No. 18057

Contig ID 58323 1.R1040

5'-most EST LIB3106-062-Q1-K1-D3

Seq. No. 18058

Contig ID 58330 1.R1040

5'-most EST LIB3106-062-Q1-K1-E1

Method BLASTX
NCBI GI g3135257
BLAST score 333
E value 5.0e-31
Match length 91
% identity 70

NCBI Description (AC003058) unknown protein [Arabidopsis thaliana]

Seq. No. 18059

Contig ID 58336\_1.R1040 5'-most EST eep700869760.h1

Method BLASTX
NCBI GI g3236247
BLAST score 765
E value 2.0e-81
Match length 225



% identity (ACO04684) SCARECROW-like protein [Arabidopsis thaliana] NCBI Description Seq. No. 18060 Contig ID 58345 1.R1040 dpv701103069.h1 5'-most EST Method BLASTX g4559380 NCBI GI BLAST score 287 1.0e-39 E value Match length 156 % identity 56 (AC006526) putative auxin-responsive GH3 protein NCBI Description [Arabidopsis thaliana] Seq. No. 18061 58345 2.R1040 Contig ID LIB3106-062-Q1-K1-C12 5'-most EST Seq. No. 18062 Contig ID 58346 1.R1040 uC-qmropic071h03b1 5'-most EST Method BLASTX NCBI GI g2505874 BLAST score 794 E value 1.0e-106 238 Match length % identity 79 (Y12776) putative kinase [Arabidopsis thaliana] NCBI Description 18063 Seq. No. 58348 1.R1040 Contig ID LIB3170-022-Q1-K1-A4 5'-most EST BLASTX Method g3329506 NCBI GI BLAST score 242 2.0e-20 E value Match length 122 % identity 44 (AF074723) RNA polymerase transcriptional regulation NCBI Description mediator [Homo sapiens] 18064 Seq. No. 58359 1.R1040 Contig ID 5'-most EST V4L-02-Q1-B1-C6 Method BLASTX q1785613 NCBI GI BLAST score 373

E value 1.0e-35 Match length 165 % identity 47

(U83274) polyphenol oxidase [Vitis vinifera] NCBI Description

Seq. No.

18065

Contig ID

58364 1.R1040

5'-most EST

LIB3139-049-P1-N1-E8

Method

BLASTX



```
g1019946
NCBI GI
                  492
BLAST score
E value
                  1.0e-49
Match length
                  120
% identity
                  78
NCBI Description (U37060) ascorbate peroxidase [Gossypium hirsutum]
                  18066
Seq. No.
                  58372 1.R1040
Contig ID
5'-most EST
                  kl1701202569.h1
Method
                  BLASTX
                  q4063748
NCBI GI
BLAST score
                  440
                  2.0e-43
E value
                  121
Match length
% identity
                   62
NCBI Description (AC005851) unknown protein [Arabidopsis thaliana]
                   18067
Seq. No.
                   58374 1.R1040
Contig ID
                  LIB3106-061-Q1-K1-F9
5'-most EST
                   18068
Seq. No.
                   58393 1.R1040
Contig ID
                   LIB3106-061-Q1-K1-E12
5'-most EST
                   18069
Seq. No.
                   58400 1.R1040
Contig ID
                   LIB3106-061-Q1-K1-E8
5'-most EST
                   18070
Seq. No.
                   58408 1.R1040
Contig ID
                   LIB3139-040-P1-N1-C10
5'-most EST
                   18071
Seq. No.
                   58409 2.R1040
Contig ID
5'-most EST
                   dpv701101608.h1
Seq. No.
                   18072
                   58417 1.R1040
Contig ID
                   sat701012903.hl
5'-most EST
                   BLASTX
Method
                   g2160166
NCBI GI
                   676
BLAST score
E value
                   8.0e-71
                   279
Match length
                   49
% identity
                   (AC000132) No definition line found [Arabidopsis thaliana]
NCBI Description
                   18073
Seq. No.
Contig ID
                   58419 1.R1040
                   LIB3107-035-Q1-K1-C11
 5'-most EST
```

Method BLASTX
NCBI GI g4249419
BLAST score 457
E value 1.0e-45
Match length 165



% identity (AC006072) hypothetical protein, 3' partial [Arabidopsis NCBI Description thaliana]

Seq. No. 18074

Contig ID 58427 1.R1040 kl1701209622.hl 5'-most EST

BLASTN Method q1223925 NCBI GI BLAST score 221 E value 1.0e-121 320 Match length 93 % identity

NCBI Description Vigna radiata carboxypeptidase II mRNA, partial cds

Seq. No. 18075

58430 1.R1040 Contig ID pxt700942520.h1 5'-most EST

18076 Seq. No.

58439 1.R1040 Contig ID

LIB3167-077-P1-K2-A8 5'-most EST

18077 Seq. No.

58443 1.R1040 Contig ID

LIB3106-003-Q1-K1-A10 5'-most EST

BLASTX Method NCBI GI q119931 BLAST score 284 2.0e-25 E value 123 Match length 52 % identity

FERREDOXIN I PRECURSOR >gi 65740 pir FEPM1 ferredoxin [2Fe-2S] I precursor - garden pea >gi 169087 (M31713) NCBI Description

ferredoxin I precursor [Pisum sativum]

18078 Seq. No.

58449 1.R1040 Contig ID 5'-most EST kl1701204782.hl

BLASTN Method g3004543 NCBI GI BLAST score 33 9.0e-09 E value Match length 53 91 % identity

Arabidopsis thaliana chromosome II BAC F19F24 genomic NCBI Description

sequence, complete sequence [Arabidopsis thaliana]

18079 Seq. No.

58449 2.R1040 Contig ID

5'-most EST uC-qmflminsoy030a11b1

18080 Seq. No.

58449 3.R1040 Contig ID 5'-most EST ncj700976889.h1

BLASTX Method g3004556 NCBI GI



BLAST score 184 E value 2.0e-13 Match length 49 % identity 84

NCBI Description (AC003673) hypothetical protein [Arabidopsis thaliana]

Seq. No. 18081

Contig ID 58451\_1.R1040 5'-most EST 2DC-01-Q1-B1-F3

Seq. No. 18082

Contig ID 58455 1.R1040

5'-most EST LIB3138-014-Q1-N2-C7

Method BLASTX
NCBI GI g133447
BLAST score 1645
E value 0.0e+00
Match length 411
% identity 81

NCBI Description DNA-DIRECTED RNA POLYMERASE BETA" CHAIN

>gi\_81957\_pir\_\_S07137 DNA-directed RNA polymerase (EC
2.7.7.6) beta'-2 chain - garden pea chloroplast (fragment)
>gi\_829325\_emb\_CAA27545\_ (X03912) ORF with large areas of
homology to RNA polymerase subunit beta [Pisum sativum]

Seq. No. 18083

Contig ID 58458 1.R1040

5'-most EST LIB31 $\overline{0}6$ -060-Q1-K1-E7

Seq. No. 18084

Contig ID 58490\_1.R1040 5'-most EST epx701104721.h1

Seq. No. 18085

Contig ID 58490\_2.R1040 5'-most EST gsv701055937.h1

Seq. No. 18086

Contig ID 58500\_1.R1040 5'-most EST pxt700945186.h1

Method BLASTX
NCBI GI g2736147
BLAST score 797
E value 3.0e-85
Match length 188
% identity 73

NCBI Description (AF021804) fatty acid hydroxylase Fahlp [Arabidopsis

thaliana] >gi\_3132481 (AC003096) fatty acid hydroxylase,

FAH1 [Arabidopsis thaliana]

Seq. No. 18087

Contig ID 58502\_1.R1040 5'-most EST leu701155506.h1

Seq. No. 18088

Contig ID 58510 1.R1040 5'-most EST seb700652790.h1



Method BLASTX
NCBI GI g3169719
BLAST score 621
E value 2.0e-64
Match length 215
% identity 61

NCBI Description (AF007109) similar to yeast dcpl [Arabidopsis thaliana]

Seq. No. 18089

Contig ID 58510\_2.R1040 5'-most EST zzp700833033.h1

Method BLASTX
NCBI GI g3169719
BLAST score 313
E value 1.0e-28
Match length 106
% identity 62

NCBI Description (AF007109) similar to yeast dcpl [Arabidopsis thaliana]

Seq. No. 18090

Contig ID 58514\_1.R1040

5'-most EST LIB3106-059-Q1-K1-H9

Method BLASTX
NCBI GI g3482973
BLAST score 274
E value 3.0e-24
Match length 135
% identity 51

NCBI Description (AL031369) putative protein [Arabidopsis thaliana]

Seq. No. 18091

Contig ID 58519 1.R1040 5'-most EST leu701151173.h1

Seq. No. 18092

Contig ID 58539\_1.R1040 5'-most EST uC-gmronoir007b06b1

Seq. No. 18093

Contig ID 58542 1.R1040

5'-most EST LIB3138-048-Q1-N1-B9

Method BLASTX
NCBI GI g4538926
BLAST score 670
E value 6.0e-70
Match length 182
% identity 74

NCBI Description (AL049483) putative phosphatidylserine decarboxylase

[Arabidopsis thaliana]

Seq. No. 18094

Contig ID 58543 1.R1040

5'-most EST LIB3109-055-Q1-K1-C7

Seq. No. 18095

Contig ID 58545\_1.R1040 5'-most EST leu701146828.h1



```
BLASTX
Method
NCBI GI
                  g3132477
BLAST score
                   636
E value
                   2.0e-66
Match length
                   214
% identity
                   16
                  (AC003096) unknown protein [Arabidopsis thaliana]
NCBI Description
                   18096
Seq. No.
Contig ID
                   58550 1.R1040
                   pmv700894915.h1
5'-most EST
Method
                   BLASTX
                   g3063446
NCBI GI
BLAST score
                   915
E value
                   5.0e-99
Match length
                   240
% identity
                   74
                  (AC003981) F22013.8 [Arabidopsis thaliana]
NCBI Description
                   18097
Seq. No.
Contig ID
                   58552 1.R1040
                   LIB3109-038-Q1-K1-G5
5'-most EST
                   18098
Seq. No.
                   58568 1.R1040
Contig ID
                   uC\text{-}gmflminsoy108e04b1
5'-most EST
Seq. No.
                   18099
                   58573 1.R1040
Contig ID
5'-most EST
                   LIB3106-058-Q1-K1-H12
Seq. No.
                   18100
                   58583 1.R1040
Contig ID
                   LIB3106-059-Q1-K1-A2
5'-most EST
                   BLASTX
Method
                   g2224925
NCBI GI
                   742
BLAST score
E value
                   6.0e-79
                   163
Match length
% identity
                   86
                   (AF002678) kinesin-like protein [Arabidopsis thaliana]
NCBI Description
                   18101
Seq. No.
                   58584 1.R1040
Contig ID
5'-most EST
                   taw700658126.h1
                   BLASTX
Method
                   q113742
NCBI GI
BLAST score
                   415
E value
                   3.0e-40
                   223
Match length
% identity
                   42
                   AMINOPEPTIDASE N (ALPHA-AMINOACYLPEPTIDE HYDROLASE)
NCBI Description
```

>gi\_147142 (M15273) peptidase N [Escherichia coli]
>gi\_147144 (M15676) aminopeptidase N [Escherichia coli]
>gi\_1787163 (AE000195) aminopeptidase N [Escherichia coli]
>gi\_4062498\_dbj\_BAA35684\_ (D90731) Aminopeptidase n (EC
3.4.11.2) (alpha-aminoacylpeptide hydrolase). [Escherichia



## coli]

Seq. No. 18102

Contig ID 58589\_1.R1040

5'-most EST LIB3106-018-Q1-K1-C11

Seq. No. 18103

Contig ID 58605 1.R1040
5'-most EST g5677214
Method BLASTX
NCBI GI g3080389
BLAST score 678
E value 5.0e-71

Match length 246 % identity 60

NCBI Description (AL022603) putative membrane associated protein

[Arabidopsis thaliana]

Seq. No. 18104

Contig ID 58605\_2.R1040 5'-most EST dpv701097068.h1

Method BLASTX
NCBI GI g3080389
BLAST score 238
E value 7.0e-20
Match length 128
% identity 49

NCBI Description (AL022603) putative membrane associated protein

[Arabidopsis thaliana]

Seq. No. 18105

Contig ID 58605 4.R1040 5'-most EST leu701156085.h1

Seq. No. 18106

Contig ID 58611\_1.R1040 5'-most EST zhf700955121.h1

Method BLASTX
NCBI GI g3170230
BLAST score 356
E value 1.0e-33
Match length 173
% identity 47

NCBI Description (AF041848) fructose-6-phosphate 2-kinase

/fructose-2,6-bisphosphatase [Spinacia oleracea]

Seq. No. 18107

Contig ID 58614\_1.R1040 5'-most EST zpv700761779.h1

Seq. No. 18108

Contig ID 58632\_1.R1040 5'-most EST rlr700901961.h1

Seq. No. 18109

Contig ID 58640 1.R1040

5'-most EST LIB3138-040-Q1-N1-C9

NCBI Description

```
BLASTX
Method
                  g4467098
NCBI GI
                  556
BLAST score
E value
                  4.0e-57
Match length
                  178
% identity
                  67
NCBI Description (AL035538) putative protein [Arabidopsis thaliana]
                  18110
Seq. No.
                  58658 1.R1040
Contig ID
                  LIB3106-058-Q1-K1-A10
5'-most EST
Seq. No.
                  18111
                  58660 1.R1040
Contig ID
5'-most EST
                  jC-gmle01810006h05a1
Method
                  BLASTX
NCBI GI
                  g2266985
BLAST score
                  702
E value
                   4.0e-74
Match length
                  195
% identity
                  71
NCBI Description (Y13943) METRS [Arabidopsis thaliana]
Seq. No.
                  18112
                   58678 1.R1040
Contig ID
                  LIB3106-057-Q1-K1-B2
5'-most EST
                   18113
Seq. No.
                   58681 1.R1040
Contig ID
                   sat701008103.h1
5'-most EST
                   18114
Seq. No.
                   58694 1.R1040
Contig ID
                   LIB3106-009-Q1-K1-D10
5'-most EST
Seq. No.
                   18115
                   58701_1.R1040
Contig ID
5'-most EST
                   LIB3106-056-Q1-K1-H12
                   BLASTX
Method
                   g4240253
NCBI GI
BLAST score
                   145
                   8.0e-09
E value
                   65
Match length
                   45
% identity
NCBI Description (AB020689) KIAA0882 protein [Homo sapiens]
                   18116
Seq. No.
                   58708 1.R1040
Contig ID
5'-most EST
                   LIB3106-057-Q1-K1-A12
                   BLASTX
Method
NCBI GI
                   q1076301
                   167
BLAST score
                   2.0e-11
E value
                   101
Match length
                   24
% identity
```

>gi 1161514\_emb\_CAA64407\_ (X94937) CONSTANS protein

CONSTANS protein - Arabidopsis thaliana



## [Arabidopsis thaliana]

Seq. No. 18117

Contig ID 58714\_1.R1040

5'-most EST LIB3106-056-Q1-K1-F12

Seq. No. 18118

Contig ID 58715\_1.R1040 5'-most EST zhf700955643.h1

Method BLASTX
NCBI GI g2341032
BLAST score 689
E value 3.0e-72
Match length 319
% identity 48

NCBI Description (AC000104) EST gb\_ATTS0956 comes from this gene.

[Arabidopsis thaliana]

Seq. No. 18119

Contig ID 58717\_1.R1040 5'-most EST bth700848122.h1

Seq. No. 18120

Contig ID 58724\_1.R1040 5'-most EST ncj700976961.h1

Method BLASTX
NCBI GI g122087
BLAST score 632
E value 4.0e-66
Match length 133
% identity 96

NCBI Description HISTONE H3 >gi\_81849\_pir\_S04520 histone H3 (clone pH3c-1)

- alfalfa >gi\_82609\_pir\_A26014 histone H3 - wheat >gi\_19607\_emb\_CAA31964 (X13673) histone H3 (AA 1-136) [Medicago sativa] >gi\_19609\_emb\_CAA31965 (X13674) histone H3 (AA 1-136) [Medicago sativa] >gi\_21797\_emb\_CAA25451 (X00937) H3 histone [Triticum aestivum] >gi\_488565 (U09459)

histone H3.1 [Medicago sativa] >gi\_2565419 (AF026803)

histone H3 [Onobrychis viciifolia]

Seq. No. 18121

Contig ID 58728\_1.R1040

5'-most EST LIB3138-003-Q1-N1-E1

Method BLASTN
NCBI GI g2828182
BLAST score 38
E value 2.0e-11
Match length 241
% identity 84

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MOJ9, complete sequence [Arabidopsis thaliana]

Seq. No. 18122

Contig ID 58728 2.R1040 5'-most EST ncj700978629.h1

Seq. No. 18123



58728 3.R1040 Contig ID jC-gmle01810014b11d1 5'-most EST

18124 Seq. No.

58734 1.R1040 Contig ID jex700903395.hl 5'-most EST

BLASTX Method q3249086 NCBI GI 511 BLAST score 6.0e-52 E value 112 Match length 86 % identity

(AC004473) Contains similarity to 21 KD subunit of the NCBI Description Arp2/3 protein complex (ARC21) gb\_AF006086 from Homo

sapiens. EST gb\_Z37222 comes [Arabidopsis thaliana]

Seq. No. 18125

58736 1.R1040 Contig ID

LIB3106-056-Q1-K1-E6 5'-most EST

18126 Seq. No.

Contig ID 58769 1.R1040

LIB3106-055-Q1-K1-H5 5'-most EST

BLASTX Method g400986 NCBI GI BLAST score 239 E value 4.0e-20 66 Match length 76 % identity

50S RIBOSOMAL PROTEIN L15, CHLOROPLAST PRECURSOR (CL15) NCBI Description

>gi\_81947\_pir\_\_S18001 ribosomal protein L15 precursor, chloroplast - garden pea (fragment) >gi\_20867\_emb\_CAA77595\_ (Z11510) Plastid ribosomal protein CL15 [Pisum sativum]

18127 Seq. No.

58791 1.R1040 Contig ID

LIB3106-055-Q1-K1-D5 5'-most EST

BLASTX Method g3913661 NCBI GI BLAST score 220 7.0e-18 E value 66 Match length % identity 65

FERREDOXIN B (FD B) >gi\_322807\_pir\_\_S28199 ferredoxin [2Fe-2S] B - giant taro >gi\_264602\_bbs\_123934 ferredoxin B NCBI Description

isoprotein, Fd B [Alocasia macrorrhiza=elephant ear,

Schott, Peptide, 98 aa]

18128 Seq. No.

58798 1.R1040 Contig ID 5'-most EST  $gsv70\overline{1}043854.h1$ 

Method BLASTX q3176874 NCBI GI 421 BLAST score E value 3.0e-41Match length 184 % identity 47



NCBI Description (AF065639) cucumisin-like serine protease [Arabidopsis thaliana]

Seq. No. 18129

Contig ID 58806\_1.R1040

5'-most EST uC-gmflminsoy081d10b1

Seq. No. 18130

Contig ID 58809 1.R1040

5'-most EST LIB3106-054-Q1-K1-E7

Seq. No. 18131

Contig ID 58817\_1.R1040 5'-most EST crh700852024.h1

Seq. No. 18132

Contig ID 58818\_1.R1040

5'-most EST LIB3106-054-Q1-K1-F4

Method BLASTX
NCBI GI 94432865
BLAST score 599
E value 2.0e-66
Match length 148
% identity 84

NCBI Description (AC006300) putative cellulose synthase catalytic subunit

[Arabidopsis thaliana]

Seq. No. 18133

Contig ID 58823\_1.R1040 5'-most EST sat701012735.h1

Seq. No. 18134

Contig ID 58826 1.R1040 5'-most EST kl1701213544.h1

Method BLASTX
NCBI GI g3367536
BLAST score 535
E value 1.0e-54
Match length 120
% identity 89

NCBI Description (AC004392) Contains similarity to symbiosis-related like

protein F1N20.80 gi\_2961343 from A. thaliana BAC gb AL022140. EST gb\_T04695 comes from this gene.

[Arabidopsis thaliana]

Seq. No. 18135

Contig ID 58830\_1.R1040

5'-most EST jC-gmf102220144g08a1

Method BLASTX
NCBI GI g2827699
BLAST score 261
E value 2.0e-22
Match length 108
% identity 56

NCBI Description (AL021684) predicted protein [Arabidopsis thaliana]

Seq. No. 18136



Contig ID 58835\_1.R1040

5'-most EST LIB3107-064-Q1-K1-E6

Method BLASTN
NCBI GI g2262155
BLAST score 50
E value 4.0e-19
Match length 118
% identity 86

NCBI Description DNA sequence of Arabidopsis thaliana BAC F5J6 from chromosome IV, complete sequence [Arabidopsis thaliana]

Seq. No. 18137

Contig ID 58835\_2.R1040 5'-most EST kl1701203127.h1

Seq. No. 18138

Contig ID 58836 1.R1040

Seq. No. 18139

Contig ID 58842 1.R1040

5'-most EST LIB3106-054-Q1-K1-C11

Seq. No. 18140

Contig ID 58854 1.R1040

5'-most EST jC-gmle01810086f03d1

Method BLASTX
NCBI GI g3860263
BLAST score 262
E value 9.0e-23
Match length 78
% identity 60

NCBI Description (AC005824) putative cytochrome p450 protein [Arabidopsis

thaliana]

Seq. No. 18141

Contig ID 58861\_1.R1040

5'-most EST LIB3106-054-Q1-K1-A7

Seq. No. 18142

Contig ID 58864\_1.R1040

5'-most EST LIB3106-054-Q1-K1-B11

Seq. No. 18143

Contig ID 58866\_1.R1040 5'-most EST kmv700740915.h1

Method BLASTX
NCBI GI g2982469
BLAST score 428
E value 5.0e-42
Match length 110
% identity 74

NCBI Description (AL022223) putative protein [Arabidopsis thaliana]

Seq. No. 18144

Contig ID 58871\_1.R1040 5'-most EST sat701014433.h1



Method BLASTX
NCBI GI g3165581
BLAST score 489
E value 1.0e-48
Match length 362
% identity 34

NCBI Description (AF067942) similar to lysosomal acid lipases (SW:P38571)

[Caenorhabditis elegans]

Seq. No. 18145

Contig ID 58875\_1.R1040

5'-most EST LIB3106-052-Q1-K1-G5

Seq. No. 18146

Contig ID 58882\_1.R1040

5'-most EST jC-gmle01810007c06a1

Method BLASTX
NCBI GI g3776557
BLAST score 198
E value 3.0e-15
Match length 146
% identity 36

NCBI Description (AC005388) Contains similarity to gi\_2924495 hypothetical

protein Rv1920 from Mycobacterium tuberculosis genome

gb AL022020. [Arabidopsis thaliana]

Seq. No. 18147

Contig ID 58882\_2.R1040

5'-most EST LIB3106-052-Q1-K1-H3

Seq. No. 18148

Contig ID 58883\_1.R1040

5'-most EST LIB3106-052-Q1-K1-H4

Seq. No. 18149

Contig ID 58887\_1.R1040

5'-most EST uC-gmronoir074a02b1

Method BLASTX
NCBI GI g2251248
BLAST score 171
E value 1.0e-11
Match length 179
% identity 28

NCBI Description (AF003352) unknown [Mus musculus]

Seq. No. 18150

Contig ID 58892\_1.R1040

5'-most EST LIB3106-052-Q1-K1-E9

Seq. No. 18151

Contig ID 58901\_1.R1040

5'-most EST LIB3106-052-Q1-K1-F7

Seq. No. 18152

Contig ID 58925\_1.R1040 5'-most EST pmv700893843.h1



```
18153
Seq. No.
                  58926 1.R1040
Contig ID
                  LIB3106-052-Q1-K1-B10
5'-most EST
                  BLASTX
Method
                  g3341684
NCBI GI
                  151
BLAST score
                  7.0e-10
E value
                  91
Match length
% identity
NCBI Description (AC003672) hypothetical protein [Arabidopsis thaliana]
                  18154
Seq. No.
                   58930 1.R1040
Contig ID
                  LIB3106-052-Q1-K1-B3
5'-most EST
Seq. No.
                   18155
                   58939 1.R1040
Contig ID
                   jC-gmro02800038h11a1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3335372
BLAST score
                   303
E value
                   2.0e-27
                   134
Match length
                   46
% identity
NCBI Description (AC003028) putative SRG1 protein [Arabidopsis thaliana]
Seq. No.
                   18156
                   58945 1.R1040
Contig ID
                   LIB3106-051-Q1-K1-H6
5'-most EST
                   18157
Seq. No.
                   58947 1.R1040
Contig ID
                   LIB3106-052-Q1-K1-A1
5'-most EST
                   BLASTX
Method
                   g2982285
NCBI GI
BLAST score
                   364
                   2.0e-34
E value
                   88
Match length
                   69
% identity
                   (AF051227) GASA5-like protein [Picea mariana]
NCBI Description
                   18158
Seq. No.
                   58950 2.R1040
Contig ID
                   LIB3139-060-P1-N1-A11
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3786011
BLAST score
                   211
                   4.0e-32
E value
                   140
Match length
                   59
% identity
```

NCBI Description

(AC005499) putative elongation factor [Arabidopsis

thalianal

Seq. No. 18159

58950 3.R1040 Contig ID

jC-gmle01810094e08a1 5'-most EST

BLASTX Method



```
g3786011
NCBI GI
BLAST score
                  266
                   6.0e-23
E value
                  109
Match length
% identity
                  (AC005499) putative elongation factor [Arabidopsis
NCBI Description
                  thaliana]
                   18160
Seq. No.
                   58952 1.R1040
Contig ID
5'-most EST
                   g5677838
                   18161
Seq. No.
                   58955 1.R1040
Contig ID
5'-most EST
                   wvk700682003.h1
Seq. No.
                   18162
                   58966 1.R1040
Contiq ID
                   LIB3106-051-Q1-K1-G6
5'-most EST
                   18163
Seq. No.
Contig ID
                   58971 1.R1040
5'-most EST
                   LIB3106-051-Q1-K1-D6
                   BLASTX
Method
NCBI GI
                   g3061271
BLAST score
                   238
E value
                   5.0e-20
Match length
                   75
% identity
NCBI Description (AB012863) NPCA1 [Nicotiana paniculata]
Seq. No.
                   18164
                   58971 2.R1040
Contig ID
                   jex70\overline{0}903617.h1
5'-most EST
                   BLASTX
Method
                   g310921
NCBI GI
                   165
BLAST score
                   1.0e-11
E value
                   55
Match length
                   62
% identity
NCBI Description (L19255) carbonic anhydrase [Nicotiana tabacum]
                   18165
Seq. No.
                   58971 3.R1040
Contig ID
5'-most EST
                   kmv700740490.h1
                   18166
Seq. No.
                   58975 1.R1040
Contig ID
5'-most EST
                   LIB3106-051-Q1-K1-E12
Seq. No.
                   18167
                   58992 1.R1040
```

Contig ID LIB3139-037-P1-N1-H8 5'-most EST

BLASTN Method

q3510343 NCBI GI BLAST score 42 6.0e-14 E value



Match length 351 % identity 88

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MJC20, complete sequence [Arabidopsis thaliana]

Seq. No. 18168

Contig ID 59012 1.R1040

5'-most EST LIB3106-051-Q1-K1-B10

Seq. No. 18169

Contig ID 59030\_1.R1040

5'-most EST LIB3106-050-Q1-K1-H12

Method BLASTX
NCBI GI g2346966
BLAST score 170
E value 4.0e-12
Match length 41
% identity 76

NCBI Description (AB004871) CPC [Arabidopsis thaliana]

>gi\_4559383\_gb\_AAD23043.1\_AC006526\_8 (AC006526) putative

DNA binding protein CPC [Arabidopsis thaliana]

Seq. No. 18170

Contig ID 59035\_1.R1040 5'-most EST pxt700943088.h1

Method BLASTX
NCBI GI g2749939
BLAST score 235
E value 3.0e-19
Match length 78
% identity 55

NCBI Description (U70999) CCS1 [Chlamydomonas reinhardtii] >gi\_2749941

(U71000) CCS1 [Chlamydomonas reinhardtii]

Seq. No. 18171

Contig ID 59077\_1.R1040

5'-most EST LIB3106-049-Q1-K1-H1

Method BLASTX
NCBI GI g4539324
BLAST score 220
E value 2.0e-17
Match length 48
% identity 85

NCBI Description (AL035679) kinesin like protein [Arabidopsis thaliana]

Seq. No. 18172

Contig ID 59085\_1.R1040

5'-most EST jC-gmst02400049h12d1

Method BLASTX
NCBI GI g2565436
BLAST score 303
E value 2.0e-27
Match length 70
% identity 86

NCBI Description (AF028842) DegP protease precursor [Arabidopsis thaliana]

Seq. No. 18173



Contig ID 59088\_1.R1040

5'-most EST LIB3106-050-Q1-K1-A11

Seq. No. 18174

Contig ID 59090 1.R1040

5'-most EST LIB3106-050-Q1-K1-A12

Seq. No. 18175

Contig ID 59092\_1.R1040 5'-most EST leu701154508.h1

Method BLASTX
NCBI GI g2146800
BLAST score 418
E value 5.0e-41
Match length 151
% identity 56

NCBI Description anthocyanin 3 glucoside: rhamnosyltransferase - garden

petunia >gi\_454245\_emb\_CAA50376\_ (X71059) anthocyanin 3 glucoside: rhamnosyltransferase [Petunia x hybrida]

>gi 454253 emb CAA50377 (X71060) anthocyanin:

rhamnosyltransferase [Petunia x hybrida]

Seq. No. 18176

Contig ID 59094\_1.R1040

5'-most EST LIB3106-049-Q1-K1-F2

Seq. No. 18177

Contig ID 59096\_1.R1040

5'-most EST LIB3106-049-Q1-K1-F4

Method BLASTX
NCBI GI g3096947
BLAST score 243
E value 2.0e-20
Match length 118
% identity 42

NCBI Description (Y16327) putative cyclic nucleotide-regulated ion channel

[Arabidopsis thaliana]

Seq. No. 18178

Contig ID 59096\_2.R1040 5'-most EST rca700998222.h1

Seq. No. 18179

Contig ID 59110\_1.R1040 5'-most EST fua701039040.h1

Seq. No. 18180

Contig ID 59111\_1.R1040 5'-most EST 2DC-01-Q1-E1-H7

Seq. No. 18181

Contig ID 59118\_1.R1040 5'-most EST fua701043193.h1

Method BLASTX
NCBI GI g3033379
BLAST score 350
E value 1.0e-32



Match length 120 % identity 58

NCBI Description (AC004238) putative DNA-binding protein [Arabidopsis

thaliana]

Seq. No. 18182

Contig ID 59136\_1.R1040 5'-most EST rlr700900022.h1

Method BLASTX
NCBI GI g3335373
BLAST score 167
E value 1.0e-11
Match length 87
% identity 37

NCBI Description (AC003028) putative GTL1 protein [Arabidopsis thaliana]

Seq. No. 18183

Contig ID 59149\_1.R1040 5'-most EST epx701104068.h1

Seq. No. 18184

Contig ID 59153\_1.R1040

5'-most EST uC-gmrominsoy093b05b1

Method BLASTN
NCBI GI g22069
BLAST score 41
E value 1.0e-13
Match length 192
% identity 85

NCBI Description V.radiata mRNA for ACC synthase

Seq. No. 18185

Contig ID 59161\_1.R1040 5'-most EST epx701107416.h1

Seq. No. 18186

Contig ID 59175\_1.R1040 5'-most EST hrw701062928.h1

Method BLASTX
NCBI GI g3420051
BLAST score 258
E value 5.0e-35
Match length 74
% identity 92

% identity 92
NCBI Description (AC004680) unknown protein [Arabidopsis thaliana]

Seq. No. 18187

Contig ID 59175\_2.R1040 5'-most EST bth700846565.h1

Method BLASTN
NCBI GI g3420043
BLAST score 113
E value 1.0e-56
Match length 269
% identity 86

NCBI Description Arabidopsis thaliana chromosome II BAC F23F1 genomic sequence, complete sequence [Arabidopsis thaliana]



```
18188
Seq. No.
                  59184 1.R1040
Contig ID
                  LIB3106-048-Q1-K1-E9
5'-most EST
Seq. No.
                  18189
                  59185 1.R1040
Contig ID
                  uC-gmropic025e03b1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q719291
BLAST score
                  312
E value
                  1.0e-55
                  155
Match length
% identity
                  (U19134) unknown [Arabidopsis thaliana]
NCBI Description
                  >gi_1095007_prf__2107236A SABRE gene [Arabidopsis thaliana]
                   18190
Seq. No.
                   59199 1.R1040
Contig ID
                   ssr700557726.h1
5'-most EST
                   18191
Seq. No.
                   59205 1.R1040
Contig ID
                   LIB3106-048-Q1-K1-B7
5'-most EST
                   18192
Seq. No.
Contig ID
                   59216 2.R1040
                   bth700844414.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g1345933
BLAST score
                   149
E value
                   1.0e-09
Match length
                   68
                   49
% identity
                   CITRATE SYNTHASE, GLYOXYSOMAL PRECURSOR (GCS)
NCBI Description
                   >gi 1084323 pir__S53007 citrate synthase - cucurbit
                   >gi_975633_dbj_BAA07328_ (D38132) glyoxysomal citrate
                   synthase [Cucurbita sp.]
                   18193
Seq. No.
                   59226 1.R1040
Contig ID
5'-most EST
                   q5678036
                   BLASTX
Method
                   g4539330
NCBI GI
                   321
BLAST score
                   2.0e-29
E value
Match length
                   169
                   42
% identity
                   (AL035679) putative receptor-like protein kinase (fragment)
NCBI Description
```

Contig ID 59226\_2.R1040

5'-most EST LIB3106-047-Q1-K1-H5

[Arabidopsis thaliana]

Method BLASTX
NCBI GI g1809257
BLAST score 215



```
2.0e-17
E value
                  98
Match length
% identity
                  43
                  (U59316) serine/threonine protein kinase Pto [Lycopersicon
NCBI Description
                  esculentum]
                  18195
Seq. No.
                  59229 1.R1040
Contig ID
                  uC-gmronoir031f10b1
5'-most EST
                  18196
Seq. No.
                  59232 1.R1040
Contig ID
                  LIB3106-047-Q1-K1-E5
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3560141
BLAST score
                  160
                   6.0e-11
E value
Match length
                   54
                   57
% identity
                  (AL031534) ribosomal protein 133-like protein
NCBI Description
                   [Schizosaccharomyces pombe]
                   18197
Seq. No.
                   59233 2.R1040
Contig ID
                   LIB3106-047-Q1-K1-E6
5'-most EST
                   18198
Seq. No.
                   59235 1.R1040
Contig ID
                   pcp700992538.hl
5'-most EST
                   BLASTX
Method
                   g4539329
NCBI GI
                   838
BLAST score
                   4.0e-90
E value
                   204
Match length
                   72
% identity
NCBI Description (AL035679) ES43 like protein [Arabidopsis thaliana]
                   18199
Seq. No.
                   59241_1.R1040
Contig ID
5'-most EST
                   wvk700680922.h1
                   BLASTX
Method
                   q1001603
NCBI GI
                   286
BLAST score
E value
                   3.0e-25
Match length
                   169
% identity
                   38
                   (D64000) hypothetical protein [Synechocystis sp.]
NCBI Description
                   18200
Seq. No.
```

Contiq ID

59241 2.R1040

5'-most EST

LIB3138-042-Q1-N1-G11

Seq. No.

18201

Contig ID

59247 1.R1040

5'-most EST LIB3106-047-Q1-K1-G12

Seq. No.

18202



Contig ID 59282 1.R1040 5'-most EST bth700847658.h1

Seq. No. 18203

Contig ID 59291\_1.R1040

5'-most EST LIB3106-047-Q1-K1-A10

Method BLASTN
NCBI GI g871769
BLAST score 38
E value 6.0e-12
Match length 110
% identity 90

NCBI Description V.unguiculata mRNA for glycin-rich protein

Seq. No. 18204

Contig ID 59294\_1.R1040 5'-most EST ncj700985947.h1

Seq. No. 18205

Contig ID 59301\_1.R1040

5'-most EST jC-gmst02400077e12d1

Seq. No. 18206

Contig ID 59301\_2.R1040

5'-most EST LIB3106-046-Q1-K1-F6

Seq. No. 18207

Contig ID 59314 1.R1040 5'-most EST hyd700731222.h1

Method BLASTX
NCBI GI g4138265
BLAST score 419
E value 4.0e-41
Match length 136

% identity 62

NCBI Description (AJ006228) Avr9 elicitor response protein [Nicotiana

tabacum]

Seq. No. 18208

Contig ID 59316\_1.R1040

5'-most EST LIB3106-022-Q1-K1-H8

Seq. No. 18209

Contig ID 59317\_1.R1040 5'-most EST xpa700793684.h1

Seq. No. 18210

Contig ID 59317\_2.R1040

5'-most EST jC-gmro02910004e05a1

Seq. No. 18211

Contig ID 59321 1.R1040 5'-most EST ncj700984969.h1

Method BLASTX
NCBI GI g4455367
BLAST score 563
E value 7.0e-58



Match length 207 % identity 60

NCBI Description (AL035524) putative protein [Arabidopsis thaliana]

Seq. No. 18212

Contig ID 59327\_1.R1040

5'-most EST LIB31 $\overline{0}6$ -046-Q1-K1-F1

Method BLASTX
NCBI GI g4432832
BLAST score 311
E value 8.0e-30
Match length 94
% identity 73

NCBI Description (AC006283) similar to protein Htf9C [Arabidopsis thaliana]

Seq. No. 18213

Contig ID 59333\_1.R1040 5'-most EST fC-gmf1700900022a1 Method BLASTX

NCBI GI g2804278 BLAST score 1203 E value 1.0e-132 Match length 276 % identity 84

NCBI Description (AB003516) squalene epoxidase [Panax ginseng]

Seq. No. 18214

Contig ID 59343\_1.R1040

5'-most EST LIB3106-046-Q1-K1-D11

Method BLASTN
NCBI GI g535585
BLAST score 34
E value 2.0e-09
Match length 305
% identity 85

NCBI Description Medicago sativa proline-rich protein mRNA, complete cds

Seq. No. 18215

Contig ID 59343 2.R1040 5'-most EST pxt700945060.h1

Seq. No. 18216

Contig. ID 59351 1.R1040

5'-most EST LIB3106-046-Q1-K1-B1

Seq. No. 18217

Contig ID 59353\_1.R1040

5'-most EST LIB3109-028-Q1-K1-F5

Method BLASTX
NCBI GI g1755178
BLAST score 249
E value 4.0e-21
Match length 105
% identity 50

NCBI Description (U75200) germin-like protein [Arabidopsis thaliana]

Seq. No. 18218



```
59365 1.R1040
Contig ID
5'-most EST
                  leu701148949.hl
                  18219
Seq. No.
                  59371 1.R1040
Contig ID
                  LIB3106-045-Q1-K1-H9
5'-most EST
                  BLASTX
Method
                  g3402746
NCBI GI
                  159
BLAST score
                  1.0e-10
E value
                  55
Match length
                  51
% identity
                  (AL022603) putative protein [Arabidopsis thaliana]
NCBI Description
                  >gi_3402762_emb_CAA20208.1_ (AL031187) putative protein
                  [Arabidopsis thaliana]
                  18220
Seq. No.
                  59418 1.R1040
Contig ID
5'-most EST
                  LIB3106-045-Q1-K1-D1
                  18221
Seq. No.
                  59419 1.R1040
Contig ID
                  vzy700750706.hl
5'-most EST
                  BLASTX
Method
                  g4049351
NCBI GI
                   263
BLAST score
                   7.0e-23
E value
                   83
Match length
                   54
% identity
NCBI Description (AL034567) nodulin-like protein [Arabidopsis thaliana]
                   18222
Seq. No.
                   59422 1.R1040
Contig ID
5'-most EST
                   LIB3106-045-Q1-K1-D2
                   BLASTX
Method
NCBI GI
                   q4115357
BLAST score
                   368
                   6.0e-35
E value
                   160
Match length
                   47
% identity
                  (AC005957) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   18223
                   59422 2.R1040
Contig ID
5'-most EST
                   wrq700789515.h2
                   BLASTX
Method
                   q4115357
NCBI GI
BLAST score
                   146
E value
                   1.0e-09
Match length
                   62
% identity
                   (AC005957) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   18224
Seq. No.
                   59424 1.R1040
Contig ID
```

2983

 $eep70\overline{0}869728.h1$ 

BLASTX

5'-most EST

Method

Contig ID



```
q4468979
NCBI GI
BLAST score
                  575
                  5.0e-59
E value
                  226
Match length
% identity
NCBI Description (AL035605) putative protein [Arabidopsis thaliana]
                  18225
Seq. No.
                  59431 1.R1040
Contig ID
                  LIB3167-077-P1-K2-A11
5'-most EST
Method
                  BLASTX
                  g1532135
NCBI GI
BLAST score
                  374
                   9.0e-36
E value
                   96
Match length
% identity
                   74
                   (U49442) chloroplast mRNA-binding protein CSP41 precursor
NCBI Description
                   [Spinacia oleracea]
                   18226
Seq. No.
                   59432 1.R1040
Contig ID
                   jC-gmst02400058d11a1
5'-most EST
                   BLASTX
Method
                   q2895866
NCBI GI
BLAST score
                   1535
                   1.0e-171
E value
Match length
                   376
                   76
% identity
                   (AF045770) methylmalonate semi-aldehyde dehydrogenase
NCBI Description
                   [Oryza sativa]
Seq. No.
                   18227
                   59442 1.R1040
Contig ID
                   LIB3106-045-Q1-K1-C2
5'-most EST
                   BLASTX
Method
                   g1077345
NCBI GI
                   156
BLAST score
                   3.0e-10
E value
                   72
Match length
                   44
% identity
                   hypothetical protein YLR290c - yeast (Saccharomyces
NCBI Description
                   cerevisiae) >gi_596046 (U17243) L8003.16 gene product
                   [Saccharomyces cerevisiae]
                   18228
Seq. No.
                   59448 1.R1040
Contig ID
                   LIB3106-043-Q1-K1-H12
5'-most EST
                   BLASTX
Method
                   g2623295
NCBI GI
BLAST score
                   1060
E value
                   1.0e-116
Match length
                   349
                   61
 % identity
                   (AC002409) hypothetical protein [Arabidopsis thaliana]
NCBI Description
```

59472\_1.R1040

Contig ID

18238

59547 1.R1040



```
LIB3106-043-Q1-K1-G11
5'-most EST
                  18230
Seq. No.
                  59482 1.R1040
Contig ID
                  jC-gmle01810070f08a1
5'-most EST
                  BLASTX
Method
                  g3924606
NCBI GI
                  682
BLAST score
                  1.0e-71
E value
                  248
Match length
% identity
                   40
NCBI Description (AF069442) hypothetical protein [Arabidopsis thaliana]
                  18231
Seq. No.
Contig ID
                   59483 1.R1040
                  jC-gmf102220115g11d1
5'-most EST
                   18232
Seq. No.
                   59497 1.R1040
Contig ID
                   wrq700791996.hl
5'-most EST
Method
                   BLASTX
                   g3822036
NCBI GI
                   157
BLAST score
                   1.0e-10
E value
Match length
                   89
                   39
% identity
NCBI Description (AF072326) endo-1,3-1,4-beta-D-glucanase [Zea mays]
                   18233
Seq. No.
                   59499 1.R1040
Contig ID
                   LIB3109-035-Q1-K6-E9
5'-most EST
                   18234
Seq. No.
                   59501 1.R1040
Contig ID
                   LIB31\overline{0}6-020-Q1-K1-E1
5'-most EST
                   BLASTX
Method
                   g3702327
NCBI GI
BLAST score
                   151
                   1.0e-09
E value
                   70
Match length
% identity
                   44
NCBI Description (AC005397) unknown protein [Arabidopsis thaliana]
                   18235
Seq. No.
Contig ID
                   59518 1.R1040
                   LIB3106-043-Q1-K1-A3
5'-most EST
                   18236
Seq. No.
                   59524 1.R1040
Contig ID
5'-most EST
                   LIB3106-042-Q1-K1-F4
                   18237
 Seq. No.
                   59539 1.R1040
 Contig ID
                   uC-gmropic037c05b1
 5'-most EST
```



```
q4300855
5'-most EST
                  18239
Seq. No.
                  59556 1.R1040
Contig ID
                 jC-gmf102220079g04a1
5'-most EST
                  18240
Seq. No.
                  59565 1.R1040
Contig ID
                  qsv701053091.hl
5'-most EST
                  BLASTX
Method
                  g4468733
NCBI GI
                  519
BLAST score
                  1.0e-52
E value
                  168
Match length
                  58
% identity
NCBI Description (AJ012839) replication factor C subunit
                  [Schizosaccharomyces pombe]
                  18241
Seq. No.
                  59565 2.R1040
Contig ID
                  uaw700662757.h1
5'-most EST
                  BLASTX
Method
                  g4468733
NCBI GI
                  154
BLAST score
                  8.0e-18
E value
Match length
                  76
                  58
% identity
NCBI Description (AJ012839) replication factor C subunit
                   [Schizosaccharomyces pombe]
                  18242
Seq. No.
                   59570 2.R1040
Contig ID
                  uC-gmropic020g07b1
5'-most EST
                  18243
Seq. No.
                   59575_1.R1040
Contig ID
                  LIB3106-042-Q1-K1-A1
5'-most EST
                   18244
Seq. No.
                   59578 1.R1040
Contig ID
                   LIB3106-042-Q1-K1-A2
5'-most EST
                   BLASTX
Method
                   g3721856
NCBI GI
                   810
BLAST score
                   1.0e-109
E value
Match length
                   243
                   73
% identity
NCBI Description (AB014057) beta-Amyrin Synthase [Panax ginseng]
                   18245
Seq. No.
                   59592 1.R1040
 Contig ID
                   epx701109151.hl
 5'-most EST
                   18246
 Seq. No.
                   59595 1.R1040
 Contig ID
```

2986

epx701105443.h1

BLASTX

5'-most EST

Method

```
NCBI GI
                   q3668151
BLAST score
                   147
                   3.0e-09
E value
Match length
                   48
% identity
                   60
                  (AL031764) putative FAD synthetase [Schizosaccharomyces
NCBI Description
                  pombe]
                   18247
Seq. No.
                   59596 1.R1040
Contig ID
                  LIB3106-041-Q1-K1-G4
5'-most EST
Method
                  BLASTX
NCBI GI
                   g115813
BLAST score
                   153
E value
                   6.0e-13
Match length
                   73
% identity
                   53
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE III PRECURSOR
                   (CAB-8) >gi 19182 emb CAA33330 (X15258) Type III
                   chlorophyll a/b-binding protein [Lycopersicon esculentum]
Seq. No.
                   18248
Contig ID
                   59633 1.R1040
                   LIB3106-041-Q1-K1-D4
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4455239
BLAST score
                   152
                   6.0e-10
E value
Match length
                   73
% identity
                   38
                  (AL035523) abscisic acid-induced-like protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   18249
                   59641 1.R1040
Contig ID
5'-most EST
                   uC-gmropic096c04b1
Method
                   BLASTX
NCBI GI
                   q4539335
BLAST score
                   349
E value
                   9.0e-33
Match length
                   90
                   64
% identity
NCBI Description
                  (AL035539) putative protein [Arabidopsis thaliana]
                   18250
Seq. No.
                   59641 2.R1040
Contig ID
                   LIB31\overline{3}8-119-Q1-N1-H12
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4539335
BLAST score
                   720
```

E value 3.0e-76

Match length 182 % identity 66

NCBI Description (AL035539) putative protein [Arabidopsis thaliana]

Seq. No. 18251

59641 3.R1040 Contig ID



5'-most EST

q5605769

```
18252
Seq. No.
                   59645 1.R1040
Contig ID
5'-most EST
                   eep700868359.hl
Method
                   BLASTX
                   g2981475
NCBI GI
                   1385
BLAST score
E value
                   1.0e-154
                   325
Match length
% identity
                  (AF053084) putative cinnamyl alcohol dehydrogenase [Malus
NCBI Description
                   domestica]
                   18253
Seq. No.
                   59653 1.R1040
Contig ID
                   LIB3106-041-Q1-K1-B5
5'-most EST
Method
                   BLASTX
                   q1839188
NCBI GI
BLAST score
                   550
                   2.0e-56
E value
Match length
                   126
                   83
% identity
NCBI Description (U86081) root hair defective 3 [Arabidopsis thaliana]
                   18254
Seq. No.
                   59655 1.R1040
Contig ID
                   LIB3106-040-Q1-K1-G12
5'-most EST
                   BLASTX
Method
                   g2905643
NCBI GI
                   218
BLAST score
                   2.0e-17
E value
                   125
Match length
                   38
% identity
NCBI Description (AF045244) ribitol kinase [Klebsiella pneumoniae]
                   18255
Seq. No.
                   59655 2.R1040
Contig ID
                   uC-gmronoir024c08b1
5'-most EST
                   18256
Seq. No.
                   59664 1.R1040
Contig ID
                   awf700841148.h1
 5'-most EST
                   BLASTX
Method
                    g1706396
NCBI GI
                    433
BLAST score
                    2.0e-50
E value
                    287
Match length
                    43
 % identity
                   ESTRADIOL 17 BETA-DEHYDROGENASE 4 (17-BETA-HSD 4)
 NCBI Description
                    (17-BETA-HYDROXYSTEROID DEHYDROGENASE 4)
                    >gi_2134658_pir__S59136 17beta-hydroxysteroid dehydrogenase
IV - human >gi_1050517_emb_CAA60643_ (X87176)
                    17beta-hydroxysteroid dehydrogenase [Homo sapiens]
                    >gi_4165049 (AF057740) 17-beta-hydroxysteroid dehydrogenase
                    IV [Homo sapiens] >gi 4504505_ref_NP_000405.1_pHSD17B4_
                    hydroxysteroid (17-beta) dehydrogenase
```



Contig ID 59673\_1.R1040 5'-most EST gsv701053327.h1

Method BLASTX
NCBI GI g3763923
BLAST score 309
E value 3.0e-28
Match length 74
% identity 81

NCBI Description (AC004450) hypothetical protein [Arabidopsis thaliana]

Seq. No. 18258

Contig ID 59679\_1.R1040

5'-most EST LIB3106-040-Q1-K1-E4

Seq. No. 18259

Contig ID 59720 1.R1040 5'-most EST pcp700994707.h1

Seq. No. 18260

Contig ID 59720\_2.R1040 5'-most EST hrw701061801.h1

Seq. No. 18261

Contig ID 59721\_1.R1040

5'-most EST LIB3106-040-Q1-K1-B10

Method BLASTX
NCBI GI g4090662
BLAST score 585
E value 2.0e-60
Match length 174
% identity 68

NCBI Description (U96880) maturase [Alangium platanifolium]

Seq. No. 18262

Contig ID 59723 1.R1040

5'-most EST LIB3106-040-Q1-K1-B12

Seq. No. 18263

Contig ID 59725 1.R1040

5'-most EST uC-gmflminsoy079c11b1

Seq. No. 18264

Contig ID 59743\_1.R1040

5'-most EST LIB3106-039-Q1-K1-H10

Seq. No. 18265

Contig ID 59745 1.R1040

5'-most EST LIB3106-039-Q1-K1-H12

Seq. No. 18266

Contig ID 59748\_1.R1040 5'-most EST uC-gmropic043f11b1

Method BLASTX
NCBI GI g2735764
BLAST score 286



E value 1.0e-25
Match length 107
% identity 53

NCBI Description (AF008651) MADS transcriptional factor; STMADS16 [Solanum

tuberosum]

Seq. No. 18267

Contig ID 59763\_1.R1040

5'-most EST LIB3106-039-Q1-K1-F7

Seq. No. 18268

Contig ID 59764\_1.R1040

5'-most EST LIB3106-039-Q1-K1-F8

Method BLASTX
NCBI GI g3845297
BLAST score 157
E value 4.0e-10
Match length 107
% identity 37

NCBI Description (AE001421) hypothetical protein [Plasmodium falciparum]

Seq. No. 18269

Contig ID 59764 2.R1040

5'-most EST LIB3139-064-P1-N1-E12

Seq. No. 18270

Contig ID 59769\_1.R1040 5'-most EST wrg700789445.h2

Seq. No. 18271

Contig ID 59769\_2.R1040 5'-most EST hrw701059589.h1

Seq. No. 18272

Contig ID 59777\_1.R1040 5'-most EST 2DC-02-Q1-B1-A2

Method BLASTX
NCBI GI 94467098
BLAST score 148
E value 2.0e-09
Match length 36
% identity 69

NCBI Description (AL035538) putative protein [Arabidopsis thaliana]

Seq. No. 18273

Contig ID 59778 1.R1040

5'-most EST LIB3106-039-Q1-K1-E11

Method BLASTX
NCBI GI g4538992
BLAST score 230
E value 4.0e-19
Match length 87
% identity 57

NCBI Description (AL049481) putative protein [Arabidopsis thaliana]

Seq. No. 18274

Contig ID 59781 1.R1040



epx701105684.hl 5'-most EST BLASTX Method

q3080448 NCBI GI 238 BLAST score 5.0e-20 E value 114 Match length % identity 49

(AL022605) putative protein [Arabidopsis thaliana] NCBI Description

18275 Seq. No.

59789 1.R1040 Contig ID

LIB3106-039-Q1-K1-C5 5'-most EST

BLASTX Method q3176709 NCBI GI BLAST score 302 2.0e-27 E value 155 Match length 43 % identity

(AC002392) putative anthranilate NCBI Description

N-hydroxycinnamoyl/benzoyltransferase [Arabidopsis

thaliana]

18276 Seq. No.

59790 1.R1040 Contig ID zhf700953876.h1 5'-most EST

18277 Seq. No.

59793 1.R1040 Contig ID

LIB3106-038-Q1-K1-G5 5'-most EST

BLASTX Method g3914239 NCBI GI 225 BLAST score 1.0e-18 E value 85 Match length 53 % identity

PROTEIN PHOSPHATASE 2C ABI2 (PP2C) NCBI Description

>gi\_1945140\_emb\_CAA70163\_ (Y08966) ABI2 protein phosphatase
2C [Arabidopsis thaliana] >gi\_1945142\_emb\_CAA70162\_

(Y08965) ABI2 protein phosphatase 2C [Arabidopsis thaliana]

>gi 2564213\_emb\_CAA72538\_ (Y11840) ABI2 [Arabidopsis

thalianal

18278 Seq. No.

59807 1.R1040 Contig ID

jC-gmro02910012g03a1 5'-most EST

BLASTX Method q3063453 NCBI GI 236 BLAST score E value 1.0e-19 52 Match length % identity

(AC003981) F22013.15 [Arabidopsis thaliana] NCBI Description

18279 Seq. No.

59816 1.R1040 Contig ID

LIB3106-038-Q1-K1-F12 5'-most EST



Contig ID 59822\_1.R1040 5'-most EST fC-gmle700741530a3

Seq. No. 18281

Contig ID 59822 2.R1040 5'-most EST kl1701214986.h1

Seq. No. 18282

Contig ID 59837 1.R1040

5'-most EST jC-gmf102220084c08d1

Method BLASTN
NCBI GI g3128143
BLAST score 38
E value 1.0e-11
Match length 74

% identity 88
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MTI20, complete sequence [Arabidopsis thaliana]

Seq. No. 18283

Contig ID 59862\_1.R1040 5'-most EST taw700658265.h1

Method BLASTX
NCBI GI g3138972
BLAST score 283
E value 4.0e-35
Match length 109
% identity 72

NCBI Description (AF038505) dihydrolipoylacyltransferase subunit of the

branched-chain alpha-keto acid dehydrogenase complex

[Arabidopsis thaliana]

Seq. No. 18284

Contig ID 59866\_1.R1040

5'-most EST jC-gmle01810063c08a1

Method BLASTX
NCBI GI g2511715
BLAST score 173
E value 2.0e-12
Match length 57
% identity 12

NCBI Description (AF019380) putative phosphatidylinositol-4-phosphate

5-kinase [Arabidopsis thaliana]

Seq. No. 18285

Contig ID 59873\_1.R1040 5'-most EST leu701155991.h1

Method BLASTX
NCBI GI g2501986
BLAST score 243
E value 2.0e-20
Match length 183
% identity 38

NCBI Description (AF022178) TAFII250 transcription factor [Mus musculus]

Seq. No. 18286



Contig ID 59894\_1.R1040 5'-most EST LIB3106-037-Q1-K1-G11

Seq. No. 18287

Contig ID 59916\_1.R1040 5'-most EST wrg700788005.h1

Method BLASTX
NCBI GI g1906830
BLAST score 868
E value 2.0e-93
Match length 276
% identity 61

NCBI Description (Y11829) heat shock protein [Arabidopsis thaliana]

Seq. No. 18288

Contig ID 59925\_1.R1040 5'-most EST zhf700962227.h1

Method BLASTX
NCBI GI g3287688
BLAST score 436
E value 3.0e-57
Match length 163
% identity 72

NCBI Description (AC003979) Contains similarity to ycf37 gene product gb\_1001425 from Synechocystis sp. genome gb\_D63999. ESTs gb\_T43026, gb\_R64902, gb\_Z18169 and gb\_N37374 come from

this gene. [Arabidopsis thaliana]

Seq. No. 18289

Contig ID 59938\_1.R1040

5'-most EST LIB3106-037-Q1-K1-A7

Method BLASTN
NCBI GI g170645
BLAST score 318
E value 1.0e-179
Match length 518
% identity 90

NCBI Description Vigna aconitifolia pyrroline-5-carboxylate synthetase associated mRNA sequence. >gi 2471746\_gb\_I47781\_I47781

Sequence 1 from patent US

Seq. No. 18290

Contig ID 59940 1.R1040

5'-most EST LIB3106-032-Q1-K1-A9

Seq. No. 18291

Contig ID 59947 1.R1040

5'-most EST jC-gmf102220089f06a1

Method BLASTX
NCBI GI g4512705
BLAST score 748
E value 4.0e-85
Match length 229
% identity 73

NCBI Description (AC006569) putative serine/threonine protein kinase

[Arabidopsis thaliana]



59952 1.R1040 Contig ID

5'-most EST

LIB3106-037-Q1-K1-A6

Seq. No.

18293

Contig ID 5'-most EST

59960 1.R1040 pxt700944508.h1

Seq. No.

18294

Contig ID 5'-most EST 59964 1.R1040 zzp700832278.hl

Seq. No.

18295

Contig ID 5'-most EST 59976 1.R1040 trc700565783.hl

Method NCBI GI BLASTX

BLAST score

g2347189 453

E value

5.0e-45

165

Match length % identity

NCBI Description

(AC002338) hypothetical protein [Arabidopsis thaliana]

>gi 3150399 (AC004165) hypothetical protein (Arabidopsis

thaliana]

Seq. No.

18296

Contig ID 5'-most EST

59977 1.R1040 pmv700888324.hl

Seq. No.

18297

Contig ID

59986\_1.R1040

5'-most EST

LIB3106-036-Q1-K1-E12

Method

BLASTX g3935170

NCBI GI

BLAST score

908

E value

3.0e-98

Match length

223

% identity

73

NCBI Description (AC004557) F17L21.13 [Arabidopsis thaliana]

Seq. No.

18298

Contig ID 5'-most EST 59999 1.R1040 zsq701126830.h1

Seq. No.

18299

Contig ID

60008 1.R1040

5'-most EST

LIB3106-036-Q1-K1-D11

Seq. No.

18300

Contig ID

60010 1.R1040 zhf700964390.h1

5'-most EST

18301

Contig ID

60018 1.R1040

5'-most EST

kl1701211613.hl

Seq. No.

Seq. No.

% identity

82

NCBI Description (AF045286)



```
60029 1.R1040
Contig ID
5'-most EST
                  gsv701056111.h1
                  18303
Seq. No.
                  60032 1.R1040
Contig ID
                  LIB3106-036-Q1-K1-C10
5'-most EST
                  BLASTN
Method
NCBI GI
                  g633606
BLAST score
                  38
                  6.0e-12
E value
                  152
Match length
                  87
% identity
NCBI Description P.sativum mRNA for chloroplastic outer envelope membrane
                  protein (OEP75)
                  18304
Seq. No.
                  60032 2.R1040
Contig ID
                  uaw700665759.h1
5'-most EST
                  18305
Seq. No.
                  60037 1.R1040
Contig ID
                  hyd700727254.hl
5'-most EST
                  BLASTX
Method
                  g3298439
NCBI GI
BLAST score
                   305
                   5.0e-28
E value
                   75
Match length
                   77
% identity
                  (AB010878) chloroplast ribosomal protein L4 [Nicotiana
NCBI Description
                   tabacuml
                   18306
Seq. No.
                   60063 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400027g08a1
                   18307
Seq. No.
Contig ID
                   60077 1.R1040
                   zhf700951813.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q559713
BLAST score
                   413
                   2.0e-40
E value
                   168
Match length
                   49
% identity
                   (D38552) The half39 protein is related to cyclophilin.
NCBI Description
                   [Homo sapiens]
Seq. No.
                   18308
                   60080 1.R1040
Contig ID
                   jC-gmro02910073f01d1
5'-most EST
                   BLASTX
Method
                   q2865623
NCBI GI
                   350
BLAST score
                   5.0e-33
E value
Match length
                   78
```



GDP-4-keto-6-deoxy-D-mannose-3,5-epimerase-4-reductase [Arabidopsis thaliana]

18309 Seq. No.

60115 1.R1040 Contig ID

 $LIB31\overline{7}0-077-Q1-J1-H12$ 5'-most EST

BLASTX Method NCBI GI q3152613 417 BLAST score 7.0e-41 E value 122 Match length % identity

NCBI Description (AC004482) hypothetical protein [Arabidopsis thaliana]

18310 Seq. No.

60119 1.R1040 Contig ID

LIB3106-035-Q1-K1-A12 5'-most EST

Method BLASTX q1619300 NCBI GI 191 BLAST score 3.0e-14 E value 84 Match length % identity

NCBI Description (X95269) LRR protein [Lycopersicon esculentum]

18311 Seq. No.

60121 1.R1040 Contig ID fua701043109.hl 5'-most EST

BLASTX Method q1711370 NCBI GI 153 BLAST score 7.0e-10 E value 102 Match length 32 % identity

NCBI Description

NUCLEAR PORE PROTEIN SEH1 >gi\_2133124\_pir\_\_S62137 SEC13 protein homolog YGL100w - yeast (Saccharomyces cerevisiae) >gi\_1177640 emb\_CAA62480\_ (X90994) Sec13p-like protein [Saccharomyces cerevisiae] >gi\_1322639\_emb\_CAA96806\_

(Z72622) ORF YGL100w [Saccharomyces cerevisiae]

18312 Seq. No.

60123 1.R1040 Contig ID

 $jC-gm\overline{f}102220071b11a1$ 5'-most EST

BLASTN Method g2580439 NCBI GI 71 BLAST score 1.0e-31 E value 179 Match length 85 % identity

NCBI Description Oryza sativa mRNA for PCF2, complete cds

Seq. No. 18313

60123 2.R1040 Contig ID

jC-gmst02400062g06a1 5'-most EST

BLASTX Method NCBI GI g2580440 303 BLAST score



E value 1.0e-27

Match length 62 % identity 89

NCBI Description (D87261) PCF2 [Oryza sativa]

Seq. No. 18314

Contig ID 60134\_1.R1040 5'-most EST uaw700664349.h1

Seq. No. 18315

Contig ID 60178\_1.R1040

5'-most EST LIB3106-034-Q1-K1-C12

Seq. No. 18316

Contig ID 60181 1.R1040

5'-most EST LIB3106-033-Q1-K1-H7

Seq. No. 18317

Contig ID 60185 1.R1040

5'-most EST LIB3106-034-Q1-K1-A10

Seq. No. 18318

Contig ID 60195 1.R1040

E value 9.0e-65 Match length 181 % identity 30

NCBI Description (X98474) mitochondrial energy transfer protein [Solanum

tuberosum]

Seq. No. 18319

Contig ID 60200\_1.R1040

5'-most EST LIB3106-033-Q1-K1-G2

Seq. No. 18320

Contig ID 60223\_1.R1040 5'-most EST taw700658223.h1

Method BLASTX
NCBI GI g3024874
BLAST score 440
E value 4.0e-43
Match length 245
% identity 41

NCBI Description HYPOTHETICAL 50.0 KD PROTEIN SLR0076

>gi\_1001707\_dbj\_BAA10544\_ (D64004) hypothetical protein

[Synechocystis sp.]

Seq. No. 18321

Contig ID 60236\_1.R1040

5'-most EST LIB3106-033-Q1-K1-C9

Seq. No. 18322

Contig ID 60236\_2.R1040 5'-most EST txt700735327.h1



```
18323
Seq. No.
                  60246 1.R1040
Contig ID
5'-most EST
                  dpv701098957.hl
                  BLASTX
Method
                  g2244771
NCBI GI
                  632
BLAST score
                  7.0e-66
E value
                  232
Match length
                  59
% identity
NCBI Description (Z97335) kinesin homolog [Arabidopsis thaliana]
                  18324
Seq. No.
Contig ID
                  60247 1.R1040
                  zsg701124992.h1
5'-most EST
                  18325
Seq. No.
                  60253 1.R1040
Contig ID
5'-most EST
                  leu701155634.h1
                  BLASTX
Method
                  g3023751
NCBI GI
                  374
BLAST score
                  1.0e-35
E value
                  137
Match length
% identity
                  54
                  70 KD PEPTIDYLPROLYL ISOMERASE (PEPTIDYLPROLYL CIS-TRANS
NCBI Description
                  ISOMERASE) (CYCLOPHILIN) (PPIASE) >gi_1076772_pir__S55383
                  peptidylprolyl isomerase (EC 5.2.1.8) - wheat
                  >gi 854626 emb CAA60505_ (X86903) peptidylprolyl isomerase
                   [Triticum aestivum]
                  18326
Seq. No.
                  60255 1.R1040
Contig ID
5'-most EST
                  zsq701120921.h1
                  18327
Seq. No.
                   60255 2.R1040
Contig ID
5'-most EST
                  LIB3107-011-Q1-K1-A8
Seq. No.
                   18328
                   60269 1.R1040
Contig ID
                  uC-gmropic096f07b1
5'-most EST
                  BLASTX
Method
NCBI GI
                   g322787
BLAST score
                   343
                   7.0e-32
E value
Match length
                  199
% identity
                   42
NCBI Description pyruvate kinase (EC 2.7.1.40), cytosolic - potato
                   18329
Seq. No.
                   60279 1.R1040
```

Contig ID

5'-most EST LIB3106-032-Q1-K1-H8

18330 Seq. No.

60286 1.R1040 Contig ID 5'-most EST wrg700789329.h2



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18331
Seq. No.
                  60317 1.R1040
Contig ID
                  LIB3106-032-Q1-K1-E4
5'-most EST
                  18332
Seq. No.
                  60325 1.R1040
Contig ID
                  jex700907044.h1
5'-most EST
                  18333
Seq. No.
                  60326 1.R1040
Contig ID
                  r1r70\overline{0}898371.h1
5'-most EST
                  18334
Seq. No.
                  60326 2.R1040
Contig ID
                  txt700737170.h1
5'-most EST
                  18335
Seq. No.
                  60331 1.R1040
Contig ID
                  zvp700764236.h1
5'-most EST
Method
                  BLASTX
                  g2213591
NCBI GI
                  224
BLAST score
                  8.0e-18
E value
                  149
Match length
% identity
                  40
NCBI Description (AC000348) T7N9.11 [Arabidopsis thaliana]
Seq. No.
                  18336
                   60333 1.R1040
Contig ID
                  LIB3106-032-Q1-K1-B3
5'-most EST
                  18337
Seq. No.
                   60339 1.R1040
Contig ID
                  LIB3106-032-Q1-K1-A2
5'-most EST
                   18338
Seq. No.
                   60345 1.R1040
Contig ID
                   jC-gmro02800032d04a1
5'-most EST
                   18339
Seq. No.
                   60356 1.R1040
Contig ID
                   jex700903072.hl
5'-most EST
                   BLASTX
Method
NCBI GI
                   g1871196
                   549
BLAST score
                   8.0e-56
E value
                   134
Match length
% identity
                   (U90439) GMP kinase isolog [Arabidopsis thaliana]
NCBI Description
                   >gi_2335091 (AC002339) putative GMP kinase [Arabidopsis
```

Contig ID 60356\_2.R1040

5'-most EST uC-gmflminsoy097d02b1

thaliana]



18341 Seq. No. 60395 1.R1040 Contig ID LIB3106-031-Q1-K1-A8 5'-most EST Method BLASTX q4454051 NCBI GI 457 BLAST score 2.0e-52 E value 118 Match length % identity (AL035394) putative polygalacturonase [Arabidopsis NCBI Description thaliana] 18342 Seq. No. Contig ID 60415 1.R1040 pcp700990894.h1 5'-most EST BLASTX Method

g1513180 NCBI GI 219 BLAST score 9.0e-18 E value 113 Match length 36

% identity NCBI Description (U65511) stellacyanin [Cucumis sativus]

18343 Seq. No.

60416 1.R1040 Contig ID

LIB3106-018-Q1-K1-F11 5'-most EST

18344 Seq. No.

60416 2.R1040 Contig ID zsq701120527.h1 5'-most EST

18345 Seq. No.

60425 1.R1040 Contig ID

5'-most EST jC-gmle01810020d06a1

18346 Seq. No.

60425 2.R1040 Contig ID

LIB3106-027-Q1-K1-D10 5'-most EST

18347 Seq. No.

60472 1.R1040 Contig ID

LIB3106-028-Q1-K1-F9 5'-most EST

18348 Seq. No.

60481 1.R1040 Contig ID zhf700960821.h1 5'-most EST

BLASTX Method g1084454 NCBI GI BLAST score 715 E value 1.0e-75 173 Match length 76 % identity

peptidylprolyl isomerase (EC 5.2.1.8) Cyp1 - rice NCBI Description >gi 600765 (L29471) cyclophilin 1 [Oryza sativa]

18349 Seq. No.

60481 2.R1040 Contig ID



5'-most EST jC-gmro02800038d04d1 Method

BLASTX NCBI GI q1084454 BLAST score 217

E value 2.0e-17 Match length 55 % identity 71

NCBI Description peptidylprolyl isomerase (EC 5.2.1.8) Cyp1 - rice

>gi\_600765 (L29471) cyclophilin 1 [Oryza sativa]

Seq. No. 18350

Contig ID 60489 1.R1040

5'-most EST uC-gmflminsoy047a01b1

Seq. No. 18351

Contig ID 60492 1.R1040

5'-most EST LIB3106-028-Q1-K1-B6

Seq. No. 18352

Contig ID 60507 1.R1040 5'-most EST hrw701057709.h1

Method BLASTX NCBI GI g4262236 BLAST score 742 1.0e-78 E value Match length 236

% identity 63

NCBI Description (AC006200) putative ribose 5-phosphate isomerase

[Arabidopsis thaliana]

Seq. No.

Contig ID 60517 1.R1040 5'-most EST pmv700891952.hl

Seq. No.

18354

18353

Contig ID 60523 1.R1040

5'-most EST LIB3106-026-Q1-K1-G5

Seq. No.

18355

Contig ID 60532 1.R1040 5'-most EST rlr700895888.h1

Seq. No.

18356

Contig ID 60535 1.R1040

5'-most EST LIB3106-026-Q1-K1-E5

Method BLASTX NCBI GI g3928758 BLAST score 827 E value 4.0e-93 Match length 193 % identity 85

NCBI Description

(AB007987) Lipoic acid synthase [Arabidopsis thaliana] >gi 4454462\_gb\_AAD20909\_ (AC006234) putative lipoic acid

synthase [Arabidopsis thaliana]

Seq. No. 18357

Contig ID 60536\_1.R1040



5'-most EST uC-gmropic073g08b1
Method BLASTX
NCBI GI g1001309

NCBI GI g1001309
BLAST score 505
E value 1.0e-50
Match length 374
% identity 33

NCBI Description (D64006) aspartate aminotransferase [Synechocystis sp.]

Seq. No. 18358

Contig ID 60536\_2.R1040

5'-most EST uC-gmflminsoy077f05b1

Seq. No. 18359

Contig ID 60541\_1.R1040

5'-most EST LIB3106-026-Q1-K1-F2

Method BLASTX
NCBI GI g3955021
BLAST score 417
E value 5.0e-41
Match length 105
% identity 77

NCBI Description (AJ010811) HB2 homeodomain protein [Populus tremula x

Populus tremuloides]

Seq. No. 18360

Contig ID 60541\_2.R1040 5'-most EST hyd700730891.h1

Method BLASTX
NCBI GI g3955021
BLAST score 149
E value 6.0e-10
Match length 54
% identity 61

NCBI Description (AJ010811) HB2 homeodomain protein [Populus tremula x

Populus tremuloides]

Seq. No. 18361

Contig ID 60554\_1.R1040

5'-most EST LIB3106-026-Q1-K1-D5

Seq. No. 18362

Contig ID 60573 1.R1040

5'-most EST jC-gmro02910004a06d1

Method BLASTX
NCBI GI g3128168
BLAST score 197
E value 4.0e-15
Match length 59
% identity 58

NCBI Description (AC004521) putative carboxyl-terminal peptidase

[Arabidopsis thaliana]

Seq. No. 18363

Contig ID 60582\_1.R1040 5'-most EST zzp700831919.h1



```
18364
Seq. No.
                  60592 1.R1040
Contig ID
                  leu701148729.h1
5'-most EST
Method
                  BLASTX
                  g2828293
NCBI GI
                  208
BLAST score
                  2.0e-16
E value
Match length
                   65
% identity
                   65
                  (ALO21687) putative protein [Arabidopsis thaliana]
NCBI Description
                   18365
Seq. No.
                   60605 1.R1040
Contig ID
                   uaw700663688.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2459408
BLAST score
                   430
                   2.0e-42
E value
Match length
                   118
                   63
% identity
                   (AC002332) unknown protein [Arabidopsis thaliana]
NCBI Description
                   >qi 2924769 (AC002334) unknown protein [Arabidopsis
                   thaliana]
                   18366
Seq. No.
Contig ID
                   60611 1.R1040
                   LIB3106-025-Q1-K1-B2
5'-most EST
Seq. No.
                   18367
                   60639 1.R1040
Contig ID
                   LIB3106-025-Q1-K1-A7
5'-most EST
                   18368
Seq. No.
                   60640 1.R1040
Contig ID
                   LIB3106-025-Q1-K1-A9
5'-most EST
                   BLASTX
Method
                   g2827524
NCBI GI
                   262
BLAST score
                   1.0e-22
E value
Match length
                   67
% identity
                   69
                  (AL021633) predicted protein [Arabidopsis thaliana]
NCBI Description
                   18369
Seq. No.
                   60663 1.R1040
Contig ID
                   jC-gmro02800038e08a1
5'-most EST
                   BLASTN
Method
```

g2760167 NCBI GI 36 BLAST score 2.0e-10 E value 84 Match length 86 % identity

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MCO15, complete sequence [Arabidopsis thaliana]

18370 Seq. No.

60695 1.R1040 Contig ID



```
LIB3106-022-Q1-K1-C12
5'-most EST
                  18371
Seq. No.
                  60695 2.R1040
Contig ID
                  uaw700661871.hl
5'-most EST
                  18372
Seq. No.
                   60697 1.R1040
Contig ID
                   jC-gmro02800031b04d1
5'-most EST
                   18373
Seq. No.
                   60698 1.R1040
Contig ID
                  LIB3106-022-Q1-K1-D11
5'-most EST
Seq. No.
                   18374
Contig ID
                   60732 1.R1040
                   LIB31\overline{0}6-021-Q1-K1-G2
5'-most EST
                   18375
Seq. No.
                   60739 1.R1040
Contig ID
5'-most EST
                   LIB3106-021-Q1-K1-D4
Method
                   BLASTX
                   g2529672
NCBI GI
BLAST score
                   254
                   7.0e-22
E value
Match length
                   86
% identity
                   56
NCBI Description (AC002535) putative pectinesterase [Arabidopsis thaliana]
                   18376
Seq. No.
                   60745_1.R1040
Contig ID
5'-most EST
                   g5058131
                   BLASTX
Method
                   g4567310
NCBI GI
                   160
BLAST score
                   6.0e-15
E value
                   71
Match length
                   68
% identity
                  (AC005956) unknown protein [Arabidopsis thaliana]
NCBI Description
                   18377
Seq. No.
                   60751 1.R1040
Contig ID
                   pcp700989809.h1
5'-most EST
                   18378
Seq. No.
                   60756_1.R1040
Contig ID
                   jex700907520.h1
5'-most EST
                   BLASTX
Method
                   g3033388
NCBI GI
BLAST score
                   185
                   1.0e-13
E value
Match length
                   53
```

% identity

Contig ID 60808\_1.R1040

51

NCBI Description (AC004238) hypothetical protein [Arabidopsis thaliana]



uC-gmrominsoy108a02b1 5'-most EST BLASTX Method g4558672 NCBI GI 861 BLAST score 1.0e-92 E value 247 Match length % identity (AC007063) putative 1,3-beta-D-glucan synthase [Arabidopsis NCBI Description thaliana] 18380 Seq. No. 60820 1.R1040 Contig ID sat701010144.h2 5'-most EST BLASTX Method g130897 NCBI GI BLAST score 421 3.0e-41E value 151 Match length % identity 52 DNA PRIMASE SMALL SUBUNIT (DNA PRIMASE 49 KD SUBUNIT) (P49) NCBI Description >gi\_423418\_pir\_\_D46642 DNA primase (EC 2.7.7.-) 46K chain  $mouse > gi_3036\overline{61}_{dbj_BAA02744_{doc}}$  (D13544) primase small subunit [Mus musculus] 18381 Seq. No. 60821 1.R1040 Contig ID fua701042757.hl 5'-most EST 18382 Seq. No. 60828 1.R1040 Contig ID uC-gmflminsoy064g05b1 5'-most EST BLASTX Method g452593 NCBI GI 326 BLAST score 3.0e-61 E value 189 Match length 61 % identity (D21814) ORF [Lilium longiflorum] NCBI Description 18383 Seq. No. 60843 1.R1040 Contig ID LIB3106-019-Q1-K1-F6 5'-most EST BLASTX Method q534982 NCBI GI BLAST score 724 8.0e-77 E value 177 Match length 77 % identity NCBI Description (X75898) phosphoglucomutase [Spinacia oleracea]

Seq. No. 18384

60880 1.R1040 Contig ID qsv701048835.h1 5'-most EST

BLASTX Method NCBI GI g3023280 210 BLAST score 1.0e-16 E value



Match length 89 % identity 42

NCBI Description AUGMENTER OF LIVER REGENERATION >gi\_4096810 (U40494) ALR

[Mus musculus]

Seq. No. 18385

Contig ID 60881\_1.R1040 5'-most EST ssr700555772.h1

Seq. No. 18386

Contig ID 60935 1.R1040

5'-most EST LIB3106-015-Q1-K1-G6

Seq. No. 18387

Contig ID 60936 1.R1040

5'-most EST LIB3106-015-Q1-K1-H7

Method BLASTX
NCBI GI g3386596
BLAST score 355
E value 1.0e-33
Match length 121
% identity 58

NCBI Description (AC004665) unknown protein [Arabidopsis thaliana]

>gi 3702346 (AC005397) unknown protein [Arabidopsis

thaliana]

Seq. No. 18388

Contig ID 60968\_1.R1040 5'-most EST seb700653603.h1

Seq. No. 18389

Contig ID 60970\_1.R1040

5'-most EST LIB3106-015-Q1-K1-D6

Seq. No. 18390

Contig ID 60970 2.R1040 5'-most EST vwf700677026.h1

Seq. No. 18391

Contig ID 60973 1.R1040

5'-most EST LIB3106-015-Q1-K1-D9

Method BLASTX
NCBI GI g2244818
BLAST score 273
E value 5.0e-24
Match length 147
% identity 48

NCBI Description (Z97336) hypothetical protein [Arabidopsis thaliana]

Seq. No. 18392

Contig ID 60984 1.R1040

5'-most EST LIB3106-015-Q1-K1-D3

Method BLASTX
NCBI GI g2499005
BLAST score 186
E value 8.0e-14
Match length 103

3006



% identity 4-METHYL-5 (B-HYDROXYETHYL) -THIAZOLE MONOPHOSPHATE NCBI Description BIOSYNTHESIS ENZYME >gi 1100872 (U34923) ThiJ [Escherichia coli] >gi 1773108 (U826 $\overline{64}$ ) 4-methyl $-\overline{5}$  (b-hydroxyethyl)-thiazole monophosphate biosynthesis protein [Escherichia coli] >gi 1786626 (AE000148) 4-methyl-5(beta-hydroxyethyl)-thiazole monophosphate synthesis [Escherichia coli] Seq. No. 18393 Contig ID 60985 1.R1040 5'-most EST LIB3106-015-Q1-K1-B7 Seq. No. 18394 Contig ID 60991 1.R1040 5'-most EST LIB3106-015-Q1-K1-C3 Method BLASTX g2289010 NCBI GI BLAST score 338 E value 1.0e-31 Match length 81 % identity 80 NCBI Description (AC002335) FKBP type peptidyl-prolyl cis-trans isomerase isolog [Arabidopsis thaliana] 18395 Seq. No. Contig ID 61008 1.R1040 5'-most EST  $ncj70\overline{0}987379.h1$ 18396 Seq. No. 61009\_1.R1040 Contig ID 5'-most EST ncj700985536.h1 Method BLASTX q1946364 NCBI GI BLAST score 235 E value 1.0e-19 Match length 63 % identity 60 NCBI Description (U93215) lipase isolog [Arabidopsis thaliana] Seq. No. 18397 61012 1.R1040 ncj700985515.h1 Seq. No. 18398 61025 1.R1040

Contig ID 5'-most EST

Contig ID

5'-most EST LIB3167-038-P1-K1-F11

Method BLASTN NCBI GI q170087 BLAST score 57 E value 2.0e-23 Match length 218 % identity 78

NCBI Description G.max vegetative storage protein mRNA (VSP25 gene)

Seq. No. 18399

Contig ID 61039 1.R1040



```
5'-most EST
                   jC-qmf102220054b02d1
Method
                   BLASTN
NCBI GI
                   q1619324
BLAST score
                   176
E value
                   4.0e-94
Match length
                  350
% identity
                  88
NCBI Description P.sativum mRNA for ADP-glucose pyrophosphorylase
Seq. No.
                  18400
                  61059 1.R1040
Contig ID
5'-most EST
                  LIB3106-013-Q1-K1-G7
                  18401
Seq. No.
                  61060 1.R1040
Contig ID
5'-most EST
                  LIB3106-013-Q1-K1-G8
Method
                  BLASTN
NCBI GI
                   g3821780
BLAST score
                   36
E value
                   2.0e-10
Match length
                   37
% identity
                   61
NCBI Description Xenopus laevis cDNA clone 27A6-1
                   18402
Seq. No.
                   61060 2.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy104c09b1
                   18403
Seq. No.
                   61073 1.R1040
Contig ID
5'-most EST
                  pxt700946124.h1
Seq. No.
                   18404
                   61084 1.R1040
Contig ID
5'-most EST
                   LIB3106-013-Q1-K1-D4
                   18405
Seq. No.
                   61100 1.R1040
Contig ID
5'-most EST
                   ncj70\overline{0}980526.h1
Seq. No.
                   18406
                   61104 1.R1040
Contig ID
5'-most EST
                   LIB3106-013-Q1-K1-D10
Seq. No.
                   18407
Contig ID
                   61105 1.R1040
5'-most EST
                   LIB3106-013-Q1-K1-D11
Method
                   BLASTX
NCBI GI
                   g3219785
BLAST score
                   217
E value
                   3.0e-17
Match length
                   66
```

NCBI Description PUTATIVE CYSTEINE SYNTHASE (O-ACETYLSERINE SULFHYDRYLASE) (O-ACETYLSERINE (THIOL)-LYASE) (CSASE)

>gi\_2104433\_emb\_CAB08745\_ (Z95395) putative cysteine

synthase [Schizosaccharomyces pombe]

59

% identity

% identity

56



```
18408
Seq. No.
Contig ID
                  61112 1.R1040
5'-most EST
                  LIB3106-013-Q1-K1-B1
                  BLASTX
Method
NCBI GI
                  g1652779
BLAST score
                  124
E value
                  4.0e-12
Match length
                  89
                  44
% identity
NCBI Description (D90908) hypothetical protein [Synechocystis sp.]
Seq. No.
                  18409
                  61114 1.R1040
Contig ID
5'-most EST
                  LIB3106-013-Q1-K1-B11
                  BLASTX
Method
NCBI GI
                  g3510252
BLAST score
                  414
                  2.0e-40
E value
                  168
Match length
% identity
NCBI Description (AC005310) putative RNA-binding protein [Arabidopsis
                  thaliana]
                  18410
Seq. No.
                  61117 1.R1040
Contig ID
                  smc700749863.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g4512694
BLAST score
                  199
E value
                  2.0e-15
Match length
                  101
% identity
                  43
NCBI Description (AC006569) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  18411
                  61123 1.R1040
Contig ID
5'-most EST
                  LIB3106-011-Q1-K1-G4
                  18412
Seq. No.
Contig ID
                  61141 1.R1040
                  jC-gmf102220079c08d1
5'-most EST
Seq. No.
                  18413
Contig ID
                  61145 1.R1040
5'-most EST
                  sat701007985.h1
                  18414
Seq. No.
                  61178 1.R1040
Contig ID
5'-most EST
                  vwf700675420.h1
                  BLASTX
Method
                  g1653702
NCBI GI
BLAST score
                  519
E value
                  2.0e-74
Match length
                  280
```

NCBI Description (D90915) dihydrolipoamide acetyltransferase component (E2)

Method

BLASTX



## of pyruvate dehydrogenase complex [Synechocystis sp.]

```
Seq. No.
                  18415
                  61178 2.R1040
Contig ID
5'-most EST
                  fC-gmle700558355f2
                  BLASTX
Method
NCBI GI
                  g564024
BLAST score
                  154
                  5.0e-13
E value
                  44
Match length
% identity
NCBI Description (U16254) dihydrolipoamide acetyl transferase [Zea mays]
                  18416
Seq. No.
                  61187 1.R1040
Contig ID
5'-most EST
                  bth700845865.h1
Method
                  BLASTX
NCBI GI
                  q547911
BLAST score
                  148
E value
                  3.0e-09
Match length
                  123
                  29
% identity
NCBI Description MO25 PROTEIN >gi_2143483_pir___157997 hypothetical
                  calcium-binding protein - mouse >gi_262934_bbs_121784
                  (S51858) putative Ca2+ binding protein [mice, embryos,
                  Peptide, 341 aa] [Mus sp.]
                  18417
Seq. No.
Contig ID
                  61197 1.R1040
5'-most EST
                  LIB3106-010-Q1-K1-F5
Method
                  BLASTX
NCBI GI
                  g3292822
BLAST score
                  352
                  2.0e-33
E value
                  107
Match length
% identity
                  61
NCBI Description (AL031018) putative protein [Arabidopsis thaliana]
                  18418
Seq. No.
                  61220 1.R1040
Contig ID
5'-most EST
                  vzy700751009.hl
                  BLASTX
Method
NCBI GI
                  q2979555
BLAST score
                  372
                  1.0e-35
E value
Match length
                  166
% identity
                  49
NCBI Description (AC003680) unknown protein [Arabidopsis thaliana]
                  18419
Seq. No.
Contig ID
                  61235 1.R1040
5'-most EST
                  LIB3106-010-Q1-K1-E5
                  18420
Seq. No.
                  61241 1.R1040
Contig ID
5'-most EST
                  dpv701101553.h1
```



```
NCBI GI g4263771
BLAST score 322
E value 3.0e-29
Match length 84
% identity 67
NCBI Description (AC00621
```

NCBI Description (AC006218) putative nonspecific lipid-transfer protein precursor [Arabidopsis thaliana]

Seq. No. 18421

Contig ID 61260 1.R1040

5'-most EST uC-gmflminsoy003f08b1

Method BLASTX
NCBI GI g1465368
BLAST score 149
E value 2.0e-09
Match length 110
% identity 36

NCBI Description (X99548) bHLH protein [Arabidopsis thaliana]

Seq. No. 18422

Contig ID 61260\_2.R1040 5'-most EST vzy700755034.h1

Method BLASTX
NCBI GI g1465368
BLAST score 236
E value 1.0e-19
Match length 149
% identity 36

NCBI Description (X99548) bHLH protein [Arabidopsis thaliana]

Seq. No. 18423

Contig ID 61263\_1.R1040

5'-most EST jC-gmf102220064g03a1

Method BLASTX
NCBI GI 94455225
BLAST score 283
E value 3.0e-25
Match length 89
% identity 55

NCBI Description (AL035440) putative protein [Arabidopsis thaliana]

Seq. No. 18424

Contig ID 61266\_1.R1040

5'-most EST LIB3106-010-Q1-K1-B4

Method BLASTX
NCBI GI g2281090
BLAST score 221
E value 6.0e-18
Match length 112
% identity 50

NCBI Description (AC002333) hypothetical protein [Arabidopsis thaliana]

Seq. No. 18425

Contig ID 61271 1.R1040 5'-most EST fde700872534.h1

Method BLASTX NCBI GI g2129656



BLAST score 210 E value 3.0e-21 Match length 100 % identity 60

NCBI Description OBP33pep protein - Arabidopsis thaliana (fragment) >gi\_1022801 (U37699) OBP33pep [Arabidopsis thaliana]

Seq. No. 18426

Contig ID 61276\_1.R1040

5'-most EST LIB3167-002-Q1-K1-A11

Method BLASTX
NCBI GI g4468992
BLAST score 352
E value 2.0e-44
Match length 135
% identity 70

NCBI Description (AL035605) putative protein [Arabidopsis thaliana]

Seq. No. 18427

Contig ID 61276\_2.R1040

5'-most EST uC-gmflminsoy118g11b1

Method BLASTX
NCBI GI g4468992
BLAST score 183
E value 1.0e-13
Match length 62
% identity 58

NCBI Description (AL035605) putative protein [Arabidopsis thaliana]

Seq. No. 18428

Contig ID 61292\_1.R1040

5'-most EST jC-gmf102220052c04a1

Seq. No. 18429

Contig ID 61302\_1.R1040

5'-most EST jC-gmro02910049h07d1

Seq. No. 18430

Contig ID 61307\_1.R1040 5'-most EST LIB3106-009-Q1-K1-E1

Seq. No. 18431

Contig ID 61307\_2.R1040

5'-most EST jC-gmro02910041060a1

Seq. No. 18432

Contig ID 61307\_3.R1040 5'-most EST wvk700686513.h1

Seq. No. 18433

Contig ID 61308\_1.R1040 5'-most EST zvj700605252.h2

Seq. No. 18434

Contig ID 61311\_1.R1040 5'-most EST leu701155239.h1

3012



```
Seq. No.
                  18435
                  61315 1.R1040
Contig ID
5'-most EST
                  LIB3106-009-Q1-K1-B6
                  BLASTX
Method
NCBI GI
                  g4531444
BLAST score
                  826
E value
                  2.0e-88
                  268
Match length
% identity
                  59
NCBI Description (AC006224) putative protein kinase [Arabidopsis thaliana]
                  18436
Seq. No.
                  61322 1.R1040
Contig ID
5'-most EST
                  djj700606020.h2
Seq. No.
                  18437
Contig ID
                  61335 1.R1040
5'-most EST
                  LIB3139-011-P1-N1-B12
Method
                  BLASTX
                  q1651865
NCBI GI
BLAST score
                  177
                  3.0e-12
E value
Match length
                  87
                  48
% identity
NCBI Description (D90900) hypothetical protein [Synechocystis sp.]
                  18438
Seq. No.
                  61336_1.R1040
Contig ID
5'-most EST
                  asn701140584.h1
                  18439
Seq. No.
Contig ID
                   61339 1.R1040
5'-most EST
                  LIB3106-009-Q1-K1-A8
Method
                  BLASTX
NCBI GI
                  g3176725
BLAST score
                  604
                  1.0e-68
E value
Match length
                  160
                  73
% identity
NCBI Description (AC002392) unknown protein [Arabidopsis thaliana]
                  18440
Seq. No.
                  61347 1.R1040
Contig ID
5'-most EST
                  rry700808376.hl
Seq. No.
                  18441
Contig ID
                   61351 3.R1040
5'-most EST
                  LIB3106-008-Q1-K1-D8
                  18442
Seq. No.
```

Contig ID 61360 1.R1040

5'-most EST LIB3170-021-Q1-K1-B10

18443 Seq. No.

Contig ID 61377 1.R1040

5'-most EST uC-gmflminsoy045c05b1

BLASTX Method



NCBI GI q544184 BLAST score 952 E value 1.0e-103 Match length 209 % identity 81 4-ALPHA-GLUCANOTRANSFERASE PRECURSOR (AMYLOMALTASE) NCBI Description (DISPROPORTIONATING ENZYME) (D-ENZYME) >gi\_322785\_pir\_\_A45049 4-alpha-glucanotransferase (EC 2.4.1.25) - potato >gi 296692 emb CAA48630 (X68664) 4-alpha-glucanotransferase [Solanum tuberosum]

Seq. No. 61382 1.R1040 Contig ID LIB3106-008-Q1-K1-C1 5'-most EST BLASTX Method NCBI GI g1293835 BLAST score 124 3.0e-11 E value 69 Match length 51 % identity

18444

NCBI Description (U56965) C15H9.5 gene product [Caenorhabditis elegans]

Seq. No. 18445 61382 2.R1040 Contig ID zpv700763456.h1 5'-most EST Method BLASTX NCBI GI q1293835

BLAST score 352 2.0e-33 E value Match length 130 % identity 47

NCBI Description (U56965) C15H9.5 gene product [Caenorhabditis elegans]

Seq. No. 18446

61383 1.R1040 Contig ID

5'-most EST jC-qmst02400066b09a2

Method BLASTX q3540207 NCBI GI 297 BLAST score 8.0e-27 E value 81 Match length 72 % identity

NCBI Description (AC004260) Putative protein kinase [Arabidopsis thaliana]

Seq. No. 18447

61389 1.R1040 Contig ID

5'-most EST LIB3106-007-Q1-K1-F9

Seq. No. 18448

61409 1.R1040 Contig ID

5'-most EST LIB3106-007-Q1-K1-E3

Seq. No. 18449

61418 1.R1040 Contig ID pmv700889115.hl 5'-most EST

Method BLASTX NCBI GI g2827141



BLAST score 2.0e-75 E value Match length 150 % identity 83

NCBI Description (AF027173) cellulose synthase catalytic subunit

[Arabidopsis thaliana]

Seq. No. 18450

61442 1.R1040 Contig ID

5'-most EST jC-gmst02400067e06a1

Seq. No. 18451

Contig ID 61454 1.R1040 5'-most EST ncj700976548.h1

Method BLASTX NCBI GI q2673915 BLAST score 529 E value 7.0e-88 Match length 372 % identity 46

NCBI Description (AC002561) putative cytochrome P-450 [Arabidopsis thaliana]

Seq. No. 18452

61455 1.R1040 Contig ID

5'-most EST LIB3106-006-Q1-K1-F10

18453 Seq. No.

61462\_1.R1040 Contig ID 5'-most EST epx701106357.hl

Method BLASTX NCBI GI q1708972 BLAST score 400 E value 1.0e-38 Match length 265 % identity 38

(R)-MANDELONITRILE LYASE ISOFORM 3 PRECURSOR NCBI Description

(HYDROXYNITRILE LYASE 3) ((R)-OXYNITRILASE 3) >gi 1262279

(U51562) (R)-(+)-mandelonitrile lyase isoform  $MDL\overline{3}$ precursor [Prunus serotina] >gi 2343181 (AF013161)

(R)-(+)-mandelonitrile lyase isoform MDL3 precursor [Prunus

serotina]

Seq. No. 18454

Contig ID 61469 1.R1040

5'-most EST LIB3106-006-Q1-K1-F9

Seq. No. 18455

61470 1.R1040 Contig ID 5'-most EST uxk700669643.h1

Method BLASTN g1657381 NCBI GI 230 BLAST score 1.0e-126 E value Match length 398 90 % identity

NCBI Description P.sativum mRNA for cholinephosphate cytidylyltransferase



```
18456
Seq. No.
                  61473 1.R1040
Contig ID
5'-most EST
                  pmv700888759.h1
Seq. No.
                  18457
                  61483 1.R1040
Contig ID
                  LIB3170-080-Q1-K1-E4
5'-most EST
                  BLASTX
Method
                  g3287270
NCBI GI
BLAST score
                  515
                  4.0e-52
E value
                  112
Match length
% identity
                  87
NCBI Description (Y09533) involved in starch metabalism [Solanum tuberosum]
                  18458
Seq. No.
                  61496 1.R1040
Contig ID
                  LIB3106-006-Q1-K1-E4
5'-most EST
Seq. No.
                  18459
                   61505 1.R1040
Contig ID
                  LIB3106-006-Q1-K2-B11
5'-most EST
                   18460
Seq. No.
                   61525 1.R1040
Contig ID
                   LIB3106-006-Q1-K1-A1
5'-most EST
                   BLASTX
Method
                   g2245029
NCBI GI
                   349
BLAST score
                   5.0e-33
E value
                   133
Match length
                   53
% identity
NCBI Description (Z97341) limonene cyclase homolog [Arabidopsis thaliana]
                   18461
Seq. No.
                   61535 2.R1040
Contig ID
                   uC-gmrominsoy113a11b1
5'-most EST
Seq. No.
                   18462
                   61535 3.R1040
Contig ID
                   epx701105028.h1
5'-most EST
                   18463
Seq. No.
Contig ID
                   61562 1.R1040
 5'-most EST
                   qsv701056808.hl
                   BLASTX
Method
```

q4455367 NCBI GI 215 BLAST score 2.0e-17 E value

123 Match length % identity 47

(AL035524) putative protein [Arabidopsis thaliana] NCBI Description

Seq. No.

18464

Contig ID

61575 1.R1040

5'-most EST

LIB3106-005-Q1-K1-H9



Seq. No. 18465

Contig ID 61593 1.R1040

5'-most EST uC-gmflminsoy016d10b1

Method BLASTX
NCBI GI g3122671
BLAST score 687
E value 2.0e-72
Match length 160
% identity 73

NCBI Description HYPOTHETICAL RAE1-LIKE PROTEIN >gi 2129676 pir S71241

probable export protein - Arabidopsis thaliana >gi\_1297188 (U53501) Theoretical protein with similarity to Swiss-Prot

Accession Number P41838 poly A+ RNA export protein

[Arabidopsis thaliana]

Seq. No. 18466

Contig ID 61594\_1.R1040 5'-most EST kmv700742024.h1

Method BLASTN
NCBI GI 94220640
BLAST score 48
E value 7.0e-18
Match length 116
% identity 85

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MPE11, complete sequence [Arabidopsis thaliana]

Seq. No. 18467

Contig ID 61597 1.R1040

5'-most EST LIB3106-005-Q1-K2-H12

Method BLASTX
NCBI GI g4510368
BLAST score 226
E value 1.0e-18
Match length 135
% identity 41

NCBI Description (AC007017) putative transcription factor E2F5 [Arabidopsis

thaliana]

Seq. No. 18468

Contig ID 61599 1.R1040

5'-most EST LIB3106-005-Q1-K1-H3

Method BLASTX
NCBI GI 94544408
BLAST score 494
E value 5.0e-50
Match length 108
% identity 81

NCBI Description (AC006955) unknown protein [Arabidopsis thaliana]

Seq. No. 18469

Contig ID 61603\_1.R1040

5'-most EST LIB3106-005-Q1-K2-G12

Seq. No. 18470

Contig ID 61605\_1.R1040

5'-most EST LIB3106-005-Q1-K1-E8



Method BLASTX
NCBI GI g4314378
BLAST score 322
E value 1.0e-29
Match length 164
% identity 41
NCBI Description (AC006232) putative lipase [Arabidopsis thaliana]

Seq. No. 18471

Contig ID 61605\_2.R1040

5'-most EST jC-gmf102220091g09a1

Method BLASTX
NCBI GI g4314378
BLAST score 190
E value 3.0e-14
Match length 63
% identity 54

NCBI Description (AC006232) putative lipase [Arabidopsis thaliana]

Seq. No. 18472

Contig ID 61609\_1.R1040

5'-most EST LIB3106-005-Q1-K2-F2

Seq. No. 18473

Contig ID 61617\_1.R1040

5'-most EST jC-gmst02400065f08a2

Method BLASTX
NCBI GI g3023818
BLAST score 185
E value 1.0e-13
Match length 37
% identity 89

NCBI Description GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CHOLOROPLAST ISOFORM

PRECURSOR (G6PD) >gi\_1197385\_emb\_CAA58775\_ (X83923) glucose-6-phosphate dehydrogenase [Solanum tuberosum]

Seq. No. 18474

Contig ID 61618\_1.R1040 5'-most EST ncj700984252.h1

Method BLASTX
NCBI GI g2651303
BLAST score 179
E value 3.0e-13
Match length 116
% identity 38

NCBI Description (AC002336) putative potassium transporter [Arabidopsis

thaliana]

Seq. No. 18475

Contig ID 61627\_1.R1040

5'-most EST LIB3106-005-Q1-K1-E1

Seq. No. 18476

Contig ID 61628\_1.R1040

5'-most EST LIB3106-005-Q1-K1-E10

Method BLASTN NCBI GI g3821780



BLAST score 36 E value 1.0e-10 38 Match length 61 % identity

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No.

18477

Contig ID 5'-most EST 61630 1.R1040 jC-gmst02400059d05a1

BLASTN Method NCBI GI q18695 BLAST score 118 1.0e-59 E value Match length 178

92 % identity

NCBI Description Soybean nodulin 22 gene

Seq. No.

18478

Contig ID 5'-most EST Method NCBI GI

61630 2.R1040 q5752975 BLASTN g18695

BLAST score E value Match length % identity

118 1.0e-59 186

NCBI Description Soybean nodulin 22 gene

Seq. No.

18479

91

Contig ID 5'-most EST

61636 1.R1040 sat701007438.h2

Method BLASTX NCBI GI g2314805 BLAST score 741 9.0e-79 E value 185 Match length

75 % identity

(U85045) 2-oxoglutarate-dependent dioxygenase [Pisum NCBI Description

sativum] >gi 2316036 (AF001219) gibberellin 3

beta-hydroxylase [Pisum sativum]

Seq. No.

18480

Contig ID

61638 1.R1040

5'-most EST

LIB3106-005-Q1-K1-C11

Seq. No.

18481

g2500026

1.0e-178

1445

Contig ID

61639 1.R1040

5'-most EST

uC-gmflminsoy097f04b1 BLASTX

Method NCBI GI BLAST score E value

Match length 356 88 % identity

NCBI Description ADENYLOSUCCINATE SYNTHETASE PRECURSOR (IMP--ASPARTATE LIGASE) >gi\_1616657 (U49389) adenylosuccinate synthetase

[Arabidopsis thaliana]



```
18482
Seq. No.
                   61645 1.R1040
Contig ID
5'-most EST
                  LIB3106-005-Q1-K1-C8
Seq. No.
                   18483
Contig ID
                   61651 1.R1040
5'-most EST
                  LIB3106-005-Q1-K2-A4
Method
                  BLASTX
NCBI GI
                   q4454459
BLAST score
                   302
                   2.0e-27
E value
Match length
                   96
                   66
% identity
NCBI Description
                  (AC006234) unknown protein [Arabidopsis thaliana]
Seq. No.
                   18484
                   61662 1.R1040
Contig ID
5'-most EST
                   txt700737693.hl
Method
                  BLASTX
                   g1707480
NCBI GI
                   839
BLAST score
E value
                   4.0e-90
Match length
                   253
% identity
                   61
NCBI Description
                  (Y08614) CRM1 [Homo sapiens]
                   18485
Seq. No.
Contig ID
                   61663 1.R1040
5'-most EST
                   gsv701045378.h1
Method
                   BLASTX
NCBI GI
                   g1362021
BLAST score
                   191
                   2.0e-14
E value
                   116
Match length
                   44
% identity
                  zink finger protein 7 - Arabidopsis thaliana >gi_790685
NCBI Description
                   (L39650) zinc finger protein [Arabidopsis thaliana]
                   >gi 2213609 (AC000103) F21J9.3 [Arabidopsis thaliana]
Seq. No.
                   18486
Contig ID
                   61737 1.R1040
5'-most EST
                   LIB3106-004-Q1-K1-G9
Method
                   BLASTX
NCBI GI
                   g3192704
BLAST score
                   285
                   2.0e-25
E value
                   150
Match length
% identity
                   39
NCBI Description
                  (AF064539) gp21 [Bacteriophage N15]
```

Seq. No. 18487

Contig ID 61739 1.R1040

5'-most EST LIB3106-004-Q1-K1-H12

Seq. No. 18488

Contig ID 61749\_1.R1040

3020



```
5'-most EST
                  LIB3106-004-Q1-K1-G4
Seq. No.
                  18489
                  61775 1.R1040
Contig ID
5'-most EST
                  LIB3106-004-Q1-K1-C12
                  BLASTX
Method
NCBI GI
                  g1729927
BLAST score
                  557
E value
                  6.0e-57
Match length
                  289
% identity
                  43
NCBI Description QUEUINE TRNA-RIBOSYLTRANSFERASE (TRNA-GUANINE
                  TRANSGLYCOSYLASE) (GUANINE INSERTION ENZYME) >gi 940182
                  (U30888) tRNA-Guanine Transglycosylase [Homo sapiens]
Seq. No.
                  18490
Contig ID
                  61783 1.R1040
5'-most EST
                  uC-gmrominsoy060e12b1
Seq. No.
                  18491
                  61783 2.R1040
Contig ID
5'-most EST
                  LIB3107-044-Q1-K1-H6
                  18492
Seq. No.
Contig ID
                  61801 1.R1040
5'-most EST
                  g5752487
Method
                  BLASTX
                  g2832625
NCBI GI
BLAST score
                  647
E value
                  2.0e-67
Match length
                  173
% identity
                  68
NCBI Description (AL021711) putative protein [Arabidopsis thaliana]
Seq. No.
                  18493
                  61818 1.R1040
Contig ID
5'-most EST
                  LIB3106-003-Q1-K1-G1
Seq. No.
                  18494
Contig ID
                  61821 2.R1040
5'-most EST
                  zhf700958641.h1
Seq. No.
                  18495
Contig ID
                  61830 1.R1040
5'-most EST
                  k11701212125.h1
Method
                  BLASTX
NCBI GI
                  g3236237
BLAST score
                  561
```

NCBI GI g3236237
BLAST score 561
E value 2.0e-57
Match length 190
% identity 57
NCBI Description (AC00468

NCBI Description (AC004684) putative ribotol dehydrogenase [Arabidopsis

thaliana]

Seq. No. 18496

Contig ID 61851 1.R1040 5'-most EST LIB3106-009-Q1-K1-C8



```
18497
Seq. No.
Contig ID
                  61884 1.R1040
                  LIB3106-018-Q1-K1-B7
5'-most EST
Method
                  BLASTX
                  q4539335
NCBI GI
BLAST score
                  285
E value
                  2.0e-25
Match length
                  103
                  45
% identity
NCBI Description (AL035539) putative protein [Arabidopsis thaliana]
Seq. No.
                  18498
                  61899 1.R1040
Contig ID
5'-most EST
                  uaw700662319.hl
Seq. No.
                  18499
Contig ID
                  61913 1.R1040
5'-most EST
                  LIB3106-018-Q1-K1-G8
Method
                  BLASTX
NCBI GI
                  g3738325
                  230
BLAST score
                  2.0e-19
E value
Match length
                  79
% identity
                  55
NCBI Description (AC005170) putative CaMB-channel protein [Arabidopsis
                  thaliana]
Seq. No.
                  18500
                  61953 1.R1040
Contig ID
5'-most EST
                  g4297683
Seq. No.
                  18501
Contig ID
                  61964 1.R1040
5'-most EST
                  LIB3107-001-Q1-K1-G11
Seq. No.
                  18502
                  61972 1.R1040
Contig ID
5'-most EST
                  fde700872524.h1
Method
                  BLASTX
NCBI GI
                  q2465923
BLAST score
                  844
                  1.0e-90
E value
Match length
                  266
% identity
                  63
NCBI Description (AF024648) receptor-like serine/threonine kinase
                  [Arabidopsis thaliana]
Seq. No.
                  18503
Contig ID
                  61975 1.R1040
```

5'-most EST LIB3106-022-Q1-K1-G6

Seq. No. 18504

61976 1.R1040 Contig ID 5'-most EST jsh701067419.h1

Method BLASTX NCBI GI g3915070



BLAST score 591 E value 3.0e-61 Match length 183 % identity 63

NCBI Description HISTIDYL-TRNA SYNTHETASE (HISTIDINE--TRNA LIGASE) (HISRS)

>gi\_1841704\_emb\_CAB06653\_ (Z85984) histidyl tRNA Synthetase

[Oryza sativa]

Seq. No. 18505

Contig ID 61979 1.R1040 5'-most EST jsh701070111.h1

Seq. No. 18506

Contig ID 62003 1.R1040

5'-most EST jC-gmle01810091g12d1

Seq. No. 18507

Contig ID 62005\_1.R1040
5'-most EST g5510313
Method BLASTX
NCBI GI g3643608
BLAST score 418
E value 9.0e-41

E value 9.00
Match length 118
% identity 70

NCBI Description (AC005395) hypothetical protein [Arabidopsis thaliana]

Seq. No. 18508

Contig ID 62115\_1.R1040 5'-most EST leu701155281.h1

Seq. No. 18509

Contig ID 62130 1.R1040 5'-most EST zsg701127512.h1

Seq. No. 18510

Contig ID 62139 1.R1040

5'-most EST LIB3106-073-Q1-K1-G4

Seq. No. 18511

Contig ID 62146 1.R1040

5'-most EST LIB3106-075-Q1-K1-H4

Seq. No. 18512

Contig ID 62159\_1.R1040 5'-most EST zsg701126001.h1

Method BLASTX
NCBI GI g3928862
BLAST score 157
E value 3.0e-10
Match length 176
% identity 24

NCBI Description (AF089710) disease resistance protein RPP8 [Arabidopsis

thaliana]

Seq. No. 18513

Contig ID 62174 1.R1040



5'-most EST jsh701065525.h1

Seq. No. 18514

Contig ID 62181 1.R1040

5'-most EST LIB3106-089-Q1-K1-F8

Seq. No. 18515

Contig ID 62186 1.R1040

5'-most EST LIB3170-083-Q1-J1-H4

Seq. No. 18516

Contig ID 62186 2.R1040

5'-most EST uC-gmflminsoy016d03b1

Seq. No. 18517

Contig ID 62212\_1.R1040 5'-most EST ncj700986922.h1

Method BLASTX
NCBI GI g2500098
BLAST score 219
E value 8.0e-18
Match length 57
% identity 79

NCBI Description DNA REPAIR PROTEIN RECA PRECURSOR >gi\_289208 (L15229) DNA

repair protein [Arabidopsis thaliana] >gi\_3152570

(AC002986) Match to nuclear-encoded chloroplast DNA repair protein (E. coli recA homolog) gb L15229. [Arabidopsis

thalianal

Seq. No. 18518

Contig ID 62223\_1.R1040 5'-most EST uC-gmropic104c02b1

Method BLASTX
NCBI GI g2367392
BLAST score 339
E value 2.0e-31
Match length 121
% identity 54

NCBI Description (U82513) random slug cDNA25 protein [Dictyostelium

discoideum]

Seq. No. 18519

Contig ID 62227\_1.R1040 5'-most EST fde700870559.h1

Seq. No. 18520

Contig ID 62242 1.R1040

5'-most EST LIB3106-107-Q1-K1-A10

Seq. No. 18521

Contig ID 62247\_1.R1040 5'-most EST uC-gmropic009a08b1

Seq. No. 18522

Contig ID 62250\_1.R1040

5'-most EST jC-gmle01810094g06a1



Seq. No. 18523

Contig ID 62251\_1.R1040

5'-most EST jC-gmst02400051h01a1 Method BLASTX

NCBI GI g3128168
BLAST score 638
E value 1.0e-66
Match length 174
% identity 60

NCBI Description (AC004521) putative carboxyl-terminal peptidase

[Arabidopsis thaliana]

Seq. No. 18524

Contig ID 62254 1.R1040

5'-most EST LIB3106-109-Q1-K1-E6

Method BLASTX
NCBI GI g113742
BLAST score 928
E value 1.0e-122
Match length 492
% identity 48

NCBI Description AMINOPEPTIDASE N (ALPHA-AMINOACYLPEPTIDE HYDROLASE)

>gi\_147142 (M15273) peptidase N [Escherichia coli]
>gi\_147144 (M15676) aminopeptidase N [Escherichia coli]
>gi\_1787163 (AE000195) aminopeptidase N [Escherichia coli]
>gi\_4062498\_dbj\_BAA35684\_ (D90731) Aminopeptidase n (EC 3.4.11.2) (alpha-aminoacylpeptide hydrolase). [Escherichia

coli]

Seq. No. 18525

Contig ID 62255\_1.R1040

5'-most EST LIB3106-109-Q1-K1-G12

Seq. No. 18526

Contig ID 62264\_1.R1040

5'-most EST LIB3139-117-P1-N1-H6

Seq. No. 18527

Contig ID 62266 1.R1040

5'-most EST LIB3106-112-Q1-K1-F4

Seq. No. 18528

Contig ID 62272 1.R1040

5'-most EST jC-gmle01810043c10d1

Seq. No. 18529

Contig ID 62279\_1.R1040

5'-most EST uC-gmrominsoy245c07b1

Method BLASTX
NCBI GI g3420050
BLAST score 173
E value 6.0e-12
Match length 98
% identity 40

NCBI Description (AC004680) hypothetical protein [Arabidopsis thaliana]

Seq. No. 18530



```
Contig ID
                   62283 1.R1040
5'-most EST
                  LIB3170-076-Q1-J1-A5
Method
                  BLASTX
NCBI GI
                  g2827619
BLAST score
                  143
E value
                  1.0e-20
```

69

75

% identity NCBI Description (AL021636) hypothetical protein [Arabidopsis thaliana]

Seq. No. 18531 Contig ID 62283 3.R1040 5'-most EST sat701006229.h2 Method BLASTX q2827619

NCBI GI BLAST score 411 E value 1.0e-40 Match length 90 % identity 91

Match length

NCBI Description (AL021636) hypothetical protein [Arabidopsis thaliana]

18532 Seq. No.

Contig ID 62293 1.R1040 5'-most EST fua701043515.h1

18533 Seq. No.

62300 1.R1040 Contig ID

5'-most EST LIB3107-041-Q1-K1-E8

Seq. No. 18534

Contig ID 62304 1.R1040

5'-most EST LIB3107-041-Q1-K1-G8

Seq. No. 18535

Contig ID 62305 1.R1040

5'-most EST LIB3107-041-Q1-K1-H11

Seq. No. 18536

62323 1.R1040 Contig ID

5'-most EST LIB3109-031-Q1-K1-D12

Seq. No. 18537

Contig ID 62323 2.R1040

5'-most EST LIB3107-049-Q1-K1-D12

Method BLASTX NCBI GI q3298540 BLAST score 453 E value 3.0e-45Match length 115 % identity 77

NCBI Description (AC004681) unknown protein [Arabidopsis thaliana]

Seq. No. 18538

Contig ID 62335\_1.R1040

5'-most EST LIB3107-036-Q1-K1-G4

Seq. No. 18539



```
Contig ID
                  62335 2.R1040
                  LIB3107-053-Q1-K1-B2
5'-most EST
                  18540
Seq. No.
Contig ID
                  62341 1.R1040
                  LIB3107-053-Q1-K1-B9
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4263831
BLAST score
                  338
E value
                  1.0e-31
Match length
                  162
                  40
% identity
NCBI Description
                  (AC006067) putative reverse transcriptase [Arabidopsis
                  thaliana]
Seq. No.
                  18541
Contig ID
                  62344 1.R1040
5'-most EST
                  LIB3109-047-Q1-K1-F1
Method
                  BLASTX
                  g1946368
NCBI GI
BLAST score
                  771
                  3.0e-86
E value
                  254
Match length
% identity
                  69
NCBI Description
                 (U93215) unknown protein [Arabidopsis thaliana]
Seq. No.
                  18542
Contig ID
                  62357 1.R1040
5'-most EST
                  LIB3107-053-Q1-K1-E10
Seq. No.
                  18543
                  62357 2.R1040
Contig ID
5'-most EST
                  jC-gmro02910052h12a1
Seq. No.
                  18544
                  62357 3.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy228c03b1
                  18545
Seq. No.
                  62364 1.R1040
Contig ID
5'-most EST
                  gsv701052234.h1
Method
                  BLASTX
NCBI GI
                  g3411152
BLAST score
                  393
                  5.0e-38
E value
Match length
                  98
% identity
NCBI Description
                  (AF066050) thymidine kinase [Oryza sativa]
```

18546 Seq. No.

Contig ID 62368 1.R1040

5'-most EST jC-gmf102220054a07a1

Method BLASTX NCBI GI g3063693 BLAST score 175 E value 1.0e-12 Match length 77



% identity (AL022537) putative protein [Arabidopsis thaliana] NCBI Description

18547 Seq. No.

62368 2.R1040 Contig ID

LIB3107-053-Q1-K1-F2 5'-most EST

BLASTX Method q3063693 NCBI GI 159 BLAST score 1.0e-10 E value 30 Match length

% identity

(AL022537) putative protein [Arabidopsis thaliana] NCBI Description

Seq. No.

62368 3.R1040 Contig ID 5'-most EST pcp700990904.h1

18549 Seq. No.

62369 1.R1040 Contig ID

LIB3107-063-Q1-K1-G12 5'-most EST

18548

18550 Seq. No.

62371 1.R1040 Contig ID

LIB3107-055-Q1-K1-A10 5'-most EST

18551 Seq. No.

62379 1.R1040 Contig ID

LIB3107-055-Q1-K1-A9 5'-most EST

BLASTX Method q4508068 NCBI GI 209 BLAST score 2.0e-16 E value 94 Match length

48 % identity

(AC005882) 3063 [Arabidopsis thaliana] NCBI Description

Seq. No. 18552

62379 2.R1040 Contig ID uC-gmropic108f12b1 5'-most EST

BLASTX Method q4508068 NCBI GI 152 BLAST score 6.0e-10 E value 46 Match length 65 % identity

(AC005882) 3063 [Arabidopsis thaliana] NCBI Description

18553 Seq. No.

62380 1.R1040 Contig ID

LIB3107-055-Q1-K1-B1 5'-most EST

18554 Seq. No.

62385 1.R1040 Contig ID 5'-most EST uC-gmropic073a11b1

18555 Seq. No.



```
62394 1.R1040
Contig ID
                  xpa700794075.hl
5'-most EST
                  BLASTX
Method
NCBI GI
                  q600855
BLAST score
                  867
                  2.0e-93
E value
                  240
Match length
                  69
% identity
NCBI Description (U17887) bZIP protein [Arabidopsis thaliana]
                  18556
Seq. No.
                   62403 1.R1040
Contig ID
                  LIB3107-058-Q1-K1-H4
5'-most EST
                   18557
Seq. No.
                   62403 2.R1040
Contig ID
                   sat701014011.hl
5'-most EST
                   18558
Seq. No.
                   62406 1.R1040
Contig ID
                   LIB3107-058-Q1-K1-H9
5'-most EST
                   BLASTX
Method
                   g1657382
NCBI GI
                   672
BLAST score
                   1.0e-70
E value
                   139
Match length
                   86
% identity
                  (Y09101) cholinephosphate cytidylyltransferase [Pisum
NCBI Description
                   sativum]
                   18559
Seq. No.
                   62406 2.R1040
Contig ID
                   asn70\overline{1}141957.h1
5'-most EST
                   BLASTX
Method
                   g1657382
NCBI GI
                   589
BLAST score
                   5.0e-61
E value
                   113
Match length
                   93
% identity
                   (Y09101) cholinephosphate cytidylyltransferase [Pisum
NCBI Description
                   sativum]
                   18560
 Seq. No.
                   62423 1.R1040
 Contig ID
 5'-most EST
                   zsg701120383.hl
                   BLASTX
Method
                   q2498943
 NCBI GI
                   189
 BLAST score
                   3.0e-14
 E value
                   89
 Match length
 % identity
                   38
                   PUTATIVE SPERMIDINE SYNTHASE (PUTRESCINE
 NCBI Description
                   AMINOPROPYLTRANSFERASE) (SPDSY) >gi_2129288_pir__B64339
```

spermidine synthase (EC 2.5.1.16) - Methanococcus

jannaschii >gi\_1591033 (U67486) spermidine synthase (speE)

[Methanococcus jannaschii]



```
Seq. No.
                  18561
                  62434 1.R1040
Contig ID
5'-most EST
                  asn701138713.h1
                  BLASTX
Method
                  g4539369
NCBI GI
BLAST score
                  390
E value
                  3.0e-74
                  220
Match length
% identity
                 (AL049525) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  18562
Contig ID
                  62447 1.R1040
5'-most EST
                  zzp700833443.hl
Seq. No.
                  18563
Contig ID
                  62449 1.R1040
5'-most EST
                  hyd700727763.h1
Method
                  BLASTX
NCBI GI
                  q1172441
BLAST score
                  550
                  6.0e-56
E value
Match length
                  175
                  70
% identity
NCBI Description
                  POSSIBLE TRANSCRIPTION FACTOR POSF21 >gi 99685 pir S21883
                  DNA-binding protein POSF21 - Arabidopsis thaliana
                  >gi 16429 emb CAA43366 (X61031) posF21 [Arabidopsis
                  thaliana]
                  18564
Seq. No.
                  62455 1.R1040
Contig ID
                  fua701040928.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q4455330
BLAST score
                  281
                  5.0e-27
E value
                  159
Match length
                  48
% identity
                 (AL035525) contains EST gb:T44002 [Arabidopsis thaliana]
NCBI Description
                  18565
Seq. No.
                  62465 1.R1040
Contig ID
5'-most EST
                  smc700745046.h1
Method
                  BLASTX
NCBI GI
                  g2980806
BLAST score
                  426
E value
                  8.0e-42
Match length
                  165
% identity
                  (AL022197) putative protein [Arabidopsis thaliana]
NCBI Description
```

Seq. No. 18566

62473 1.R1040 Contig ID

5'-most EST LIB3107-065-Q1-K1-H2

18567 Seq. No.

Contig ID 62493 1.R1040

3030



```
5'-most EST
                  LIB3107-030-Q1-K1-C5
                  18568
Seq. No.
                  62494 1.R1040
Contig ID
                  uC-gmflminsoy030f03b1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g2982444
BLAST score
                  244
                  2.0e-20
E value
Match length
                  119
% identity
                 (AL022224) CLV1 receptor kinase like protein [Arabidopsis
NCBI Description
                  thaliana]
                  18569
Seq. No.
Contig ID
                  62496 1.R1040
5'-most EST
                  jC-gmst02400042b10a1
Method
                  BLASTX
NCBI GI
                  g4510375
BLAST score
                  934
E value
                  1.0e-101
Match length
                  453
% identity
                  51
                  (AC007017) putative homeotic protein BEL1 [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  18570
                  62496 2.R1040
Contig ID
5'-most EST
                  jC-qmle01810046d06a1
Method
                  BLASTX
                  g4510375
NCBI GI
BLAST score
                  332
E value
                  4.0e-31
Match length
                  138
% identity
                  57
                  (AC007017) putative homeotic protein BEL1 [Arabidopsis
NCBI Description
                  thaliana]
                  18571
Seq. No.
                  62501 1.R1040
Contig ID
5'-most EST
                  LIB3107-065-Q1-K1-D9
Seq. No.
                  18572
                  62504 1.R1040
Contig ID
5'-most EST
                  LIB3107-065-Q1-K1-E11
                  BLASTX
Method
NCBI GI
                  q2288985
BLAST score
                  235
E value
                  2.0e-19
                  198
Match length
                  36
```

% identity

NCBI Description (AC002335) hypothetical protein [Arabidopsis thaliana]

18573 Seq. No.

Contig ID 62505 1.R1040

LIB3107-065-Q1-K1-E12 5'-most EST

Method BLASTX



```
q4220481
NCBI GI
BLAST score
                  560
                  2.0e-57
E value
                  159
Match length
% identity
NCBI Description (AC006069) unknown protein [Arabidopsis thaliana]
                  18574
Seq. No.
                   62514 1.R1040
Contig ID
5'-most EST
                  LIB3107-066-Q1-K1-D6
Method
                  BLASTX
                   g4249385
NCBI GI
BLAST score
                   384
                   4.0e-37
E value
                  79
Match length
% identity
                   82
NCBI Description (AC005966) T2K10.11 [Arabidopsis thaliana]
                   18575
Seq. No.
                   62515 1.R1040
Contig ID
5'-most EST
                   LIB3107-066-Q1-K1-D11
                   18576
Seq. No.
                   62522 1.R1040
Contig ID
                   LIB3107-066-Q1-K1-G9
5'-most EST
                   BLASTX
Method
NCBI GI
                   g1469882
BLAST score
                   444
                   6.0e-44
E value
Match length
                   150
% identity
                   52
NCBI Description (D63484) The KIAA0150 gene product is novel. [Homo sapiens]
                   18577
Seq. No.
                   62555 1.R1040
Contig ID
                   pcp700994459.hl
5'-most EST
                   18578
Seq. No.
                   62575 1.R1040
Contig ID
                   LIB3107-074-Q1-K1-D1
5'-most EST
                   18579
Seq. No.
                   62597 1.R1040
Contig ID
                   LIB3107-074-Q1-K1-F8
5'-most EST
                   BLASTX
Method
                   g4490321
NCBI GI
BLAST score
                   595
                   9.0e-62
E value
                   163
Match length
                   72
```

% identity

NCBI Description (AJ011604) nitrate transporter [Arabidopsis thaliana]

Seq. No.

62599 1.R1040 Contig ID

5'-most EST LIB3107-074-Q1-K1-G12

18580

Method BLASTX NCBI GI g3924596

3032



BLAST score 571 E value 5.0e-59 Match length 144 % identity 76

NCBI Description (AF069442) putative phospho-ser/thr phosphatase

[Arabidopsis thaliana]

Seq. No. 18581

Contig ID 62611\_1.R1040

5'-most EST LIB3107-076-Q1-K1-A3

Seq. No. 18582

Contig ID 62636\_1.R1040

5'-most EST LIB3139-018-P1-N1-D1

Method BLASTX
NCBI GI g4092771
BLAST score 430
E value 8.0e-42
Match length 331
% identity 31

NCBI Description (AF105139) disease resistance gene homolog 1A [Brassica

napus]

Seq. No. 18583

Contig ID 62644\_1.R1040

5'-most EST LIB3107-076-Q1-K1-F3

Seq. No. 18584

Contig ID 62644\_2.R1040 5'-most EST uC-gmropic106b11b1

Seq. No. 18585

Contig ID 62645 1.R1040

5'-most EST LIB3109-037-Q1-K1-C6

Seq. No. 18586

Contig ID 62646\_1.R1040 5'-most EST bth700847268.h1

Seq. No. 18587

Contig ID 62653\_1.R1040 5'-most EST epx701107486.h1

Method BLASTX
NCBI GI g3063444
BLAST score 450
E value 2.0e-44
Match length 181
% identity 57

NCBI Description (AC003981) F22013.5 [Arabidopsis thaliana]

Seq. No. 18588

Contig ID 62653\_2.R1040

5'-most EST LIB3139-012-P1-N1-A12

Seq. No. 18589

Contig ID 62656\_1.R1040 5'-most EST jex700908731.h1

3033



Method BLASTX
NCBI GI g2244850
BLAST score 446
E value 3.0e-44
Match length 135
% identity 70

NCBI Description (Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No. 18590

Contig ID 62661\_1.R1040

5'-most EST LIB3107-078-Q1-K1-A8

Method BLASTN
NCBI GI g2264303
BLAST score 36
E value 2.0e-10
Match length 127
% identity 87

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MBB18, complete sequence [Arabidopsis thaliana]

Seq. No. 18591

Contig ID 62661\_2.R1040 5'-most EST fde700877095.h1

Seq. No. 18592

Contig ID 62668\_1.R1040 5'-most EST g4260133

Seq. No. 18593

Contig ID 62687\_1.R1040

5'-most EST LIB3107-078-Q1-K1-E9

Seq. No. 18594

Contig ID 62689 1.R1040 5'-most EST dpv701101788.h1

Method BLASTX
NCBI GI g4263779
BLAST score 386
E value 3.0e-37
Match length 127
% identity 61

NCBI Description (AC006068) hypothetical protein [Arabidopsis thaliana]

Seq. No. 18595

Contig ID 62689\_2.R1040 5'-most EST hrw701058456.h1

Seq. No. 18596

Contig ID 62714\_1.R1040

5'-most EST LIB3107-079-Q1-K1-G2

Seq. No. 18597

Contig ID 62723\_1.R1040

5'-most EST LIB3107-079-Q1-K1-H7

Seq. No. 18598

Contig ID 62724\_2.R1040

```
5'-most EST
                  LIB3139-099-P1-N1-E9
Method
                  BLASTX
NCBI GI
                  g4204303
BLAST score
                  379
                   5.0e-36
E value
Match length
                  82
% identity
                   (AC003027) 1cl prt seq No definition line found
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  18599
Contig ID
                   62727 1.R1040
5'-most EST
                  LIB3107-080-Q1-K1-A2
Method
                  BLASTX
NCBI GI
                   q4220461
BLAST score
                  151
E value
                  7.0e-10
Match length
                  81
```

Seq. No. 18600 Contig ID 62733 1.R1040 5'-most EST LIB3107-065-Q1-K1-G10 Method BLASTX NCBI GI g2130080 BLAST score 654 E value 2.0e-68 Match length 225

protein [Oryza sativa]

 Seq. No.
 18601

 Contig ID
 62750 1.R1040

 5'-most EST
 gsv701051625.h1

 Method
 BLASTX

 NCBI GI
 g3142300

 BLAST score
 680

 E value
 3.0e-71

E value 3.0e-7
Match length 240
% identity 57

NCBI Description (AC002411) Contains similarity to pre-mRNA processing protein PRP39 gb L29224 from S. cerevisiae. ESTs gb R64908 and gb T88158, gb N38703 and gb AA651043 come from this

gene. [Arabidopsis thaliana]

 Seq. No.
 18602

 Contig ID
 62774\_1.R1040

 5'-most EST
 LIB3107-082-Q1-K1-G7

 Method
 BLASTX

 NCBI GI
 g2213613

 BLAST score
 301



E value 5.0e-27
Match length 140
% identity 49

NCBI Description (AC000103) F21J9.7 [Arabidopsis thaliana]

Seq. No. 18603

Contig ID 62774 2.R1040

5'-most EST LIB3107-082-Q1-K1-D11

Method BLASTX
NCBI GI g2213613
BLAST score 191
E value 1.0e-14
Match length 76
% identity 57

NCBI Description (AC000103) F21J9.7 [Arabidopsis thaliana]

Seq. No. 18604

Contig ID 62777 1.R1040

5'-most EST LIB3107-082-Q1-K1-D6

Method BLASTX
NCBI GI g627469
BLAST score 113
E value 1.0e-08
Match length 122
% identity 10

NCBI Description hypothetical protein 2 - human (fragment)

Seq. No. 18605

Contig ID 62780 1.R1040

5'-most EST LIB3107-082-Q1-K1-D9

Seq. No. 18606

Contig ID 62780 2.R1040 5'-most EST zzp700831440.h1

Seq. No. 18607

Contig ID 62791\_1.R1040

5'-most EST LIB3107-082-Q1-K1-F3

Seq. No. 18608

Contig ID 62794 1.R1040

5'-most EST LIB3107-054-Q1-K1-B8

Seq. No. 18609

Contig ID 62796\_1.R1040 5'-most EST zsg701124385.h1

Method BLASTX
NCBI GI g2618699
BLAST score 921
E value 1.0e-99
Match length 281
% identity 64

NCBI Description (AC002510) unknown protein [Arabidopsis thaliana]

Seq. No. 18610

Contig ID 62797\_1.R1040

5'-most EST LIB3107-054-Q1-K1-C2



Seq. No. 18611

Contig ID 62808 1.R1040

5'-most EST LIB3107-054-Q1-K1-D6

Seq. No. 18612

Contig ID 62819\_1.R1040 5'-most EST leu701149614.h1

Method BLASTX
NCBI GI g3608133
BLAST score 410
E value 1.0e-39
Match length 123
% identity 59

NCBI Description (AC005314) hypothetical protein [Arabidopsis thaliana]

Seq. No. 18613

Contig ID 62819 2.R1040

5'-most EST LIB3107-054-Q1-K1-E7

Method BLASTX
NCBI GI g3608133
BLAST score 367
E value 6.0e-35
Match length 98
% identity 65

NCBI Description (AC005314) hypothetical protein [Arabidopsis thaliana]

Seq. No. 18614

Contig ID 62823\_1.R1040 5'-most EST dpv701100913.h1

Method BLASTX
NCBI GI g4467119
BLAST score 827
E value 1.0e-88
Match length 157
% identity 94

NCBI Description (AL035538) Histone deacetylase [Arabidopsis thaliana]

Seq. No. 18615

Contig ID 62848 1.R1040

5'-most EST uC-gmflminsoy041c09b1

Method BLASTN
NCBI GI g516102
BLAST score 472
E value 0.0e+00
Match length 529
% identity 98

NCBI Description Soybean phytochrome B (phyB) gene exons 1-5, complete cds

Seq. No. 18616

Contig ID 62859 1.R1040

5'-most EST jC-gmle01810080a08a1

Method BLASTX
NCBI GI g2982462
BLAST score 717
E value 1.0e-75
Match length 317



% identity 45

NCBI Description (AL022223) putative protein [Arabidopsis thaliana]

Seq. No.

18617

Contig ID 5'-most EST

62861\_2.R1040 eep700864206.h1

Seq. No.

18618

Contig ID 5'-most EST

62861\_3.R1040 ncj700988346.h1

Seq. No.

18619

Contig ID

62869 1.R1040

5'-most EST

LIB3139-047-P1-N1-A3

Method NCBI GI BLASTX g2497012

BLAST score E value 205 7.0e-16

Match length % identity

118 31

NCBI Description

HYPOTHETICAL 26.6 KD PROTEIN T19C3.4 IN CHROMOSOME III >qi 849238 (U28412) similar to polyposis locus protein 1

(SP:DP1 HUMAN, Q00765) [Caenorhabditis elegans]

Seq. No.

18620

Contig ID 5'-most EST

62869\_2.R1040 gsv701054891.h1

Seq. No.

18621

Contig ID 5'-most EST

62871\_1.R1040 uC-gmropic075e03b1

Seq. No.

18622

Contig ID 5'-most EST

62885 1.R1040 zhf700955021 h

Method

zhf700955021.h1 BLASTX

NCBI GI BLAST score

g1771160 2659

E value

0.0e+00 771

Match length % identity

65

NCBI Description

(X98929) SBT1 [Lycopersicon esculentum]

>gi\_3687305\_emb\_CAA06999\_ (AJ006378) subtilisin-like

protease [Lycopersicon esculentum]

Seq. No.

18623

Contig ID 5'-most EST

62888\_1.R1040 trc700565862.h1

Method

BLASTX g1669664

NCBI GI BLAST score

342

E value Match length 9.0e-32

% identity

188 45

NCBI Description

(Z49706) GTP cyclohydrolase I [Dictyostelium discoideum]

Seq. No.

18624



Contig ID 62897\_1.R1040

5'-most EST LIB3107-060-Q1-K1-D6

Method BLASTX
NCBI GI 94220535
BLAST score 561
E value 2.0e-57
Match length 134
% identity 78

NCBI Description (AL035356) clathrin coat assembly like protein [Arabidopsis

thaliana]

Seq. No. 18625

Contig ID 62910\_1.R1040

5'-most EST LIB3107-060-Q1-K1-F2

Method BLASTN
NCBI GI g1150683
BLAST score 127
E value 4.0e-65
Match length 343
% identity 88

NCBI Description V.radiata atpB, rbcL and trnK genes

Seq. No. 18626

Contig ID 62955 1.R1040

5'-most EST LIB3107-063-Q1-K1-C8

Seq. No. 18627

Contig ID 62966\_1.R1040 5'-most EST sat701013405.h1

Method BLASTX
NCBI GI g1430846
BLAST score 724
E value 2.0e-76
Match length 226
% identity 66

NCBI Description (X99210) myb-related transcription factor [Lycopersicon

esculentum]

Seq. No. 18628

Contig ID 62966 2.R1040 5'-most EST jex700904208.h1

Method BLASTN
NCBI GI g1430845
BLAST score 121
E value 2.0e-61
Match length 321
% identity 85

NCBI Description L.esculentum mRNA for myb-related transcription factor,

THM16

Seq. No. 18629

Contig ID 62967\_2.R1040 5'-most EST eep700869128.h1

Method BLASTN
NCBI GI g2182289
BLAST score 60
E value 8.0e-25



Match length 128 % identity 87

NCBI Description Arabidopsis thaliana chromosome I BAC F11P17 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 18630

Contig ID 62972 1.R1040

LIB3107-063-Q1-K1-C4 5'-most EST

BLASTX Method NCBI GI q585155 BLAST score 158 E value 2.0e-10 Match length 54 52 % identity

FOLYLPOLYGLUTAMATE SYNTHASE (FOLYLPOLY-GAMMA-GLUTAMATE NCBI Description SYNTHETASE) (FPGS) >gi 421496 pir B40646 folC - Bacillus

> subtilis >gi 142936 (L04520) folyl-polyglutamate synthetase [Bacillus subtilis] >gi 2635273 emb CAB14768 (Z99118)

folyl-polyglutamate synthetase [Bacillus subtilis]

Seq. No. 18631

62972 2.R1040 Contig ID 5'-most EST leu701152653.h1

Seq. No.

62981 1.R1040

Contig ID

5'-most EST LIB3107-063-Q1-K1-D3

18632

18633 Seq. No.

62989 1.R1040 Contig ID

LIB3107-063-Q1-K1-E2 5'-most EST

Method BLASTX NCBI GI g2245109 BLAST score 619 E value 2.0e-64 Match length 166 70 % identity

NCBI Description (Z97343) carboxyl-terminal proteinase homolog [Arabidopsis

thaliana]

Seq. No. 18634

62994 1.R1040 Contig ID

5'-most EST LIB3107-002-Q1-K1-D3

BLASTX Method NCBI GI q2137562 BLAST score 250 2.0e-21 E value 80 Match length 60 % identity

NCBI Description mouse Dhm1 protein - mouse >gi 1060921 dbj BAA07524

(D38517) Dhm1 protein [Mus musculus]

Seq. No. 18635

Contig ID 62997 1.R1040

5'-most EST LIB3170-070-Q1-K2-F2

Method BLASTX NCBI GI g4406759



BLAST score 190 E value 2.0e-14 Match length 129 % identity 40

NCBI Description (AC006836) hypothetical protein [Arabidopsis thaliana]

Seq. No.

18636

63004 1.R1040 Contig ID 5'-most EST g4395902 Method BLASTX NCBI GI g462322 BLAST score 259 E value 5.0e-22 Match length 154 % identity 42

NCBI Description 18.3 KD CLASS I HEAT SHOCK PROTEIN (HSP 18.3)

>gi\_479366\_pir\_\_S33566 heat shock protein (clone CHEN421) red goosefoot >gi 18216 emb CAA37864 (X53870) heat-shock

protein [Chenopodium rubrum]

Seq. No.

18637

Contig ID 63005 1.R1040

5'-most EST jC-gmro02800042h08d1

Seq. No.

18638

Contig ID 63018\_1.R1040 5'-most EST uC-gmropic034d09b1

Seq. No.

18639

Contig ID 63018\_2.R1040

5'-most EST LIB3107-004-Q1-K1-G6

Seq. No.

18640

Contig ID 63018 3.R1040

5'-most EST LIB3107-002-Q1-K1-C6

Seq. No.

18641

Contig ID 63028\_1.R1040

5'-most EST LIB3107-001-Q1-K1-H6

Method BLASTX
NCBI GI g1362078
BLAST score 450
E value 1.0e-44
Match length 108
% identity 78

NCBI Description endo-1,4-beta-D-glucanase, xyloglucan-specific (clone NXG1)

- common nasturtium >gi 311835 emb CAA48324 (X68254)

cellulase [Tropaeolum majus]

Seq. No. 18642

Contig ID 63032 1.R1040

5'-most EST LIB3170-072-Q1-J1-F2

Method BLASTN
NCBI GI g558922
BLAST score 98
E value 1.0e-47
Match length 174



% identity

Lupinus albus farnesyl pyrophosphate synthase (fps1) mRNA, NCBI Description

complete cds

Seq. No. Contig ID 18643

5'-most EST

63033 1.R1040 smw700646141.h1

Seq. No.

18644

Contig ID 5'-most EST

63033 3.R1040 rca700996225.hl

Seq. No.

18645

Contig ID

63034 1.R1040

5'-most EST

LIB3109-013-Q1-K1-F8

Method NCBI GI BLASTX g4455309

BLAST score E value

296 8.0e-27

Match length

106

% identity

58

NCBI Description

(AL035528) hypothetical protein [Arabidopsis thaliana]

Seq. No.

18646

Contig ID

63036 1.R1040

5'-most EST

LIB3107-002-Q1-K1-B2

Method

BLASTX q4432840

NCBI GI

498

BLAST score E value

3.0e-50

Match length

156

% identity

64

NCBI Description

(AC006283) unknown protein [Arabidopsis thaliana]

Seq. No.

18647

Contig ID 5'-most EST 63038 1.R1040  $rca70\overline{0}998455.h1$ 

Method NCBI GI BLASTX

BLAST score

g3122638 955

E value

1.0e-104

Match length

% identity

198 35

NCBI Description

PP1/PP2A PHOSPHATASES PLEIOTROPIC REGULATOR PRL1

>gi 1076381 pir S49820 PRL1 protein - Arabidopsis thaliana

>gi\_577733\_emb\_CAA58031\_ (X82824) PRL1 [Arabidopsis

thaliana] >qi 577735 emb CAA58032 (X82825) PRL1

[Arabidopsis thaliana] >gi 2244947 emb CAB10369.1 (Z97339)

PRL1 protein - Arabidopsis thaliana

Seq. No.

18648

63043 1.R1040

Contig ID 5'-most EST

LIB3170-071-Q1-K1-E7

Method NCBI GI

BLASTX

BLAST score E value

q3461814 270

8.0e-24



Match length 113 50 % identity

NCBI Description (AC004138) hypothetical protein [Arabidopsis thaliana]

Seq. No.

18649

Contig ID

63063 1.R1040

5'-most EST

LIB3107-001-Q1-K1-E1

Seq. No.

18650

Contig ID 5'-most EST

63064 1.R1040 pcp700995190.h1

Seq. No.

18651

Contig ID 5'-most EST 63074 1.R1040

LIB3107-001-Q1-K1-A5

Seg. No.

18652

Contig ID

63080 1.R1040

5'-most EST

LIB3170-070-Q1-K2-C12

Method NCBI GI BLAST score BLASTX g4185507

E value Match length

268 2.0e-23

% identity

139 41

NCBI Description

(AF100163) EZA1 [Arabidopsis thaliana]

Seq. No.

18653

Contig ID

63088 1.R1040

5'-most EST

LIB3107-001-Q1-K1-E4

Seq. No.

18654

Contig ID

63089 1.R1040

5'-most EST

LIB3107-001-Q1-K1-A4

Seq. No.

18655

Contig ID 5'-most EST

63093 1.R1040 pxt700945202.h1

Method

BLASTX

NCBI GI

g1854443

BLAST score

536

E value

9.0e-55

Match length

150

% identity

71

NCBI Description

(D83970) CPRD8 protein [Vigna unquiculata]

Seq. No.

18656

Contig ID

63097 1.R1040

5'-most EST

LIB3107-003-Q1-K1-E1

Seq. No.

18657

Contig ID

63102 1.R1040

5'-most EST Method

LIB3107-003-Q1-K1-E6 BLASTX

NCBI GI

g1817584

BLAST score

142

E value

1.0e-08



Match length 113 % identity 31

NCBI Description (Y08991) adaptor protein [Homo sapiens]

Seq. No.

Contig ID 63103\_1.R1040

5'-most EST LIB3170-071-Q1-K1-D2

18658

Seq. No. 18659

Contig ID 63104 1.R1040

5'-most EST LIB3107-003-Q1-K1-F1

Seq. No. 18660

Contig ID 63115 1.R1040

5'-most EST LIB3170-070-Q1-J1-G6

Seq. No. 18661

Contig ID 63117\_1.R1040

5'-most EST LIB3107-003-Q1-K1-G7

Method BLASTX
NCBI GI g3080416
BLAST score 196
E value 4.0e-15
Match length 77
% identity 49

NCBI Description (AL022604) UDP-galactose transporter - like protein

[Arabidopsis thaliana]

Seq. No. 18662

Contig ID 63118 1.R1040

5'-most EST LIB3107-003-Q1-K1-G9

Seq. No. 18663

Contig ID 63121 1.R1040

5'-most EST LIB3107-003-Q1-K1-H11

Seq. No. 18664

Contig ID 63126 1.R1040

5'-most EST LIB3107-003-Q1-K1-H5

Seq. No. 18665

Contig ID 63127\_1.R1040

5'-most EST LIB3107-003-Q1-K1-H6

Seq. No. 18666

Contig ID 63128 1.R1040

5'-most EST LIB3107-003-Q1-K1-H8

Method BLASTX
NCBI GI g2352492
BLAST score 402
E value 4.0e-39
Match length 100
% identity 63

NCBI Description (AF005047) transport inhibitor response 1 [Arabidopsis

thaliana] >gi\_2352494 (AF005048) transport inhibitor

response 1 [Arabidopsis thaliana]



Seq. No. 18667

Contig ID 63128 2.R1040

5'-most EST LIB3170-077-Q1-K1-C5

Method BLASTX
NCBI GI g2352492
BLAST score 392
E value 6.0e-38
Match length 83
% identity 82

NCBI Description (AF005047) transport inhibitor response 1 [Arabidopsis

thaliana] >gi 2352494 (AF005048) transport inhibitor

response 1 [Arabidopsis thaliana]

Seq. No. 18668

Contig ID 63138 1.R1040

5'-most EST LIB3107-004-Q1-K1-H4

Seq. No. 18669

Contig ID 63144 1.R1040

5'-most EST LIB3107-005-Q1-K1-A12

Seq. No. 18670

Contig ID 63145\_1.R1040 5'-most EST fua701043161.h1

Seq. No. 18671

Contig ID 63145\_2.R1040 5'-most EST uC-gmropic074b08b1

Seq. No. 18672

Contig ID 63146 1.R1040

5'-most EST LIB3107-005-Q1-K1-A5

Method BLASTN
NCBI GI g3025869
BLAST score 35
E value 3.0e-10
Match length 85
% identity 92

NCBI Description Oryza sativa ribosomal protein S4 (rps4) gene, complete cds

Seq. No. 18673

Contig ID 63147 1.R1040

5'-most EST LIB3107-034-Q1-K1-E5

Method BLASTN
NCBI GI g12245
BLAST score 227
E value 1.0e-124
Match length 424
% identity 92

NCBI Description Spinach chloroplast DNA inversion containing ORF

Seq. No. 18674

Contig ID 63148 1.R1040

5'-most EST LIB3107-005-Q1-K1-B1

Seq. No. 18675

Contig ID 63150 1.R1040

3045

E value

Match length

NCBI Description

% identity

2.0e-64

173

70



5'-most EST LIB3170-071-Q1-K1-D4 Method BLASTX NCBI GI q3668091 BLAST score 254 5.0e-22 E value 74 Match length % identity 36 NCBI Description (AC004667) hypothetical protein [Arabidopsis thaliana] Seq. No. 18676 63153\_1.R1040 Contig ID 5'-most EST LIB3107-005-Q1-K1-C11 Method BLASTX NCBI GI g2443348 BLAST score 910 E value 2.0e-98 Match length 251 % identity 68 (AB001379) cytochrome P450 [Glycyrrhiza echinata] NCBI Description Seq. No. 18677 Contig ID 63154 1.R1040 5'-most EST uC-gmropic007d11b1 Method BLASTX NCBI GI g2245378 BLAST score 168 E value 1.0e-11 Match length 36 % identity 81 NCBI Description (U83245) auxin response factor 1 [Arabidopsis thaliana] 18678 Seq. No. Contig ID 63163 1.R1040 5'-most EST LIB3170-071-Q1-K1-G4 Seq. No. 18679 63167 1.R1040 Contig ID 5'-most EST LIB3107-005-Q1-K1-H12 BLASTX Method NCBI GI g2351160 BLAST score 237 6.0e-20 E value Match length 82 % identity 52 NCBI Description (D85214) S glycoprotein [Brassica rapa] Seq. No. 18680 63170\_1.R1040 Contig ID 5'-most EST uC-gmropic109d09b1 Method BLASTX g3091216 NCBI GI BLAST score 618

(AF060192) putative resistance protein [Glycine max]

```
18681
Seq. No.
Contig ID
                   63172 1.R1040
                  LIB3107-006-Q1-K1-A3
5'-most EST
                   18682
Seq. No.
                   63185 1.R1040
Contig ID
5'-most EST
                   fjg700968314.hl
                  BLASTX
Method
NCBI GI
                   q4469014
BLAST score
                   785
E value
                   1.0e-83
                   284
Match length
                   57
% identity
                  (AL035602) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   18683
                   63192 1.R1040
Contig ID
5'-most EST
                  LIB3107-007-Q1-K1-A3
Method
                  BLASTX
```

NCBI GI q1546706 BLAST score 529 E value 5.0e - 54Match length 126 % identity 80

(X98855) peroxidase ATP8a [Arabidopsis thaliana] NCBI Description

18684 Seq. No. 63194 1.R1040 Contig ID epx701106215.hl 5'-most EST Method BLASTX g1709885 NCBI GI BLAST score 277 3.0e-24

E value Match length 128 % identity

PHYTOENE SYNTHASE PRECURSOR >gi 1086122 pir S54135 NCBI Description

phytoene synthase - Narcissus pseudonarcissus

>gi\_780275\_emb\_CAA55391\_ (X78814) phytoene synthase

[Narcissus pseudonarcissus]

18685 Seq. No.

63194 2.R1040 Contig ID

5'-most EST LIB3107-007-Q1-K1-A6

18686 Seq. No.

Contig ID 63204 1.R1040

5'-most EST LIB3109-044-Q1-K1-D5

Method BLASTX NCBI GI g939779 BLAST score 477 1.0e-47 E value 154 Match length % identity 62

NCBI Description (L46397) MADS box protein [Zea mays]

Seq. No. 18687

Contig ID 63206 1.R1040



5'-most EST LIB3107-007-Q1-K1-C3

Seq. No. 18688

Contig ID 63213 1.R1040

5'-most EST LIB3170-070-Q1-K1-A10

Seq. No. 18689

Contig ID 63214 1.R1040

5'-most EST LIB3107-007-Q1-K1-D11

Method BLASTX
NCBI GI g3983665
BLAST score 1019
E value 1.0e-111
Match length 229
% identity 85

NCBI Description (AB011271) importin-beta2 [Oryza sativa]

Seq. No. 18690

Contig ID 63215 1.R1040

5'-most EST LIB3109-022-Q1-K1-C10

Method BLASTX
NCBI GI g968973
BLAST score 144
E value 9.0e-09
Match length 77
% identity 13

NCBI Description (U29156) involved in signaling by the epidermal growth

factor receptor; Method: conceptual translation supplied

by author. [Mus musculus]

Seq. No. 18691

Contig ID 63218\_1.R1040 5'-most EST ssr700555231.h1

Method BLASTX
NCBI GI g4415924
BLAST score 464
E value 2.0e-46
Match length 168
% identity 51

NCBI Description (AC006282) putative glucosyl transferase [Arabidopsis

thalianal

Seq. No. 18692

Contig ID 63221\_1.R1040

5'-most EST LIB3107-007-Q1-K1-D8

Seq. No. 18693

Contig ID 63222\_1.R1040

5'-most EST LIB3170-070-Q1-K2-B10

Seq. No. 18694

Contig ID 63225 1.R1040

5'-most EST LIB3107-007-Q1-K1-E3

Method BLASTX
NCBI GI 94454484
BLAST score 173
E value 2.0e-12



Match length 68 % identity 56

% identity 56 NCBI Description (A

(AC006234) putative diacylglycerol kinase [Arabidopsis

thaliana]

Seq. No.

18695

Contig ID

63236\_1.R1040

5'-most EST

LIB3107-008-Q1-K1-D7

Seq. No.

18696

Contig ID 5'-most EST

63239\_1.R1040 zhf700953971.h1

Seq. No.

18697

Contig ID

63255 1.R1040

5'-most EST

LIB3170-070-Q1-K2-F11

Seq. No.

18698

Contig ID 5'-most EST

63263\_1.R1040 jex700904484.h1

Seq. No.

18699

Contig ID 5'-most EST

63268\_1.R1040 ncj700987844.h1

Method NCBI GI BLASTX g4115377 807

BLAST score E value Match length

2.0e-86 251

% identity NCBI Description

(AC005967) unknown protein [Arabidopsis thaliana]

Seq. No.

18700

62

Contig ID

63272\_1.R1040

5'-most EST

LIB3107-009-Q1-K1-G8

Seq. No.

18701

Contig ID 5'-most EST

63274\_1.R1040

J THOSE EST

LIB3107-011-Q1-K1-H12 BLASTX

Method NCBI GI BLAST score

g3269282 260

E value Match length 3.0e-25

% identity

146 47

NCBI Description

(AL030978) putative protein [Arabidopsis thaliana]

Seq. No.

18702

Contig ID

63276 1.R1040

5'-most EST

LIB3107-011-Q1-K1-H4

Seq. No.

18703

Contig ID

63282 1.R1040

5'-most EST

LIB3107-010-Q1-K1-A11

Seq. No.

18704

Contig ID

63286 1.R1040



5'-most EST LIB3170-074-Q1-K1-A1

Method BLASTX
NCBI GI 94234854
BLAST score 336
E value 2.0e-31
Match length 123
% identity 58

NCBI Description (AF082134) pol polyprotein [Zea mays]

Seq. No. 18705

Contig ID 63295\_1.R1040 5'-most EST hyd700727981.h1

Method BLASTX
NCBI GI g3337361
BLAST score 142
E value 1.0e-08
Match length 138
% identity 30

NCBI Description (AC004481) ankyrin-like protein [Arabidopsis thaliana]

Seq. No. 18706

Contig ID 63295\_2.R1040 5'-most EST dpv701102831.h1

Method BLASTX
NCBI GI g3337361
BLAST score 142
E value 1.0e-08
Match length 127
% identity 21

NCBI Description (AC004481) ankyrin-like protein [Arabidopsis thaliana]

Seq. No. 18707

Contig ID 63306 1.R1040

5'-most EST LIB3170-081-Q1-K1-H12

Seq. No. 18708

Contig ID 63307 1.R1040

5'-most EST LIB3107-010-Q1-K1-D4

Seq. No. 18709

Contig ID 63312 1.R1040

5'-most EST LIB3170-083-Q1-K1-B12

Method BLASTN
NCBI GI g725331
BLAST score 377
E value 0.0e+00
Match length 381
% identity 100

NCBI Description Glycine max mitochondrion polymorphic marker DNA sequence

Seq. No. 18710

Contig ID 63316 1.R1040

Method BLASTX
NCBI GI g4510375
BLAST score 465
E value 3.0e-46



Match length 121 % identity 79

NCBI Description (AC007017) putative homeotic protein BEL1 [Arabidopsis

thaliana]

Seq. No. 18711

Contig ID 63316\_2.R1040 5'-most EST fde700876519.h1

Method BLASTX
NCBI GI g4006884
BLAST score 162
E value 6.0e-11
Match length 100
% identity 45

NCBI Description (Z99707) BEL1-like homeodomain protein [Arabidopsis

thaliana]

Seq. No. 18712

Contig ID 63328 1.R1040 5'-most EST sat701014091.h1

Seq. No. 18713

Contig ID 63336 1.R1040

5'-most EST LIB3107-011-Q1-K1-D3

Method BLASTX
NCBI GI g2088647
BLAST score 430
E value 3.0e-42
Match length 130
% identity 65

NCBI Description (AF002109) hypothetical protein [Arabidopsis thaliana]

>gi 3158394 (AF036340) LRR-containing F-box protein

[Arabidopsis thaliana]

Seq. No. 18714

Contig ID 63340\_1.R1040

5'-most EST LIB3107-011-Q1-K1-D7

Seq. No. 18715

Contig ID 63342 1.R1040

5'-most EST LIB3107-011-Q1-K1-E10

Seq. No. 18716

Contig ID 63343 1.R1040

5'-most EST LIB3107-015-Q1-K1-E9

Method BLASTX
NCBI GI g3549664
BLAST score 396
E value 2.0e-38
Match length 137
% identity 55

NCBI Description (AL031394) putative protein [Arabidopsis thaliana]

Seq. No. 18717

Contig ID 63344 1.R1040

5'-most EST LIB3107-011-Q1-K1-E2



```
Seq. No.
                  18718
Contig ID
                  63356 1.R1040
                  LIB3107-011-Q1-K1-F4
5'-most EST
Seq. No.
                  18719
Contig ID
                  63358 1.R1040
5'-most EST
                  LIB3107-011-Q1-K1-F6
```

18720 Seq. No. 63360 1.R1040 Contig ID LIB3107-011-Q1-K1-F8 5'-most EST Method BLASTX NCBI GI g2739376 989 BLAST score E value 1.0e-107

Match length 271 % identity 69

NCBI Description (AC002505) putative permease [Arabidopsis thaliana]

18721 Seq. No. 63360 2.R1040 Contig ID 5'-most EST awf700842602.h1 Method BLASTX g2739376 NCBI GI

BLAST score 131 E value 2.0e-09 Match length 42 % identity 86

NCBI Description (AC002505) putative permease [Arabidopsis thaliana]

18722 Seq. No.

63362 1.R1040 Contig ID 5'-most EST

LIB3107-011-Q1-K1-G1

Seq. No. 18723

63363\_1.R1040 Contig ID 5'-most EST gsv701054866.h1

Seq. No. 18724

63367 1.R1040 Contig ID

5'-most EST LIB3107-012-Q1-K1-F12

Method BLASTX NCBI GI q3402684 BLAST score 173 E value 2.0e-12 Match length 111 33 % identity

NCBI Description (AC004697) hypothetical protein [Arabidopsis thaliana]

Seq. No. 18725

63378 1.R1040 Contig ID 5'-most EST pmv700894018.h1

Seq. No. 18726

Contig ID 63379 1.R1040

5'-most EST LIB3107-012-Q1-K1-H5



Seq. No. 18727

Contig ID 63395 1.R1040

5'-most EST LIB3107-013-Q1-K1-B4

Method BLASTX
NCBI GI 94512682
BLAST score 372
E value 2.0e-41
Match length 124
% identity 69

NCBI Description (AC006931) unknown protein [Arabidopsis thaliana]

Seq. No. 18728

Contig ID 63408 1.R1040

5'-most EST LIB3107-013-Q1-K1-D11

Seq. No. 18729

Contig ID 63408\_2.R1040 5'-most EST uC-gmropic038c03b1

Seq. No. 18730

Contig ID 63410 1.R1040

5'-most EST LIB3107-014-Q1-K1-B7

Seq. No. 18731

Contig ID 63430 1.R1040

5'-most EST LIB3107-014-Q1-K1-E1

Seq. No. 18732

Contig ID 63435 1.R1040

5'-most EST LIB3107-014-Q1-K1-E8

Seq. No. 18733

Contig ID 63437\_1.R1040 5'-most EST trc700566464.h1

Method BLASTN
NCBI GI g4388705
BLAST score 51
E value 2.0e-19

Match length 211 % identity 81

NCBI Description Arabidopsis thaliana chromosome I BAC F20D21 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 18734

Contig ID 63447 1.R1040

5'-most EST LIB3107-011-Q1-K1-G8

Seq. No. 18735

Contig ID 63451 1.R1040

5'-most EST LIB3107-014-Q1-K1-H1

Seq. No. 18736

Contig ID 63458\_1.R1040 5'-most EST jsh701070164.h1

Method BLASTX
NCBI GI g4001720
BLAST score 268



6.0e-23 E value Match length 197 35 % identity

(AB015894) neural specific sr protein NSSR 1 [Mus musculus] NCBI Description

Seq. No.

18737

Contig ID

63468 1.R1040

5'-most EST

LIB3107-015-Q1-K1-F2

Method NCBI GI BLAST score BLASTX g1345132

E value

1091 1.0e-119

Match length % identity

240 87

NCBI Description

(U47029) ERECTA [Arabidopsis thaliana]

>gi\_1389566\_dbj\_BAA11869\_ (D83257) receptor protein kinase
[Arabidopsis thaliana] >gi\_3075386 (AC004484) receptor

protein kinase, ERECTA [Arabidopsis thaliana]

Seq. No.

18738

Contig ID

63470 1.R1040

5'-most EST

LIB3107-034-Q1-K1-F5

Seq. No.

18739

Contig ID

63473 1.R1040

5'-most EST

LIB3107-015-Q1-K1-F8

Method NCBI GI

BLASTX

BLAST score

q4580389

513

E value

3.0e-52

Match length

127 75

% identity

NCBI Description (AC007171) unknown protein [Arabidopsis thaliana]

Seq. No.

18740

Contig ID

63477 1.R1040

5'-most EST

LIB3107-015-Q1-K1-G12 BLASTX

Method NCBI GI

g2827550

BLAST score

428

E value

3.0e-42

Match length

114

46

% identity NCBI Description

(ALO21635) leucine rich repeat receptor kinase-like protein

[Arabidopsis thaliana]

Seq. No.

18741

Contig ID

63482 1.R1040

5'-most EST

LIB3107-015-Q1-K1-G9

Seq. No.

18742

Contig ID

63488 1.R1040

5'-most EST

LIB3107-015-Q1-K1-H5

Seq. No.

18743

Contig ID

63488 2.R1040

5'-most EST

LIB3107-032-Q1-K1-H3

Seq. No. 18744

Contig ID 63491\_1.R1040 5'-most EST hyd700727491.h1

Seq. No. 18745

Contig ID 63491 3.R1040 5'-most EST uaw700662270.h1

Method BLASTX
NCBI GI g2258336
BLAST score 360
E value 4.0e-34
Match length 109
% identity 61

NCBI Description (AF007261) component involved in Haem biosynthesis

[Reclinomonas americana]

Seq. No. 18746

Contig ID 63492 1.R1040

5'-most EST LIB3107-016-Q1-K1-A11

Seq. No. 18747

Contig ID 63498 1.R1040

5'-most EST LIB3107-016-Q1-K1-B1

Seq. No. 18748

Contig ID 63500 1.R1040

5'-most EST LIB3109-041-Q1-K1-A11

Method BLASTX
NCBI GI g131150
BLAST score 2245
E value 0.0e+00
Match length 418
% identity 99

NCBI Description PHOTOSYSTEM I P700 CHLOROPHYLL A APOPROTEIN A2

>gi\_81515\_pir\_\_S00445 photosystem I protein A2 - spinach
chloroplast >gi\_12271\_emb\_CAA27745\_ (X04131) psaB gene
product (aa 1-734) P700 chlorophyll a apoprotein [Spinacia
oleracea] >gi\_225422\_prf\_\_1303218B gene psaB [Spinacia

oleracea]

Seq. No. 18749

Contig ID 63501 1.R1040

5'-most EST uC-gmflminsoy054a01b1

Method BLASTX
NCBI GI g2827139
BLAST score 257
E value 6.0e-22
Match length 172
% identity 49

NCBI Description (AF027172) cellulose synthase catalytic subunit

[Arabidopsis thaliana] >gi\_4049343\_emb\_CAA22568\_ (AL034567) cellulose synthase catalytic subunit (RSW1) [Arabidopsis

thaliana]

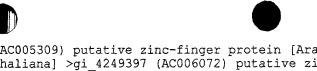
Seq. No. 18750

Contig ID 63501 2.R1040

```
5'-most EST
                  zhf700957601.h1
Method
                  BLASTX
                  g2262116
NCBI GI
BLAST score
                  488
                  9.0e-49
E value
Match length
                  240
                  40
% identity
NCBI Description (AC002343) cellulose synthase isolog [Arabidopsis thaliana]
Seq. No.
                  18751
                  63501 4.R1040
Contig ID
5'-most EST
                  kmv700739206.h1
                  BLASTX
Method
                  g2262115
NCBI GI
BLAST score
                  140
                  9.0e-13
E value
Match length
                  94
                  42
% identity
NCBI Description (AC002343) cellulose synthase isolog [Arabidopsis thaliana]
                  18752
Seq. No.
                  63511 1.R1040
Contig ID
5'-most EST
                  LIB3107-017-Q1-K1-C3
Method
                  BLASTX
NCBI GI
                  q2464914
BLAST score
                  249
E value
                  8.0e-21
Match length
                  133
% identity
                  45
NCBI Description (Z99708) hypothetical protein [Arabidopsis thaliana]
                  18753
Seq. No.
Contig ID
                  63512 1.R1040
5'-most EST
                  LIB3107-017-Q1-K1-C4
                  18754
Seq. No.
                  63519 1.R1040
Contig ID
5'-most EST
                  uC-gmflminsoy034h01b1
Method
                  BLASTX
NCBI GI
                  g3738301
BLAST score
                  345
E value
                  5.0e-32
Match length
                  209
% identity
                  43
                  (AC005309) putative zinc-finger protein [Arabidopsis
NCBI Description
                  thaliana] >gi_4249397 (AC006072) putative zinc-finger
                  protein (B-box zinc finger domain) [Arabidopsis thaliana]
                  18755
Seq. No.
Contig ID
                  63519 2.R1040
```

5'-most EST LIB3107-017-Q1-K1-D12 Method BLASTX

NCBI GI g3738301 BLAST score 538 E value 8.0e-55 Match length 214 % identity 48



```
NCBI Description
                 (AC005309) putative zinc-finger protein [Arabidopsis
                  thaliana] >qi 4249397 (AC006072) putative zinc-finger
                  protein (B-box zinc finger domain) [Arabidopsis thaliana]
Seq. No.
                  18756
Contig ID
                  63520 1.R1040
                  LIB3107-017-Q1-K1-D3
5'-most EST
Seq. No.
                  18757
                  63521 1.R1040
Contig ID
5'-most EST
                  LIB3107-050-Q1-K1-H5
Method
                  BLASTN
                  g2213606
NCBI GI
BLAST score
                  62
E value
                  3.0e-26
Match length
                  186
                  83
% identity
NCBI Description Genomic sequence for Arabidopsis thaliana BAC F21J9,
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  18758
Contig ID
                  63525 1.R1040
5'-most EST
                  LIB3107-017-Q1-K1-E11
Method
                  BLASTX
                  q3080420
NCBI GI
BLAST score
                  342
E value
                  3.0e-32
Match length
                  124
% identity
                  60
                 (AL022604) putative sugar transporter protein [Arabidopsis
NCBI Description
                  thaliana]
                  18759
Seq. No.
                  63525 2.R1040
Contig ID
5'-most EST
                  smc700747136.hl
Method
                  BLASTX
NCBI GI
                  q3080420
BLAST score
                  196
E value
                  2.0e-15
                  57
Match length
% identity
NCBI Description (AL022604) putative sugar transporter protein [Arabidopsis
                  thaliana]
                  18760
Seq. No.
Contig ID
                  63528 1.R1040
5'-most EST
                  LIB3107-017-Q1-K1-E3
Method
                  BLASTX
NCBI GI
                  q3342249
BLAST score
                  592
E value
```

4.0e-61 Match length 244 % identity

NCBI Description (AF047719) GA3 [Arabidopsis thaliana] >gi 3342251

(AF047720) GA3 [Arabidopsis thaliana]

18761 Seq. No.

3057



Contig ID 63529\_1.R1040 5'-most EST hrw701058985.h1 Method BLASTX

Method BLASTX
NCBI GI g4538897
BLAST score 378
E value 2.0e-36
Match length 111
% identity 59

NCBI Description (ALO49482) AX110P-like protein [Arabidopsis thaliana]

Seq. No. 18762

Contig ID 63542 1.R1040

5'-most EST LIB3107-041-Q1-K1-D8

Method BLASTX
NCBI GI g1621467
BLAST score 440
E value 1.0e-43
Match length 123
% identity 63

NCBI Description (U73106) laccase [Liriodendron tulipifera]

Seq. No. 18763

Contig ID 63543\_1.R1040 5'-most EST hrw70\overline{1}062596.h1

Seq. No. 18764

Contig ID 63546 1.R1040 5'-most EST pcp700993109.h1

Seq. No. 18765

Contig ID 63549 1.R1040

5'-most EST LIB3170-075-Q1-K2-F11

Method BLASTX
NCBI GI g4006833
BLAST score 161
E value 6.0e-11
Match length 76
% identity 38

NCBI Description (AC005970) putative reverse transcriptase [Arabidopsis

thaliana]

Seq. No. 18766

Contig ID 63565\_1.R1040

5'-most EST LIB3107-019-Q1-K1-C1

Method BLASTX
NCBI GI g2894612
BLAST score 408
E value 1.0e-39
Match length 177
% identity 45

NCBI Description (AL021889) putative protein [Arabidopsis thaliana]

Seq. No. 18767

Contig ID 63573 1.R1040

5'-most EST LIB3107-019-Q1-K1-D7

Seq. No. 18768



```
Contig ID
                  63576 1.R1040
5'-most EST
                  LIB3109-018-Q1-K1-G12
Method
                  BLASTN
                  g3900979
NCBI GI
BLAST score
                  40
                  4.0e-13
E value
                  60
Match length
                  92
% identity
NCBI Description Eichhornia crassipes mRNA for metallothionein-like protein,
                  clone A
```

18769 Seq. No. 63578 1.R1040 Contig ID

LIB3170-078-Q1-K1-C1 5'-most EST

Seq. No. 18770

63588 1.R1040 Contig ID

5'-most EST LIB3170-079-Q1-K1-E1

18771 Seq. No.

63589 1.R1040 Contig ID zpv700763411.h1 5'-most EST

Method BLASTX g3894171 NCBI GI BLAST score 639 E value 2.0e-66 230 Match length % identity 56

NCBI Description (AC005312) putative glutathione s-transferase [Arabidopsis

thaliana]

18772 Seq. No.

63590\_1.R1040 Contig ID

5'-most EST LIB3107-019-Q1-K1-H2

Seq. No. 18773

63591 1.R1040 Contig ID 5'-most EST smc700749803.h1

Method BLASTX NCBI GI g3860263 BLAST score 333 E value 4.0e-31 Match length 144 % identity

NCBI Description (AC005824) putative cytochrome p450 protein [Arabidopsis

thaliana]

18774 Seq. No.

63593 1.R1040 Contig ID

5'-most EST LIB3107-021-Q1-K1-C7

18775 Seq. No.

63603 1.R1040 Contig ID

LIB3107-021-Q1-K1-E4 5'-most EST

Seq. No. 18776

Contig ID 63610 1.R1040

```
LIB3107-021-Q1-K1-F5
5'-most EST
                  BLASTN
Method
                  g2656029
NCBI GI
BLAST score
                  33
E value
                  9.0e-09
Match length
                  69
% identity
                  87
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
Seq. No.
                  18777
Contig ID
                  63612 2.R1040
5'-most EST
                  LIB3107-021-Q1-K1-G3
Method
                  BLASTN
NCBI GI
                  g3242455
BLAST score
                  37
                  2.0e-11
E value
Match length
                  81
% identity
NCBI Description Arabidopsis thaliana Atrboh F mRNA, complete cds
                  18778
Seq. No.
                  63619 1.R1040
Contig ID
5'-most EST
                  LIB3107-021-Q1-K1-H5
Method
                  BLASTX
NCBI GI
                  q2465925
BLAST score
                  199
E value
                  2.0e-15
Match length
                  76
                  55
% identity
NCBI Description (AF024649) receptor-like serine/threonine kinase
                  [Arabidopsis thaliana]
Seq. No.
                  18779
Contig ID
                  63631 1.R1040
5'-most EST
                  LIB3107-022-Q1-K1-A1
Seq. No.
                  18780
Contig ID
                  63650 1.R1040
5'-most EST
                  zhf700961417.h1
Seq. No.
                  18781
                  63655 1.R1040
Contig ID
5'-most EST
                  LIB3107-039-Q1-K1-D8
Method
                  BLASTX
NCBI GI
                  g4539383
BLAST score
                  255
E value
                  1.0e-21
Match length
                  181
% identity
                  37
NCBI Description (AL035526) putative protein (fragment) [Arabidopsis
```

Seq. No. 18782

Contig ID 63663\_1.R1040

5'-most EST LIB3107-024-Q1-K1-A12

thaliana]



```
Seq. No.
                  18783
Contig ID
                  63663 2.R1040
5'-most EST
                  pxt700943612.h1
                  18784
Seq. No.
                  63678 1.R1040
Contig ID
5'-most EST
                  LIB3107-024-Q1-K1-C1
Seq. No.
                  18785
                  63679 1.R1040
Contig ID
                  LIB3107-024-Q1-K1-C10
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2980781
BLAST score
                  235
                  2.0e-19
E value
Match length
                  71
% identity
NCBI Description
                  (AL022198) putative protein [Arabidopsis thaliana]
                  18786
Seq. No.
Contig ID
                  63681 1.R1040
5'-most EST
                  LIB3107-024-Q1-K1-C4
Seq. No.
                  18787
Contig ID
                  63707 1.R1040
5'-most EST
                  LIB3107-025-Q1-K1-D8
Method
                  BLASTX
NCBI GI
                  g4234852
BLAST score
                  328
E value
                  2.0e-30
Match length
                  131
% identity
                  51
NCBI Description (AF082133) gag-pol polyprotein [Zea mays]
Seq. No.
                  18788
Contig ID
                  63710 1.R1040
5'-most EST
                  LIB3107-025-Q1-K1-E11
Seq. No.
                  18789
Contig ID
                  63711 1.R1040
5'-most EST
                  LIB3107-025-Q1-K1-E12
                  18790
Seq. No.
                  63713 1.R1040
Contig ID
5'-most EST
                  hyd700731289.h1
                  BLASTX
Method
NCBI GI
                  g2443329
BLAST score
                  704
E value
                  2.0e-85
                  230
```

Match length % identity 71

NCBI Description (D86122) Mei2-like protein [Arabidopsis thaliana]

Seq. No. 18791

Contig ID 63717 1.R1040

5'-most EST LIB3107-025-Q1-K1-F10

```
18792
Seq. No.
                  63723 1.R1040
Contig ID
5'-most EST
                  LIB3107-025-Q1-K1-F6
Seq. No.
                  18793
                  63742 1.R1040
Contig ID
5'-most EST
                  pmv700894857.h1
                  18794
Seg. No.
                  63759 1.R1040
Contig ID
5'-most EST
                  LIB3107-029-Q1-K1-A8
                  18795
Seq. No.
Contig ID
                  63760 1.R1040
5'-most EST
                  LIB3170-081-Q1-K1-C1
                  18796
Seq. No.
                  63766 1.R1040
Contig ID
5'-most EST
                  leu701153463.h1
Method
                  BLASTX
                  g3450842
NCBI GI
BLAST score
                  494
E value
                  5.0e-50
Match length
                  130
% identity
                  71
NCBI Description (AF080436) mitogen activated protein kinase kinase [Oryza
                  sativa]
Seq. No.
                  18797
                  63771 1.R1040
Contig ID
5'-most EST
                  LIB3107-029-Q1-K1-B7
Method
                  BLASTX
                  g1256509
NCBI GI
BLAST score
                  793
E value
                  1.0e-84
Match length
                  213
% identity
                  69
NCBI Description (X92943) pectate lyase [Musa acuminata]
```

Seq. No. 18798 63771 2.R1040 Contig ID 5'-most EST LIB3109-010-Q1-K1-A12 Method BLASTX NCBI GI g4220512 BLAST score 217 E value 3.0e-17 Match length 76

% identity 54
NCBI Description (AL035356) putative pectate lyase [Arabidopsis thaliana]

Seq. No. 18799

Contig ID 63771\_3.R1040

5'-most EST jC-gmf102220068h04d1

Method BLASTX
NCBI GI g1256509
BLAST score 517
E value 2.0e-52



Match length 139 % identity 68

NCBI Description (X92943) pectate lyase [Musa acuminata]

Seq. No. Contig ID 18800

BLASTX

191

g2465923

5'-most EST

63778 1.R1040

LIB3107-029-Q1-K1-C7

Method NCBI GI BLAST score E value

2.0e-14 Match length 68 49 % identity

NCBI Description (AF024648) receptor-like serine/threonine kinase

[Arabidopsis thaliana]

Seq. No.

18801

Contig ID 63780 1.R1040

5'-most EST LIB3170-081-Q1-K1-H1

Seq. No.

18802

Contig ID

63782 1.R1040

5'-most EST

LIB3170-083-Q1-K1-C1

Method BLASTN NCBI GI g507033 BLAST score 112 E value 4.0e-56 Match length 273

% identity 86

NCBI Description H.annuus mitochondrial DNA for tRNA-Cys, tRNA-Asn and

tRNA-Tyr

Seq. No.

18803

Contig ID

63783 1.R1040

5'-most EST

LIB3107-029-Q1-K1-D12

Seq. No.

18804

Contig ID 5'-most EST

63787 1.R1040 LIB3170-083-Q1-K1-B1

Seq. No.

18805

Contig ID

63788 1.R1040

5'-most EST

LIB3107-029-Q1-K1-E1

Method NCBI GI BLAST score BLASTN g402616 33

E value Match length 1.0e-08 342

% identity NCBI Description G.max satellite DNA

87

Seq. No.

18806

Contig ID

63791 1.R1040

5'-most EST

LIB3170-083-Q1-K1-E1

Seq. No.

18807

Contig ID

63792 1.R1040

3063



5'-most EST LIB3107-029-Q1-K1-E6

Seq. No. 18808

Contig ID 63795 1.R1040

5'-most EST LIB3170-082-Q1-K1-A6

Seq. No. 18809

Contig ID 63797 1.R1040

5'-most EST LIB3107-030-Q1-K1-D4

Method BLASTX
NCBI GI g4490743
BLAST score 477
E value 1.0e-47
Match length 213
% identity 53

NCBI Description (AL035708) putative protein [Arabidopsis thaliana]

Seq. No. 18810

Contig ID 63803 1.R1040

5'-most EST LIB3107-030-Q1-K1-E12

Seq. No. 18811

Contig ID 63805 1.R1040

5'-most EST jC-gmle01810080b06a1

Method BLASTN
NCBI GI g3985931
BLAST score 42
E value 2.0e-14
Match length 110
% identity 85

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K21H1, complete sequence [Arabidopsis thaliana]

Seq. No. 18812

Contig ID 63810\_1.R1040 5'-most EST fua701041718.h1

Method BLASTX
NCBI GI g445613
BLAST score 1049
E value 1.0e-114
Match length 242
% identity 81

NCBI Description ribosomal protein L7 [Solanum tuberosum]

Seq. No. 18813

Contig ID 63811 1.R1040

5'-most EST LIB3138-065-Q1-N1-F11

Seq. No. 18814

Contig ID 63813\_1.R1040

5'-most EST uC-gmrominsoy119a08b1

Method BLASTX
NCBI GI g3201615
BLAST score 1001
E value 1.0e-109
Match length 330
% identity 63



NCBI Description (AC004669) unknown protein [Arabidopsis thaliana]

Seq. No. 18815

Contig ID 63817 1.R1040

5'-most EST LIB3107-030-Q1-K1-G11

Method BLASTX
NCBI GI g1491615
BLAST score 553
E value 1.0e-56
Match length 187
% identity 59

NCBI Description (X99923) male sterility 2-like protein [Arabidopsis

thaliana]

Seq. No. 18816

Contig ID 63819\_1.R1040

5'-most EST LIB3107-030-Q1-K1-G3

Seq. No. 18817

Contig ID 63821 1.R1040

5'-most EST LIB3170-082-Q1-K1-F2

Method BLASTX
NCBI GI g3559816
BLAST score 465
E value 7.0e-91
Match length 184
% identity 93

NCBI Description (Y15782) transketolase 2 [Capsicum annuum]

Seq. No. 18818

Contig ID 63828\_1.R1040 5'-most EST awf700836324.h1

Method BLASTX
NCBI GI g3123130
BLAST score 693
E value 3.0e-73
Match length 155
% identity 45

NCBI Description HYPOTHETICAL 61.8 KD TRP-ASP REPEATS CONTAINING PROTEIN

T32G6.2 IN CHROMOSOME II >gi\_2618685 (AC002510) putative

small nuclear ribonucleoprotein Prp4p [Arabidopsis

thaliana] >gi 3241948 (AC004625) putative small nuclear

ribonucleoprotein Prp4p [Arabidopsis thaliana]

Seq. No. 18819

Contig ID 63833 1.R1040

5'-most EST LIB3107-031-Q1-K1-A1

Seq. No. 18820

Contig ID 63834\_1.R1040

5'-most EST LIB3170-084-Q1-K1-A3

Method BLASTX
NCBI GI g4309742
BLAST score 365
E value 5.0e-35
Match length 105
% identity 62



NCBI Description (AC006439) putative Rerl protein [Arabidopsis thaliana]

Seq. No. 18821

Contig ID 63835 1.R1040

5'-most EST LIB3107-031-Q1-K1-A11

Method BLASTN
NCBI GI g3599418
BLAST score 36
E value 1.0e-10
Match length 73
% identity 88

NCBI Description Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds

Seq. No. 18822

Contig ID 63836 1.R1040

5'-most EST LIB3170-065-Q1-K1-E7

Method BLASTX
NCBI GI g4263821
BLAST score 142
E value 1.0e-08
Match length 70
% identity 50

NCBI Description (AC006067) hypothetical protein [Arabidopsis thaliana]

Seq. No. 18823

Contig ID 63839\_1.R1040

5'-most EST LIB3107-031-Q1-K1-A5

Method BLASTN
NCBI GI g870984
BLAST score 50
E value 4.0e-19
Match length 98
% identity 88

NCBI Description C.melo PSY1 mRNA for phytoene synthase

Seq. No. 18824

Contig ID 63843\_1.R1040

5'-most EST LIB3107-031-Q1-K1-F3

Seq. No. 18825

Contig ID 63843 2.R1040 5'-most EST sat701006372.h1

Seq. No. 18826

Contig ID 63848\_1.R1040 5'-most EST jex700906409.h1

Method BLASTX
NCBI GI g2160177
BLAST score 249
E value 4.0e-21
Match length 87
% identity 57

NCBI Description (AC000132) EST gb\_R64758 comes from this gene. [Arabidopsis

thaliana]

Seq. No. 18827



Contig ID 63851\_1.R1040
5'-most EST LIB3107-031-Q1-K1-G2
Method BLASTX
NCBI GI g3157932
BLAST score 579

BLAST score 579
E value 9.0e-60
Match length 183
% identity 65

NCBI Description (AC002131) Similar to hypothetical protein HYP1 gb\_Z97338 from A. thaliana. [Arabidopsis thaliana]

Seq. No. 18828

Contig ID 63851 2.R1040

5'-most EST LIB3 $\overline{107}$ -031-Q1-K1-D3

Seq. No. 18829

Contig ID 63855 1.R1040

5'-most EST  $jC-gm\overline{f}102220063a04a1$ 

Method BLASTN
NCBI GI 94138678
BLAST score 192
E value 1.0e-103
Match length 559
% identity 84

NCBI Description V.faba mRNA for amino acid transporter

Seq. No. 18830

Contig ID 63861\_1.R1040 5'-most EST xpa700796903.h1

Method BLASTX
NCBI GI g2982459
BLAST score 185
E value 1.0e-13
Match length 118
% identity 37

NCBI Description (AL022223) putative protein [Arabidopsis thaliana]

Seq. No. 18831

Contig ID 63862 1.R1040

5'-most EST LIB3107-032-Q1-K1-A1

Seq. No. 18832

Contig ID 63863 1.R1040

5'-most EST LIB3170-082-Q1-K1-F4

Seq. No. 18833

Contig ID 63869 1.R1040

5'-most EST uC-gmrominsoy305f02b1

Method BLASTX
NCBI GI g1839188
BLAST score 843
E value 1.0e-90
Match length 256
% identity 62

NCBI Description (U86081) root hair defective 3 [Arabidopsis thaliana]

Seq. No. 18834



```
63870 1.R1040
Contig ID
                  LIB3170-081-Q1-K1-B4
5'-most EST
Seq. No.
                  18835
Contig ID
                  63873 1.R1040
5'-most EST
                  LIB3107-032-Q1-K1-D2
Method
                  BLASTX
NCBI GI
                  q4572676
BLAST score
                  150
E value
                  2.0e-09
Match length
                  107
                  36
% identity
                 (AC006954) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  18836
Contig ID
                  63873 2.R1040
5'-most EST
                  asn701140663.hl
Seq. No.
                  18837
Contig ID
                   63883 1.R1040
5'-most EST
                  LIB3107-033-Q1-K1-D6
                  18838
Seq. No.
Contig ID
                   63884 1.R1040
5'-most EST
                  LIB3170-084-Q1-K1-D5
Seq. No.
                   18839
Contig ID
                   63889 1.R1040
5'-most EST
                  LIB3107-033-Q1-K1-E3
Seq. No.
                   18840
Contig ID
                   63891 1.R1040
                  LIB3107-033-Q1-K1-E5
5'-most EST
Method
                  BLASTX
                   g4406764
NCBI GI
BLAST score
                   659
                   4.0e-69
E value
Match length
                   189
                   42
% identity
                  (AC006836) putative uridylyl transferase [Arabidopsis
NCBI Description
                   thaliana]
                   18841
Seq. No.
Contig ID
                   63903 1.R1040
5'-most EST
                   LIB3170-081-Q1-J1-F5
                   18842
Seq. No.
                   63912_1.R1040
Contig ID
5'-most EST
                   LIB31\overline{0}7-033-Q1-K1-G5
```

Seq. No. 18843

Contig ID 63914 1.R1040

LIB3107-033-Q1-K1-G7 5'-most EST

Method BLASTX q2586082 NCBI GI BLAST score 244 E value 1.0e-24



Match length 108 % identity 50

NCBI Description (U72725) retrofit [Oryza longistaminata]

Seq. No.

18844 63915 1.R1040 Contig ID

5'-most EST LIB3107-033-Q1-K1-G8

Seq. No.

18845

Contig ID 63920 1.R1040

5'-most EST LIB3107-033-Q1-K1-H2

Seq. No.

18846 63920 2.R1040

Contig ID 5'-most EST

rca700998065.h1

Seq. No.

18847

Contig ID 63921 1.R1040

5'-most EST LIB3107-033-Q1-K1-H3

Seq. No.

18848

63923 1.R1040 Contig ID

5'-most EST LIB3107-033-Q1-K1-H7

Seq. No.

18849

Contig ID 63924 1.R1040

5'-most EST LIB3107-033-Q1-K1-H6

Method BLASTX g629693 NCBI GI 390 BLAST score 8.0e-38 E value Match length 134 % identity 51

NCBI Description probable integrase - common tobacco (fragment)

>gi\_530742\_emb\_CAA56791\_ (X80830) integrase [Nicotiana

tabacum]

18850 Seq. No.

Contig ID 63926 1.R1040 5'-most EST kl1701213405.h1

Method BLASTX NCBI GI q3335378 BLAST score 348 1.0e-32 E value Match length 96 % identity 69

NCBI Description (AC003028) Myb-related transcription activator [Arabidopsis

thaliana]

Seq. No.

18851

Contig ID

63926 2.R1040

5'-most EST

LIB3107-033-Q1-K1-H9

BLASTX Method NCBI GI q3335378 BLAST score 180 E value 1.0e-12 Match length 50

3069



% identity 60

NCBI Description (AC003028) Myb-related transcription activator [Arabidopsis

thaliana]

Seq. No. 18852

Contig ID 63927\_1.R1040

5'-most EST jC-gmro02910003h04a1

Seq. No. 18853

Contig ID 63934\_1.R1040 5'-most EST pcp700991168.h1

Seq. No. 18854

Contig ID 63935 1.R1040

5'-most EST LIB3109-005-Q1-K1-D8

Seq. No. 18855

Contig ID 63935\_2.R1040

5'-most EST LIB3109-054-Q1-K1-D1

Seq. No. 18856

Contig ID 63939 1.R1040

5'-most EST LIB3170-083-Q1-K1-E6

Seq. No. 18857

Contig ID 63940 1.R1040

5'-most EST LIB3170-052-Q1-J1-C9

Seq. No. 18858

Contig ID 63943 1.R1040

5'-most EST LIB3107-034-Q1-K1-G7

Seq. No. 18859

Contig ID 63947\_1.R1040 5'-most EST hrw701059447.h1

Method BLASTX
NCBI GI g4539334
BLAST score 399
E value 2.0e-38
Match length 228
% identity 48

NCBI Description (AL035539) putative protein [Arabidopsis thaliana]

Seq. No. 18860

Contig ID 63951 1.R1040

5'-most EST LIB31 $\overline{0}$ 7-058-Q1-K1-H1

Seq. No. 18861

Contig ID 63951\_2.R1040

5'-most EST LIB3170-083-Q1-K1-F6

Seq. No. 18862

Contig ID 63954 1.R1040

5'-most EST LIB3107-032-Q1-K1-G1

Method BLASTX NCBI GI g2864621 BLAST score 253



E value 9.0e-22 Match length 139 % identity 38

NCBI Description (AL021811) hypothetical protein [Arabidopsis thaliana]

Seq. No. 18863

Contig ID 63956\_1.R1040

5'-most EST LIB3107-035-Q1-K1-A12

Seq. No. 18864

Contig ID 63958\_1.R1040 5'-most EST uaw700665948.h1

Seq. No. 18865

Contig ID 63971\_1.R1040 5'-most EST sat701002857.h1

Method BLASTX
NCBI GI g3169719
BLAST score 676
E value 4.0e-71
Match length 158
% identity 82

NCBI Description (AF007109) similar to yeast dcp1 [Arabidopsis thaliana]

Seq. No. 18866

Contig ID 63971\_2.R1040 5'-most EST pcp700993905.h1

Method BLASTX
NCBI GI g3169719
BLAST score 273
E value 4.0e-26
Match length 76
% identity 75

NCBI Description (AF007109) similar to yeast dcpl [Arabidopsis thaliana]

Seq. No. 18867

Contig ID 63973\_1.R1040

5'-most EST LIB3107-035-Q1-K1-C3

Seq. No. 18868

Contig ID 63976\_1.R1040 5'-most EST xpa700793532.h1

Method BLASTX
NCBI GI g4539373
BLAST score 216
E value 2.0e-17
Match length 82
% identity 52

NCBI Description (AL049525) putative retrotransposon polyprotein

[Arabidopsis thaliana]

Seq. No. 18869

Contig ID 63979 1.R1040

5'-most EST LIB3107-036-Q1-K1-A6

Seq. No. 18870

Contig ID 63983 1.R1040

3071



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LIB3107-036-Q1-K1-B1
5'-most EST
                  18871
Seq. No.
                  63989 1.R1040
Contig ID
5'-most EST
                  uC-qmropic114d05b1
Method
                  BLASTX
                  q2708741
NCBI GI
BLAST score
                  2128
                  0.0e + 00
E value
                  496
Match length
% identity
                  (AC003952) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  18872
Seq. No.
                   63989 2.R1040
Contig ID
5'-most EST
                  LIB3107-036-Q1-K1-E6
Method
                  BLASTX
NCBI GI
                   q2708741
                   220
BLAST score
                   7.0e-18
E value
                   74
Match length
% identity
NCBI Description (AC003952) hypothetical protein [Arabidopsis thaliana]
                   18873
Seq. No.
                   63995 1.R1040
Contig ID
                   fde700871816.h1
5'-most EST
                   18874
Seq. No.
Contig ID
                   64000 1.R1040
                   jC-gmst02400065c06a2
5'-most EST
Method
                   BLASTX
                   q3522987
NCBI GI
                   159
BLAST score
                   1.0e-10
E value
                   57
Match length
                   53
% identity
                   (AB007468) alpha-2,8-polysialyltransferase [Xenopus laevis]
NCBI Description
                   18875
Seq. No.
                   64010 1.R1040
Contig ID
                   LIB3170-081-Q1-K1-E8
5'-most EST
                   BLASTX
Method
                   g3618320
NCBI GI
                   149
BLAST score
                   1.0e-09
E value
                   33
Match length
                   79
% identity
                   (AB001888) zinc finger protein [Oryza sativa]
NCBI Description
                   18876
Seq. No.
                   64015 1.R1040
Contig ID
                   jC-gmst02400076d01a1
5'-most EST
                   BLASTX
Method
```

3072

q4567304

372 7.0e-59

NCBI GI BLAST score

E value



Match length 193 % identity 62

NCBI Description

(AC005956) unknown protein [Arabidopsis thaliana]

Seq. No. Contig ID 18877 64017 1.R1040

5'-most EST LIB3107-036-Q1-K1-E2

Seq. No.

18878

Contig ID 64018\_1.R1040

5'-most EST

LIB3107-036-Q1-K1-E3

Seq. No.

18879

Contig ID

64022\_1.R1040

5'-most EST

LIB3107-036-Q1-K1-E8

Seq. No.

18880

Contig ID

64022\_2.R1040

5'-most EST

uC-gmrominsoy246f04b1

Seq. No.

18881

Contig ID 64029 1.R1040

5'-most EST

LIB3107-036-Q1-K1-F4

Seq. No.

18882

Contig ID 64032\_1.R1040

5'-most EST

LIB3107-037-Q1-K1-C7

Seq. No.

18883

Contig ID 5'-most EST 64032\_2.R1040 kmv700742859.h1

Seq. No.

18884

Contig ID

64033\_1.R1040

5'-most EST

LIB3107-037-Q1-K1-C8

Method NCBI GI BLAST score BLASTX g3319342 174

E value

2.0e-12

Match length % identity

64 55

NCBI Description

(AF077407) similar to mitochondrial carrier proteins (Pfam:

mit carr.hmm, score: 79.74 and 42.50) [Arabidopsis

thaliana]

Seq. No.

18885

Contig ID

64035 1.R1040

5'-most EST

LIB3107-037-Q1-K1-D1

Seq. No.

18886

Contig ID 5'-most EST

64040\_1.R1040 rlr700901118.h1

Seq. No.

18887

Contig ID 5'-most EST

64040 2.R1040

LIB3139-022-P1-N1-B7

Method

BLASTX



```
g2961357
NCBI GI
                  449
BLAST score
                  2.0e-44
E value
                  110
Match length
                  75
% identity
                 (AL022140) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   64040 3.R1040
Contig ID
                  zzp700834594.h1
5'-most EST
                   18889
Seq. No.
                   64046 1.R1040
Contig ID
                  LIB3107-037-Q1-K1-E4
5'-most EST
                   18890
Seq. No.
                   64050 1.R1040
Contig ID
                   LIB3170-084-Q1-K1-F9
5'-most EST
                   18891
Seq. No.
                   64062 1.R1040
Contig ID
                   LIB3107-037-Q1-K1-G2
5'-most EST
                   BLASTX
Method
                   g4544473
NCBI GI
                   601
BLAST score
                   2.0e-62
E value
                   193
Match length
                   47
% identity
NCBI Description (AC006580) putative mei2 protein [Arabidopsis thaliana]
                   18892
Seq. No.
                   64063 1.R1040
Contig ID
5'-most EST
                   LIB3107-037-Q1-K1-G3
                   18893
Seq. No.
                   64065 1.R1040
Contig ID
                   epx701105543.h1
5'-most EST
                   18894
Seq. No.
                   64072 1.R1040
Contig ID
                   uC-qmropic062g11b1
5'-most EST
Method
                   BLASTN
NCBI GI
                   q633025
BLAST score
                   123
                   2.0e-62
E value
                   287
Match length
                   86
 % identity
                   Arabidopsis thaliana mRNA for Dr1
NCBI Description
                   18895
 Seq. No.
                   64074 1.R1040
 Contig ID
```

LIB3107-038-Q1-K1-G7 5'-most EST

Method BLASTX q3738315 NCBI GI 214 BLAST score 3.0e-17E value 61 Match length

3074



% identity 70

NCBI Description (AC005170) unknown protein [Arabidopsis thaliana]

Seq. No. 18896

Contig ID 64078 1.R1040

5'-most EST LIB3170-084-Q1-K1-G10

Method BLASTX
NCBI GI g2702268
BLAST score 279
E value 6.0e-25
Match length 72
% identity 69

NCBI Description (AC003033) putative cellulase [Arabidopsis thaliana]

Seq. No. 18897

Contig ID 64083 1.R1040

5'-most EST jC-gmle01810084f09a1

Seq. No. 18898

Contig ID 64095 1.R1040

5'-most EST LIB3107-039-Q1-K1-C8

Seq. No. 18899

Contig ID 64096 1.R1040

5'-most EST LIB3107-039-Q1-K1-C4

Seq. No. 18900

Contig ID 64102 1.R1040

5'-most EST LIB3107-039-Q1-K1-D11

Seq. No. 18901

Contig ID 64106\_1.R1040 5'-most EST uC-gmropic010e04b1

Method BLASTX
NCBI GI g2829902
BLAST score 258
E value 3.0e-22
Match length 83
% identity 54

NCBI Description (AC002311) Putative sulphate transporter protein#protein

[Arabidopsis thaliana]

Seq. No. 18902

Contig ID 64106\_2.R1040

5'-most EST LIB3139-037-P1-N1-H9

Method BLASTX
NCBI GI g2829902
BLAST score 413
E value 2.0e-40
Match length 126
% identity 61

NCBI Description (AC002311) Putative sulphate transporter protein#protein

[Arabidopsis thaliana]

Seq. No. 18903

Contig ID 64110\_1.R1040

5'-most EST LIB3170-081-Q1-K1-E11



```
18904
Seq. No.
                  64118 1.R1040
Contig ID
                  LIB3107-040-Q1-K1-C8
5'-most EST
                  18905
Seq. No.
                  64119 1.R1040
Contig ID
                  LIB3107-040-Q1-K1-D1
5'-most EST
                  18906
Seq. No.
                   64131 1.R1040
Contig ID
                  LIB3107-040-Q1-K1-E4
5'-most EST
```

18907 Seq. No. 64138 1.R1040 Contig ID  $eep70\overline{0}865787.h1$ 5'-most EST

18908 Seq. No. 64146 1.R1040 Contig ID LIB3107-040-Q1-K1-G3 5'-most EST

18909 Seq. No. 64146 2.R1040 Contig ID awf700836868.h15'-most EST

18910 Seq. No. 64148 1.R1040 Contig ID g5677556 5'-most EST BLASTX Method g3367576 NCBI GI 344 BLAST score 3.0e - 32E value 116 Match length % identity

NCBI Description (AL031135) NAM / CUC2 -like protein [Arabidopsis thaliana]

18911 Seq. No. 64151 1.R1040 Contig ID taw700659709.hl 5'-most EST BLASTX Method q2988397 NCBI GI 320 BLAST score E value 3.0e-29 127 Match length

% identity (AC004475) F23858\_1 [Homo sapiens] NCBI Description

Seq. No. 18912 64152 1.R1040 Contig ID LIB3107-040-Q1-K1-H8 5'-most EST

46

Seq. No. 18913 64155\_1.R1040 Contig ID LIB3107-041-Q1-K1-A11 5'-most EST

BLASTX Method g3859598 NCBI GI 226 BLAST score



E value 1.0e-18
Match length 90
% identity 77

NCBI Description (AF104919) contains similarity to Myb DNA-binding domains (Pfam: PF00249, E=3.7e-27 N=3) [Arabidopsis thaliana]

Seq. No. 18914

Contig ID 64156\_1.R1040

5'-most EST LIB3107-041-Q1-K1-A12

Method BLASTX
NCBI GI g2511693
BLAST score 175
E value 1.0e-12
Match length 108
% identity 36

NCBI Description (299954) cysteine proteinase precursor [Phaseolus vulgaris]

Seq. No. 18915

Contig ID 64162\_1.R1040 5'-most EST bth700848117.h1

Seq. No. 18916

Contig ID 64164 1.R1040

5'-most EST LIB3107-041-Q1-K1-F9

Seq. No. 18917

Contig ID 64165 1.R1040

5'-most EST LIB3107-041-Q1-K1-G5

Seq. No. 18918

Contig ID 64168 1.R1040

5'-most EST LIB3107-041-Q1-K1-G2

Method BLASTX
NCBI GI g3775989
BLAST score 799
E value 2.0e-85
Match length 262
% identity 60

NCBI Description (AJ010458) RNA helicase [Arabidopsis thaliana]

Seq. No. 18919

Contig ID 64175\_1.R1040

5'-most EST LIB3170-088-Q1-K1-D2

Method BLASTX
NCBI GI g1711615
BLAST score 225
E value 2.0e-18
Match length 71
% identity 58

NCBI Description HIGH AFFINITY SULPHATE TRANSPORTER 1

>gi\_1085847\_pir\_\_S51763 high affinity sulphate transporter
- Stylosanthes hamata >gi\_607184\_emb\_CAA57710\_ (X82255)
high affinity sulphate transporter [Stylosanthes hamata]

Seq. No. 18920

Contig ID 64179\_1.R1040

5'-most EST LIB3107-041-Q1-K1-H6



```
Seq. No.
                  18921
Contig ID
                  64186 1.R1040
5'-most EST
                  LIB3107-042-Q1-K1-A8
                  18922
Seq. No.
Contig ID
                  64186 2.R1040
                  zhf700952192.h1
5'-most EST
                  18923
Seq. No.
                  64186 3.R1040
Contig ID
5'-most EST
                  pcp700992875.h1
Seq. No.
                  18924
                  64202 1.R1040
Contig ID
5'-most EST
                  LIB3170-086-Q1-K1-D3
Seq. No.
                  18925
Contig ID
                  64210 1.R1040
5'-most EST
                  LIB3107-044-Q1-K1-C8
Method
                  BLASTX
NCBI GI
                  g1351303
BLAST score
                  644
                  3.0e-67
E value
Match length
                  162
                  78
% identity
                  INDOLE-3-GLYCEROL PHOSPHATE SYNTHASE PRECURSOR (IGPS)
NCBI Description
                  >gi 619732 (U18770) indole-3-glycerol phosphate synthase
                  [Arabidopsis thaliana]
                  18926
Seq. No.
Contig ID
                  64212 1.R1040
5'-most EST
                  LIB3107-044-Q1-K1-D1
Method
                  BLASTX
NCBI GI
                  g2244902
BLAST score
                  280
E value
                  7.0e-25
                  102
Match length
                  59
% identity
NCBI Description (Z97339) allene oxide synthase [Arabidopsis thaliana]
Seq. No.
                  18927
Contig ID
                  64217 1.R1040
5'-most EST
                  LIB3139-050-P1-N1-D2
Method
                  BLASTX
NCBI GI
                  g1076755
BLAST score
                  363
                  2.0e-34
E value
Match length
                  118
```

58 % identity

NCBI Description protein kinase - rice >gi\_450300 (L27821) protein kinase

[Oryza sativa]

Seq. No. 18928

64221 1.R1040 Contig ID

5'-most EST LIB3107-044-Q1-K1-E3



Seq. No.

Contig ID 64222 1.R1040 5'-most EST leu701151163.h1

Seq. No. 18930

Contig ID 64238 1.R1040

5'-most EST LIB3107-044-Q1-K1-G10

Seq. No. 18931

Contig ID 64238 2.R1040 5'-most EST eep700867767.hl

Seq. No. 18932

Contig ID 64244 1.R1040

LIB3107-049-Q1-K1-B10 5'-most EST

Method BLASTX g4490313 NCBI GI BLAST score 175 6.0e-21 E value Match length 96

59 % identity

NCBI Description (AL035678) putative protein [Arabidopsis thaliana]

Seq. No. 18933

Contig ID 64246 1.R1040

5'-most EST LIB3107-049-Q1-K1-B12

Seq. No. 18934

64251 1.R1040 Contig ID

5'-most EST LIB3107-049-Q1-K1-C9

Seq. No. 18935

64265 1.R1040 Contig ID

5'-most EST LIB3107-049-Q1-K1-E3

Seq. No. 18936

64266 1.R1040 Contig ID

5'-most EST LIB3107-049-Q1-K1-E5

Seq. No. 18937

Contig ID 64272 1.R1040 5'-most EST smc700745889.h1

Method BLASTX NCBI GI g3980413 BLAST score 180 E value 4.0e-13 Match length 145 35 % identity

NCBI Description (AC004561) pumilio-like protein [Arabidopsis thaliana]

Seq. No. 18938

Contig ID 64273 1.R1040 5'-most EST leu701145504.h1

Seq. No. 18939

64277 1.R1040 Contig ID

5'-most EST LIB3107-049-Q1-K1-G4



```
18940
Seq. No.
Contig ID
                   64282 1.R1040
5'-most EST
                  LIB3107-048-Q1-K1-H12
Method
                  BLASTX
NCBI GI
                  g2129889
BLAST score
                  206
E value
                  3.0e-21
Match length
                  87
% identity
                  68
NCBI Description methionine adenosyltransferase (EC 2.5.1.6) 2 - garden pea
Seq. No.
                  18941
                   64283 1.R1040
Contig ID
5'-most EST
                  LIB3107-049-Q1-K1-H3
Seq. No.
                  18942
Contig ID
                   64298 1.R1040
5'-most EST
                  LIB3170-086-Q1-K1-D7
Method
                  BLASTN
NCBI GI
                  q18768
BLAST score
                   53
E value
                   6.0e-21
Match length
                  363
% identity
                   36
NCBI Description Soybean Tgm6 transposable element 3' end
Seq. No.
                  18943
                   64306 1.R1040
Contig ID
5'-most EST
                  zhf70\overline{0}960222.h1
                  BLASTX
Method
NCBI GI
                   g3785989
                   449
BLAST score
                  1.0e-44
E value
Match length
                   99
% identity
                   87
NCBI Description
                  (AC005560) unknown protein [Arabidopsis thaliana]
Seq. No.
                   18944
                   64308 1.R1040
Contig ID
                  LIB3107-050-Q1-K1-H8
5'-most EST
Method
                  BLASTX
NCBI GI
                   g3482974
                   277
BLAST score
E value
                   2.0e-37
Match length
                   130
% identity
                   64
                   (AL031369) ATP-dependent Clp proteinase-like protein
NCBI Description
                   [Arabidopsis thaliana]
```

Seq. No. 18945

Contig ID 64354\_1.R1040

5'-most EST LIB3107-068-Q1-K1-B3

Seq. No. 18946

Contig ID 64359 1.R1040

5'-most EST LIB3107-068-Q1-K1-B8



```
Method
                  BLASTX
NCBI GI
                  g4204303
BLAST score
                  147
                  3.0e-09
E value
Match length
                  36
                  78
% identity
NCBI Description (AC003027) lcl_prt_seq No definition line found
                  [Arabidopsis thaliana]
Seq. No.
                  18947
Contig ID
                  64365 1.R1040
5'-most EST
                  LIB3107-068-Q1-K1-C6
Seq. No.
                  18948
                  64376 1.R1040
Contig ID
5'-most EST
                  txt700735765.hl
Seq. No.
                  18949
```

Contig ID

64379 1.R1040 5'-most EST LIB3107-071-Q1-K1-A4

Seq. No. 18950

64395 1.R1040 Contig ID 5'-most EST zzp700829601.h1

Method BLASTN NCBI GI g2326448 BLAST score 131 E value 1.0e-67 Match length 167 95 % identity

NCBI Description Glycine soja mitochondrial DNA for region 5' of atp6 gene

18951 Seq. No.

64395 2.R1040 Contig ID

5'-most EST LIB3107-072-Q1-K1-D5

BLASTN Method NCBI GI g22738 BLAST score 86 E value 1.0e-40 Match length 105 % identity 96

NCBI Description G.max mitochondrial atpA

Seq. No. 18952

64414 1.R1040 Contig ID 5'-most EST uC-gmropic019c01b1

Method BLASTX NCBI GI g3928097 BLAST score 521 E value 8.0e-53 Match length 158 % identity

NCBI Description (AC005770) unknown protein, 5' partial [Arabidopsis

thaliana]

Seq. No. 18953

64414\_2.R1040 Contig ID



```
5'-most EST
                  LIB3107-074-Q1-K1-A2
Method
                  BLASTX
NCBI GI
                  q3928097
BLAST score
                  317
E value
                  5.0e-29
                  99
Match length
% identity
                  67
                 (AC005770) unknown protein, 5' partial [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  18954
                  64434 1.R1040
Contig ID
5'-most EST
                  LIB3170-072-Q1-J1-F7
Seq. No.
                  18955
Contig ID
                  64434 2.R1040
                  LIB3170-072-Q1-K1-F6
5'-most EST
Seq. No.
                  18956
Contig ID
                  64448 1.R1040
5'-most EST
                  LIB3107-017-Q1-K1-F10
                  18957
Seq. No.
Contig ID
                  64450 1.R1040
5'-most EST
                  LIB3107-017-Q1-K1-H12
Method
                  BLASTN
                  g2065239
NCBI GI
BLAST score
                  35
E value
                  4.0e-10
Match length
                  40
% identity
                  64
NCBI Description
                  M.musculus mRNA for coxsackie and adenovirus receptor
                  homologue
                  18958
Seq. No.
                  64454 1.R1040
Contig ID
5'-most EST
                  LIB3107-018-Q1-K1-G3
Method
                  BLASTX
                  g3319342
NCBI GI
BLAST score
                  157
E value
                  4.0e-11
Match length
                  39
% identity
                  (AF077407) similar to mitochondrial carrier proteins (Pfam:
NCBI Description
                  mit carr.hmm, score: 79.74 and 42.50) [Arabidopsis
                  thalianal
                  18959
Seq. No.
Contig ID
                  64455 1.R1040
5'-most EST
                  LIB3107-019-Q1-K1-D4
                  18960
Seq. No.
Contig ID
                  64468 1.R1040
```

5'-most EST q4396509 Method BLASTX NCBI GI g3128207 BLAST score 144



1.0e-13

57

18962

```
E value
Match length
                   35
                   71
% identity
NCBI Description (AC004077) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  18961
                  64468 2.R1040
Contiq ID
                  pxt700943115.h1
5'-most EST
Method
                  BLASTX
                  g3128207
NCBI GI
BLAST score
                  182
```

% identity 67 NCBI Description (AC004077) hypothetical protein [Arabidopsis thaliana]

64471 1.R1040 Contig ID LIB3107-021-Q1-K1-F4 5'-most EST Method BLASTX q4467125 NCBI GI BLAST score 497 E value 6.0e-50 Match length 128

% identity 76

E value Match length

Seq. No.

NCBI Description (AL035538) putative protein [Arabidopsis thaliana]

18963 Seq. No. Contig ID 64472 1.R1040 5'-most EST LIB3107-021-Q1-K1-F8 Method BLASTX NCBI GI g4220445 BLAST score 302

E value 8.0e-50 Match length 140 18 % identity

NCBI Description (AC006216) Similar to gi 3004555 F19F24.14 salt inducible protein homolog from Arabidopsis thaliana BAC gb AC003673.

[Arabidopsis thaliana]

Seq. No. 18964

64479 1.R1040 Contig ID 5'-most EST LIB3107-022-Q1-K1-F1

18965 Seq. No.

Contig ID 64480 1.R1040

5'-most EST LIB3107-022-Q1-K1-H5

Method BLASTX NCBI GI g4106970 BLAST score 163 E value 6.0e-11 Match length 128 % identity 11

NCBI Description (AF113948) resistance protein candidate RGC2B [Lactuca

sativa]

Seq. No. 18966



```
Contig ID
                  64494 1.R1040
5'-most EST
                  LIB3107-002-Q1-K1-F7
                  18967
Seq. No.
Contig ID
                  64495 1.R1040
                  LIB3107-002-Q1-K1-F8
5'-most EST
                  BLASTX
Method
NCBI GI
                  q3201627
BLAST score
                  912
E value
                  1.0e-98
                  292
Match length
% identity
                  63
NCBI Description (AC004669) putative SWH1 protein [Arabidopsis thaliana]
                  18968
Seq. No.
                  64504 1.R1040
Contig ID
5'-most EST
                  uC-gmflminsoy022f04b1
Method
                  BLASTX
                  g3063445
NCBI GI
BLAST score
                  651
E value
                  7.0e-68
Match length
                  216
% identity
NCBI Description (AC003981) F22013.7 [Arabidopsis thaliana]
                  18969
Seq. No.
                  64504 2.R1040
Contig ID
5'-most EST
                  fC-gmle700872405d4
Method
                  BLASTX
NCBI GI
                  q3063445
BLAST score
                  168
E value
                  8.0e-12
Match length
                  65
                  49
% identity
NCBI Description (AC003981) F22013.7 [Arabidopsis thaliana]
Seq. No.
                  18970
                  64516 1.R1040
Contig ID
5'-most EST
                  jC-gmst02400005a01a1
                  18971
Seq. No.
Contig ID
                  64524 1.R1040
                  rca701001359.hl
5'-most EST
                  18972
Seq. No.
                  64526 1.R1040
Contig ID
                  leu701149866.hl
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4006818
BLAST score
                  907
E value
                  5.0e-98
                  260
Match length
                  70
```

18973 Seq. No.

% identity

NCBI Description

alpha subunit [Arabidopsis thaliana]

(ACO05970) putative translation initiation factor eIF-2B,



Contig ID 64529\_1.R1040

5'-most EST LIB3170-072-Q1-J1-E6

Seq. No. 18974

Contig ID 64533\_1.R1040

5'-most EST LIB3107-003-Q1-K1-C2

Seq. No. 18975

Contig ID 64536 1.R1040

5'-most EST LIB3107-003-Q1-K1-C9

Method BLASTX
NCBI GI g1778093
BLAST score 197
E value 3.0e-15
Match length 53
% identity 72

NCBI Description (U64902) putative sugar transporter; member of major

facilitative superfamily; integral membrane protein [Beta

vulgaris]

Seq. No. 18976

Contig ID 64539\_1.R1040 5'-most EST jex700904003.h1

Method BLASTX
NCBI GI g1871192
BLAST score 451
E value 1.0e-44
Match length 137
% identity 62

NCBI Description (U90439) Cys3His zinc finger protein isolog [Arabidopsis

thaliana]

Seq. No. 18977

Contig ID 64539 2.R1040

5'-most EST uC-gmflminsoy023c11b1

Seq. No. 18978

Contig ID 64543 1.R1040 5'-most EST pmv700894168.h1

Method BLASTX
NCBI GI g3800952
BLAST score 173
E value 3.0e-12
Match length 68
% identity 56

NCBI Description (AF100657) No definition line found [Caenorhabditis

elegans]

Seq. No. 18979

Contig ID 64545 1.R1040 5'-most EST fC-gmle700557301r2

Seq. No. 18980

Contig ID 64545\_2.R1040

5'-most EST jC-gmst02400071d10d1

Seq. No. 18981



Contig ID 64547 1.R1040 5'-most EST LIB3170-071-Q1-K1-C3

Seq. No. 18982

Contig ID 64548\_1.R1040

5'-most EST LIB3170-070-Q1-K2-C3

Method BLASTX
NCBI GI g1171642
BLAST score 223
E value 3.0e-18
Match length 62
% identity 69

NCBI Description PROBABLE SERINE/THREONINE-PROTEIN KINASE NAK

>gi\_481206\_pir\_\_S38326 protein kinase - Arabidopsis
thaliana >gi\_166809 (L07248) protein kinase [Arabidopsis

thaliana]

Seq. No. 18983

Contig ID 64550\_1.R1040 5'-most EST bth700844858.h1

Seq. No. 18984

Contig ID 64554 1.R1040

5'-most EST LIB3107-004-Q1-K1-D3

Seq. No. 18985

Contig ID 64556 1.R1040

5'-most EST uC-gmrominsoy308c01b1

Method BLASTX NCBI GI g1871192 BLAST score 314 E value 7.0e-29

Match length 91 % identity 67

NCBI Description (U90439) Cys3His zinc finger protein isolog [Arabidopsis

thaliana]

Seq. No. 18986

Contig ID 64558 1.R1040

5'-most EST LIB3107-004-Q1-K1-D8

Seq. No. 18987

Contig ID 64560 1.R1040

5'-most EST LIB3107-004-Q1-K1-E1

Seq. No. 18988

Contig ID 64564 1.R1040

5'-most EST LIB3107-004-Q1-K1-E2

Seq. No. 18989

Contig ID 64565 1.R1040

5'-most EST LIB3107-004-Q1-K1-E3

Seq. No. 18990

Contig ID 64568 1.R1040

5'-most EST LIB3107-004-Q1-K1-F10



Seq. No. 18991

Contig ID 64572 1.R1040

5'-most EST jC-gmro02910073a12a1

Method BLASTX
NCBI GI g3176686
BLAST score 278
E value 2.0e-24
Match length 70
% identity 76

NCBI Description (AC003671) Similar to high affinity potassium transporter,

HAK1 protein gb U22945 from Schwanniomyces occidentalis.

[Arabidopsis thaliana]

Seq. No. 18992

Contig ID 64576 1.R1040

5'-most EST LIB3170-072-Q1-K1-F8

Seq. No. 18993

Contig ID 64588 1.R1040

5'-most EST LIB3139-006-P1-N1-F6

Seq. No. 18994

Contig ID 64591 1.R1040

5'-most EST LIB3170-072-Q1-K1-E9

Seq. No. 18995

Contig ID 64597 1.R1040

5'-most EST LIB3107-006-Q1-K1-D10

Method BLASTX
NCBI GI g99922
BLAST score 338
E value 9.0e-32
Match length 92
% identity 65

NCBI Description hypothetical protein - soybean >gi\_930025\_emb\_CAA31883\_

(X13528) ORF (334 AA) [Glycine max]

Seq. No. 18996

Contig ID 64600\_1.R1040 5'-most EST zpv700761953.h1

Seq. No. 18997

Contig ID 64602\_1.R1040

5'-most EST LIB3170-071-Q1-K1-C9

Seq. No. 18998

Contig ID 64604 1.R1040

5'-most EST LIB3107-006-Q1-K1-E12

Seq. No. 18999

Contig ID 64605\_1.R1040

5'-most EST LIB3107-006-Q1-K1-E3

Method BLASTX
NCBI GI g3420054
BLAST score 183
E value 2.0e-13
Match length 150



% identity 35

NCBI Description (AC004680) unknown protein [Arabidopsis thaliana]

Seq. No. 19000

Contig ID 64612 1.R1040

5'-most EST LIB3170-070-Q1-K1-D9

Seq. No. 19001

Contig ID 64613 1.R1040

5'-most EST LIB3170-071-Q1-K1-E9

Method BLASTX
NCBI GI g2245004
BLAST score 240
E value 1.0e-21
Match length 81
% identity 73

NCBI Description (Z97341) similarity to membrane transport protein

[Arabidopsis thaliana]

Seq. No. 19002

Contig ID 64622 1.R1040

5'-most EST LIB3107-006-Q1-K1-G4

Seq. No. 19003

Contig ID 64625 1.R1040

5'-most EST LIB3107-006-Q1-K1-G7

Seq. No. 19004

Contig ID 64628 1.R1040

5'-most EST LIB3107-006-Q1-K1-H11

Seq. No. 19005

Contig ID 64629 1.R1040

5'-most EST LIB3107-006-Q1-K1-H12

Method BLASTX
NCBI GI g113540
BLAST score 258
E value 6.0e-22
Match length 148
% identity 41

NCBI Description ASPARTOKINASE I / HOMOSERINE DEHYDROGENASE I (AKI-HDI)

>gi\_421254\_pir\_\_B47057 aspartate kinase (EC 2.7.2.4) I /
homoserine dehydrogenase (EC 1.1.1.3) I - Serratia
marcescens >gi\_47273\_emb\_CAA43212\_ (X60821) aspartate

kinase [Serratia marcescens]

Seq. No. 19006

Contig ID 64650 1.R1040

5'-most EST LIB3109-043-Q1-K1-D2

Seq. No. 19007

Contig ID 64652\_1.R1040 5'-most EST uxk700672034.h1

Seq. No. 19008

Contig ID 64667\_1.R1040 5'-most EST zzp700831935.h1

3088



```
19009
Seq. No.
                   64672 1.R1040
Contig ID
                   LIB3107-008-Q1-K1-C3
5'-most EST
                   19010
Seq. No.
                   64674 1.R1040
Contig ID
                   LIB3107-009-Q1-K1-B5
5'-most EST
                   19011
Seq. No.
                   64687 1.R1040
Contig ID
                   LIB3107-009-Q1-K1-D1
5'-most EST
                   19012
Seq. No.
                   64688 1.R1040
Contia ID
                   LIB3139-039-P1-N1-G6
5'-most EST
                   19013
Seq. No.
                   64688 2.R1040
Contig ID
                   LIB3107-009-Q1-K1-D12
5'-most EST
                   19014
Seq. No.
                   64689 1.R1040
Contig ID
                   LIB3170-071-Q1-K1-B12
5'-most EST
                   19015
Seq. No.
                   64693 2.R1040
Contig ID
                   sat701009525.h1
5'-most EST
                   19016
Seq. No.
                    64696 1.R1040
Contig ID
                   LIB3170-070-Q1-K2-E12
5'-most EST
                    19017
 Seq. No.
                    64712 1.R1040
 Contig ID
                    q5606089
 5'-most EST
                    BLASTX
 Method
 NCBI GI
                    g2245136
                    1416
 BLAST score
                    1.0e-157
 E value
                    404
 Match length
 % identity
                    (Z97344) trehalose-6-phosphate synthase homolog
 NCBI Description
                    [Arabidopsis thaliana]
                    19018
 Seq. No.
                    64717 1.R1040
 Contig ID
                    LIB31\overline{0}7-010-Q1-K1-E7
 5'-most EST
                    BLASTX
 Method
```

Method BLASTX
NCBI GI g3075393
BLAST score 146
E value 5.0e-09
Match length 41
% identity 66

NCBI Description (AC004484) hypothetical protein [Arabidopsis thaliana]

Seq. No. 19019



Contig ID 64718 1.R1040

5'-most EST LIB31 $\overline{0}$ 7-010-Q1-K1-F1

Method BLASTX
NCBI GI 94512686
BLAST score 231
E value 3.0e-19
Match length 67
% identity 61

NCBI Description (AC006931) hypothetical protein [Arabidopsis thaliana]

>gi\_4559326\_gb\_AAD22988.1\_AC007087\_7 (AC007087)

hypothetical protein [Arabidopsis thaliana]

Seq. No. 19020

Contig ID 64723\_1.R1040 5'-most EST uaw700663762.h1

Seq. No. 19021

Contig ID 64724 1.R1040

5'-most EST LIB3107-010-Q1-K1-F6

Seq. No. 19022

Contig ID 64725 1.R1040

5'-most EST LIB3107-010-Q1-K1-F7

Seq. No. 19023

Contig ID 64725\_2.R1040 5'-most EST wvk700685783.h1

Seq. No. 19024

Contig ID 64731\_1.R1040

5'-most EST jC-gmro02910067h10a1

Method BLASTX
NCBI GI g4454011
BLAST score 190
E value 4.0e-14

Match length 60 % identity 62

NCBI Description (AL035396) putative protein [Arabidopsis thaliana]

Seq. No. 19025

Contig ID 64732\_1.R1040

5'-most EST LIB3107-010-Q1-K1-G9

Seq. No. 19026

Contig ID 64739 1.R1040 5'-most EST ncj700980806.h1

Seq. No. 19027

Contig ID 64739\_3.R1040 5'-most EST uaw700665192.h1

Seq. No. 19028

Contig ID 64752\_1.R1040

5'-most EST LIB3107-011-Q1-K1-B3

Method BLASTX
NCBI GI g2655889
BLAST score 275



E value 2.0e-24
Match length 124
% identity 48

NCBI Description (AL009171) 62D9.b [Drosophila melanogaster]

Seq. No. 19029

Contig ID 64763\_1.R1040 5'-most EST uC-gmropic068d03b1

Seq. No. 19030

Contig ID 64764\_1.R1040

5'-most EST LIB3107-011-Q1-K1-H11

Method BLASTX
NCBI GI g2618689
BLAST score 714
E value 1.0e-75
Match length 173
% identity 80

NCBI Description (AC002510) unknown protein [Arabidopsis thaliana]

Seq. No. 19031

Contig ID 64771\_1.R1040 5'-most EST uC-gmropic008f01b1

Method BLASTX
NCBI GI g1707010
BLAST score 334
E value 5.0e-31
Match length 135
% identity 52

NCBI Description (U78721) mitochondrial carrier protein isolog [Arabidopsis

thaliana]

Seq. No. 19032

Contig ID 64784\_1.R1040

5'-most EST LIB31 $\overline{0}$ 7-012-Q1-K1-B3

Seq. No. 19033

Contig ID 64789\_1.R1040

5'-most EST LIB3107-012-Q1-K1-C9

Seq. No. 19034

Contig ID 64793\_1.R1040 5'-most EST fC-gmro700744202a1

Seq. No.

Contig ID 64793\_2.R1040 5'-most EST awf700840527.h1

Seq. No. 19036

Contig ID 64795\_1.R1040

5'-most EST LIB31 $\overline{0}$ 7-013-Q1-K1-D6

19035

Seq. No. 19037

Contig ID 64797\_1.R1040

5'-most EST LIB3107-012-Q1-K1-D9

Method BLASTX NCBI GI g602292

3091



```
BLAST score
                  1.0e-45
E value
                  128
Match length
% identity
NCBI Description (U17987) RCH2 protein [Brassica napus]
Seq. No.
                  19038
                  64799 1.R1040
Contig ID
                  LIB3107-012-Q1-K1-E11
5'-most EST
Seq. No.
                  19039
                   64803 2.R1040
Contig ID
                  LIB3170-073-Q1-K1-H5
5'-most EST
                   BLASTX
```

Method q3450842 NCBI GI BLAST score 438 E value 6.0e-44Match length 103

% identity (AF080436) mitogen activated protein kinase kinase [Oryza NCBI Description

sativa]

19040 Seq. No. 64806 1.R1040 Contig ID LIB3107-013-Q1-K1-E1 5'-most EST BLASTN Method q3551114 NCBI GI 114 BLAST score

3.0e-57 E value 276 Match length % identity 87

NCBI Description Rosa gigantea chloroplast gene for maturase, complete cds

19041 Seq. No.

64809 1.R1040 Contig ID hrw701062881.hl 5'-most EST

BLASTX Method g2244792 NCBI GI 432 BLAST score 1.0e-42 E value 130 Match length % identity 64

(Z97336) ankyrin homolog [Arabidopsis thaliana] NCBI Description

19042 Seq. No. 64818 1.R1040 Contig ID

g5058267 5'-most EST Method BLASTX g4580398 NCBI GI 796 BLAST score 5.0e-85 E value 194 Match length % identity 77

(AC007171) putative protein kinase APK1A [Arabidopsis NCBI Description

thaliana]

19043 Seq. No.

3092



```
Contig ID
                   64818 2.R1040
                   jex700909746.hl
5'-most EST
                  BLASTX
Method
                  g4510406
NCBI GI
BLAST score
                  394
E value
                  8.0e-38
Match length
                  150
                  61
% identity
                 (AC006587) putative protein kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  19044
Contig ID
                   64818 3.R1040
5'-most EST
                  zsg701119413.h1
Seq. No.
                   19045
Contig ID
                   64819 1.R1040
5'-most EST
                  LIB3107-013-Q1-K1-F4
                   19046
Seq. No.
Contia ID
                   64830 1.R1040
5'-most EST
                   fde700876803.h1
Method
                  BLASTX
                  g3540190
NCBI GI
BLAST score
                  543
                  2.0e-55
E value
Match length
                  168
% identity
                   62
                  (AC004122) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  19047
Seq. No.
                   64830 4.R1040
Contig ID
5'-most EST
                  zzp700834065.hl
Seq. No.
                   19048
                   64835 1.R1040
Contig ID
5'-most EST
                   leu701146220.h1
Method
                  BLASTN
NCBI GI
                   q414665
BLAST score
                   424
                   0.0e+00
E value
                   748
Match length
                   98
% identity
NCBI Description G.max gene for coproporphyrinogen oxidase
                   19049
Seq. No.
                   64837 1.R1040
Contig ID
5'-most EST
                  LIB3170-074-Q1-K1-F5
                   19050
Seq. No.
Contig ID
                   64841 1.R1040
5'-most EST
                   uC-gmflminsoy026g07b1
Method
                   BLASTX
NCBI GI
```

Method BLASTX
NCBI GI g3600039
BLAST score 389
E value 1.0e-37

Match length 100 % identity 78



```
(AF080119) similar to Schizosaccharomyces pombe isp4
NCBI Description
                  protein (GB:D14061) [Arabidopsis thaliana]
                  19051
Seq. No.
                  64852 1.R1040
Contig ID
                  jsh701065591.hl
5'-most EST
                  BLASTX
Method
                  g2795805
NCBI GI
                  541
BLAST score
                  2.0e-55
E value
Match length
                  128
                  76
% identity
                   (AC003674) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                  >gi 3355493 (AC004218) putative protein kinase [Arabidopsis
                  thaliana]
Seq. No.
                  19052
Contig ID
                   64855 1.R1040
                  LIB3170-074-Q1-K1-H2
5'-most EST
                  BLASTX
Method
                   q4371292
NCBI GI
BLAST score
                   476
                   2.0e-47
E value
                   124
Match length
% identity
                  (AC006260) unknown protein [Arabidopsis thaliana]
NCBI Description
                   19053
Seq. No.
                   64855 2.R1040
Contig ID
                   sat701014127.hl
5'-most EST
                   BLASTX
Method
                   q4371292
NCBI GI
                   978
BLAST score
                   1.0e-110
E value
                   340
Match length
                   61
% identity
                   (AC006260) unknown protein [Arabidopsis thaliana]
NCBI Description
                   19054
Seq. No.
                   64863 1.R1040
 Contig ID
                   LIB3107-015-Q1-K1-B12
 5'-most EST
                   19055
 Seq. No.
                   64865 1.R1040
 Contig ID
                   hyd700727642.h1
 5'-most EST
                   19056
 Seq. No.
                   64865 2.R1040
 Contig ID
```

5'-most EST

LIB3107-037-Q1-K1-A10

Method BLASTX
NCBI GI g2342679
BLAST score 658

E value 1.0e-68
Match length 338
% identity 45

NCBI Description

45 (AC000106) Similar to Vicia sativa ENBP1 (gb\_X95995).

[Arabidopsis thaliana]



19057 Seq. No.

64865 3.R1040 Contig ID

5'-most EST jC-gmf102220144d01a1

19058 Seq. No.

64867 1.R1040 Contig ID kl1701210442.hl 5'-most EST

BLASTX Method NCBI GI g4376650 BLAST score 572 7.0e-59 E value 208 Match length 56 % identity

(AE001621) GcpE Protein [Chlamydia pneumoniae] NCBI Description

19059 Seq. No.

64876 1.R1040 Contig ID

LIB3107-015-Q1-K1-C3 5'-most EST

19060 Seq. No.

64888 1.R1040 Contig ID

LIB3107-015-Q1-K1-D4 5'-most EST

19061 Seq. No.

Contig ID 64889 1.R1040

jC-gmro02910069h09a1 5'-most EST

Method BLASTX g3236235 NCBI GI 143 BLAST score 1.0e-08 E value 70 Match length 46 % identity

(AC004684) unknown protein [Arabidopsis thaliana] NCBI Description

>qi 4056501 (AC005896) unknown protein [Arabidopsis

thaliana]

19062 Seq. No.

64890 1.R1040 Contig ID

jC-qmf102220063e04a1 5'-most EST

19063 Seq. No.

64900 1.R1040 Contig ID

LIB3107-016-Q1-K1-C3 5'-most EST

19064 Seq. No.

64915 1.R1040 Contig ID

LIB3107-016-Q1-K1-F2 5'-most EST

19065 Seq. No.

Contig ID 64919 1.R1040

LIB3107-016-Q1-K1-F9 5'-most EST

BLASTX Method g4325354 NCBI GI BLAST score 261 E value 1.0e-22 Match length 104

3095



% identity 43
NCBI Description (AF128395) contains similarity to retrovirus-related polyproteins and to CCHC zinc finger protein (Pfam: PF00098, Score=16.3, E=0.051, E= 1) [Arabidopsis thaliana]

Seq. No. 19066

Contig ID 64921 1.R1040

5'-most EST LIB3170-073-Q1-K1-H9

Seq. No. 19067

Contig ID 64925\_1.R1040 5'-most EST zsg701122266.h1

Method BLASTX
NCBI GI g2288981
BLAST score 360
E value 4.0e-34
Match length 97
% identity 44

NCBI Description (AC002335) calcium binding protein isolog [Arabidopsis thaliana] >gi 3763938 (AC004450) putative calcium binding

protein [Arabidopsis thaliana]

Seq. No. 19068

Contig ID 64925\_2.R1040

5'-most EST LIB3139-046-P1-N1-G1

Seq. No. 19069

Contig ID 64930\_1.R1040 5'-most EST zhf700954145.h1

Seq. No. 19070

Contig ID 64931\_1.R1040

5'-most EST uC-gmrominsoy299e01b1

Seq. No. 19071

Contig ID 64935\_1.R1040

5'-most EST LIB3107-017-Q1-K1-A5

Seq. No. 19072

Contig ID 64936\_1.R1040 5'-most EST smc700749959.h1

Method BLASTX
NCBI GI g2598569
BLAST score 241
E value 5.0e-20
Match length 115
% identity 47

NCBI Description (Y15290) putative start codon [Medicago truncatula]

Seq. No. 19073

Contig ID 64946\_1.R1040

5'-most EST LIB3107-017-Q1-K1-H6

Seq. No. 19074

Contig ID 64951 1.R1040

5'-most EST LIB3107-018-Q1-K1-A3



Seq. No. 19075

Contig ID 64955\_1.R1040 5'-most EST uC-gmropic040a06b1

Method BLASTX
NCBI GI g4263791
BLAST score 409
E value 2.0e-44
Match length 294
% identity 40

NCBI Description (AC006068) putative receptor protein kinase [Arabidopsis

thaliana]

Seq. No. Contig ID

19076 64975 1.R1040

5'-most EST

LIB3107-018-Q1-K1-D6

Method BLASTX
NCBI GI g3746063
BLAST score 224
E value 6.0e-18
Match length 106

Match length 106 % identity 45

NCBI Description (AC005311) unknown protein [Arabidopsis thaliana]

Seq. No.

19077

Contig ID

64975 2.R1040

5'-most EST

uC-gmrominsoy086f11b1

Seq. No.

19078

Contig ID

64976 1.R1040

5'-most EST

LIB3107-018-Q1-K1-D7

Seq. No.

19079

Contig ID

64992\_1.R1040

5'-most EST

zhf700961919.hl

Seq. No.

19080

Contig ID

64992\_2.R1040

5'-most EST

hrw701063501.h1

Seq. No.

19081

Contig ID

65002\_1.R1040

5'-most EST

uC-gmflminsoy074c04b1

Seq. No.

19082

Contig ID

65003 1.R1040

5'-most EST

LIB3107-020-01-K1-E3

Method NCBI GI BLASTX g3924611

BLAST score

460

E value

6.0e-46

Match length

167

% identity NCBI Description 61 (AF069442) hypothetical protein [Arabidopsis thaliana]

Seq. No.

19083

Contig ID 5'-most EST 65015\_1.R1040

ssr700557894.h1



Method BLASTX
NCBI GI g2894599
BLAST score 186
E value 3.0e-19
Match length 65
% identity 57

NCBI Description (AL021889) putative protein [Arabidopsis thaliana]

Seq. No. 19084

Contig ID 65022 1.R1040

5'-most EST LIB3107-021-Q1-K1-B5

Method BLASTX
NCBI GI g1619300
BLAST score 342
E value 4.0e-32
Match length 105
% identity 60

NCBI Description (X95269) LRR protein [Lycopersicon esculentum]

Seq. No. 19085

Contig ID 65025\_1.R1040 5'-most EST trc700566680.h1

Method BLASTX
NCBI GI g4323298
BLAST score 243
E value 2.0e-20
Match length 111
% identity 49

NCBI Description (AF099096) pulvinus outward-rectifying channel for

potassium SPOCK1 [Samanea saman]

Seq. No. 19086

Contig ID 65029\_1.R1040

5'-most EST LIB3107-022-Q1-K1-C1

Seq. No. 19087

Contig ID 65030\_1.R1040

5'-most EST LIB3107-022-Q1-K1-D3

Method BLASTX
NCBI GI g4063743
BLAST score 359
E value 7.0e-34
Match length 182
% identity 53

NCBI Description (AC005851) hypothetical protein [Arabidopsis thaliana]

Seq. No. 19088

Contig ID 65037 1.R1040

5'-most EST uC-gmrominsoy086e02b1

Method BLASTX
NCBI GI g2462835
BLAST score 326
E value 5.0e-30
Match length 110
% identity 63

NCBI Description (AF000657) hypothetical protein [Arabidopsis thaliana]



```
19089
Seq. No.
                  65044 1.R1040
Contig ID
                  zsq701119828.hl
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4538939
BLAST score
                  368
E value
                  4.0e-35
Match length
                  145
% identity
                  54
                  (AL049483) Col-O casein kinase I-like protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  19090
                  65044 3.R1040
Contig ID
5'-most EST
                  pcp700993125.hl
                  BLASTX
Method
NCBI GI
                  q4538939
BLAST score
                  311
                  2.0e-28
E value
                  151
Match length
% identity
                  (AL049483) Col-0 casein kinase I-like protein [Arabidopsis
NCBI Description
                  thaliana]
                  19091
Seq. No.
Contig ID
                  65048 1.R1040
5'-most EST
                  LIB3107-022-Q1-K1-E6
                  BLASTX
Method
                  g3941736
NCBI GI
                  194
BLAST score
                  1.0e-14
E value
                  133
Match length
% identity
                   44
                  (AF109719) BAT3 [Mus musculus]
NCBI Description
                  19092
Seq. No.
                   65057 1.R1040
Contig ID
                  uC-gmflminsoy069d07b1
5'-most EST
                  BLASTX
Method
NCBI GI
                   g4262167
BLAST score
                   308
                   4.0e-28
E value
```

Match length 119 52 % identity

(AC005275) putative LRR receptor-linked protein kinase NCBI Description

[Arabidopsis thaliana]

19093 Seq. No.

65082 1.R1040 Contig ID 5'-most EST sat701010480.h1

19094 Seq. No.

65085 1.R1040 Contig ID 5'-most EST epx701108888.h1

19095 Seq. No.

Contig ID 65086\_1.R1040



leu701149033.h1 5'-most EST 19096 Seq. No. 65087 1.R1040 Contig ID LIB3107-024-Q1-K1-E7 5'-most EST 19097 Seq. No. 65094 1.R1040 Contig ID LIB3170-078-Q1-K1-H7 5'-most EST BLASTX Method g4416302 NCBI GI 410 BLAST score 6.0e-43E value 127 Match length % identity (AF105716) copia-type pol polyprotein [Zea mays] NCBI Description 19098 Seq. No. 65098 1.R1040 Contig ID hrw701061832.h1 5'-most EST BLASTX Method g2129831 NCBI GI 478 BLAST score 9.0e-48 E value 100 Match length 87 % identity heat shock transcription factor 34 - soybean NCBI Description >gi\_662930\_emb\_CAA87077\_ (Z46953) heat shock transcription factor 34 [Glycine max] 19099 Seq. No. 65098 2.R1040 Contig ID LIB3107-024-Q1-K1-F8 5'-most EST BLASTN Method q662929 NCBI GI 38 BLAST score 6.0e-12 E value 74 Match length % identity G.max mRNA for heat shock transcription factor NCBI Description 19100 Seq. No. 65099 1.R1040 Contig ID LIB3107-024-Q1-K1-F9 5'-most EST 19101 Seq. No. 65102 1.R1040 Contig ID

pxt700941365.hl 5'-most EST

Method BLASTX g3135611 NCBI GI BLAST score 1006 1.0e-109 E value 221 Match length 86 % identity

(AF062485) cellulose synthase [Arabidopsis thaliana] NCBI Description

19102 Seq. No.



Contig ID 65103\_1.R1040 5'-most EST LIB3107-069-Q1-K1-F10

Seq. No. 19103

Contig ID 65104\_1.R1040

5'-most EST LIB3170-080-Q1-K1-D8

Seq. No. 19104

Contig ID 65107\_1.R1040

5'-most EST LIB3107-024-Q1-K1-G8

Method BLASTX
NCBI GI g2895095
BLAST score 294
E value 2.0e-26
Match length 143
% identity 43

NCBI Description (AF011337) putative E1-E2 ATPase [Mus musculus]

Seq. No. 19105

Contig ID 65120 1.R1040

5'-most EST LIB3107-025-Q1-K1-A5

Method BLASTX
NCBI GI g3914055
BLAST score 352
E value 2.0e-33
Match length 126
% identity 54

NCBI Description MUTS PROTEIN HOMOLOG 4 > gi 2463653 (U89293) MSH4 [Homo

sapiens] >gi 4505251 ref NP 002431.1 pMSH4 mutS (E. coli)

homolog

Seq. No. 19106

Contig ID 65123 1.R1040

5'-most EST LIB3109-032-Q1-K1-C3

Method BLASTX
NCBI GI g3063708
BLAST score 450
E value 1.0e-44
Match length 197
% identity 46

NCBI Description (AL022537) putative protein [Arabidopsis thaliana]

Seq. No. 19107

Contig ID 65127\_1.R1040 5'-most EST hyd700729183.h1

Seq. No. 19108

Contig ID 65128 1.R1040

5'-most EST LIB3170-078-Q1-K1-F8

Seq. No. 19109

Contig ID 65151\_1.R1040

5'-most EST LIB3138-064-Q1-N1-C5

Method BLASTN
NCBI GI g2924257
BLAST score 175
E value 2.0e-93



Match length 429 % identity 88

NCBI Description Tobacco chloroplast genome DNA

Seq. No. 19110

Contig ID 65152\_1.R1040 5'-most EST uC-gmronoir013f06b1

Seq. No. 19111

Contig ID 65154\_1.R1040

5'-most EST LIB3107-027-Q1-K1-C5

Seq. No. 19112

Contig ID 65155\_1.R1040

5'-most EST LIB3107-027-Q1-K1-C6

Seq. No. 19113

Contig ID 65158\_1.R1040

5'-most EST LIB3107-027-Q1-K1-D4

Seq. No. 19114

Contig ID 65179\_1.R1040

5'-most EST LIB3170-082-Q1-K1-G2

Seq. No. 19115

Contig ID 65186\_1.R1040

5'-most EST jC-gmro02800026e12a1

Method BLASTN
NCBI GI g169326
BLAST score 738
E value 0.0e+00
Match length 974
% identity 94

NCBI Description Bean (P.vulgaris) NADP-dependent malic enzyme mRNA,

complete cds

Seq. No. 19116

Contig ID 65199\_1.R1040

5'-most EST LIB3107-030-Q1-K1-A9

Method BLASTX
NCBI GI g1076746
BLAST score 1062
E value 1.0e-116
Match length 262
% identity 78

NCBI Description heat shock protein 70 - rice (fragment)

>gi\_763160\_emb\_CAA47948\_ (X67711) heat shock protein 70

[Oryza sativa]

Seq. No. 19117

Contig ID 65200\_1.R1040

5'-most EST LIB3107-030-Q1-K1-B1

Seq. No. 19118

Contig ID 65203\_1.R1040 5'-most EST vwf700675542.h1

```
Seq. No.
                   19119
                   65205 1.R1040
Contig ID
                  LIB3170-081-Q1-K1-G2
5'-most EST
                  19120
Seq. No.
                  65207 1.R1040
Contig ID
5'-most EST
                  LIB3107-030-Q1-K1-B9
Seq. No.
                  19121
                  65208 1.R1040
Contig ID
5'-most EST
                  LIB3170-083-Q1-K1-A2
                  19122
Seq. No.
Contig ID
                  65214 1.R1040
5'-most EST
                  LIB3170-081-Q1-K1-H2
Seq. No.
                  19123
Contig ID
                  65216 1.R1040
5'-most EST
                  LIB3107-030-Q1-K1-D11
                  BLASTN
Method
                  g3139138
NCBI GI
BLAST score
                  48
                  7.0e-18
E value
Match length
                  110
% identity
                  94
NCBI Description Lotus japonicus Rac small GTPase (Rac2) gene, promoter
                  region and partial mRNA sequence
Seq. No.
                  19124
                   65221 1.R1040
Contig ID
                  LIB3170-084-Q1-K1-B3
5'-most EST
Seq. No.
                  19125
                  65225 1.R1040
Contig ID
5'-most EST
                  LIB3107-031-Q1-K1-B7
Method
                  BLASTX
```

Method BLASTX
NCBI GI g3738338
BLAST score 326
E value 3.0e-30
Match length 113
% identity 56

NCBI Description (AC005170) putative polygalacturonase [Arabidopsis

thaliana]

Seq. No. 19126

Contig ID 65229 1.R1040 5'-most EST eep700866716.h1

Method BLASTX
NCBI GI g4454044
BLAST score 228
E value 2.0e-18
Match length 140
% identity 46

NCBI Description (AL035394) putative Ap2 domain protein [Arabidopsis

thaliana]

Seq. No. 19127



```
Contig ID
                   65230 1.R1040
5'-most EST
                   LIB3170-081-Q1-K1-B3
Seq. No.
                   19128
                   65230 2.R1040
Contig ID
                  ncj700976843.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g1888557
BLAST score
                  284
```

2.0e-25 E value Match length 78 63 % identity

NCBI Description (U89841) diadenosine 5',5'''-P1,P4-tetraphosphate hydrolase [Lupinus angustifolius]

Seq. No. 19129 65230 3.R1040 Contig ID 5'-most EST zhf700962505.h1 Method BLASTX NCBI GI q1888557

BLAST score 162 3.0e-11 E value Match length 47 57 % identity

NCBI Description (U89841) diadenosine 5',5'''-P1,P4-tetraphosphate hydrolase [Lupinus angustifolius]

19130 Seq. No. Contig ID 65234 1.R1040

5'-most EST LIB3107-031-Q1-K1-C6

Method BLASTX NCBI GI g3879813 BLAST score 149 3.0e-09 E value Match length 64

52 % identity

NCBI Description (Z66524) Similarity at the 3' end with the Yeast pre-mRNA splicing factor PRP9 (PIR Acc. No. S12320); cDNA EST EMBL: C08800 comes from this gene; cDNA EST EMBL: C07438 comes from this gene; cDNA EST yk494b4.3 comes from this

gene

Seq. No. 19131

Contig ID 65244 1.R1040

5'-most EST LIB3170-081-Q1-K1-F3

Seq. No. 19132

65246 1.R1040 Contig ID

5'-most EST LIB3107-031-Q1-K1-D7

19133 Seq. No.

Contig ID 65247 1.R1040

5'-most EST LIB3107-031-Q1-K1-D8

19134 Seq. No.

65250 1.R1040 Contig ID

5'-most EST jC-gmf102220115h02a1



Method BLASTX NCBI GI a2499611 BLAST score 663 E value 2.0e-69 Match length 143 87 % identity

NCBI Description MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 7 (MAP KINASE 7) (ATMPK7) >gi\_629548\_pir\_\_S40473 mitogen-activated protein kinase 7 (EC 2.7.1.-) - Arabidopsis thaliana

>gi 457406 dbj BAA04870 (D21843) MAP kinase [Arabidopsis

thaliana]

Seq. No. 19135

65251 1.R1040 Contig ID 5'-most EST kl1701212083.h1

BLASTX Method NCBI GI g3540201 BLAST score 776 1.0e-82 E value Match length 235 % identity

NCBI Description (AC004260) Putative nuclear protein [Arabidopsis thaliana]

19136 Seq. No.

65251 2.R1040 Contig ID 5'-most EST smc700747423.h1

BLASTX Method NCBI GI g3540201 BLAST score 152 E value 4.0e-10 Match length 65 48 % identity

NCBI Description (AC004260) Putative nuclear protein [Arabidopsis thaliana]

Seq. No. 19137

65275 1.R1040 Contig ID

5'-most EST LIB3107-033-Q1-K1-A1

Seq. No. 19138

Contig ID 65276 1.R1040

5'-most EST jC-gmro02910026a12d1

Seq. No. 19139

65276 2.R1040 Contig ID

LIB3170-083-Q1-K1-H4 5'-most EST

19140 Seq. No.

65281 1.R1040 Contig ID

5'-most EST LIB3109-055-Q1-K1-F6

Method BLASTX NCBI GI g3738288 BLAST score 591 E value 2.0e-61 Match length 147

73 % identity

(AC005309) auxin-responsive GH3-like protein [Arabidopsis NCBI Description

thalianal



Seq. No. 19141

Contig ID 65282\_1.R1040

5'-most EST LIB3107-033-Q1-K1-A8

Seq. No. 19142

Contig ID 65284\_1.R1040

5'-most EST LIB3107-033-Q1-K1-B3

Seq. No. 19143

Contig ID 65285\_1.R1040 5'-most EST ssr700558908.h1

Seq. No. 19144

Contig ID 65300\_2.R1040

5'-most EST LIB3107-033-Q1-K1-C6

Method BLASTX
NCBI GI 94455225
BLAST score 383
E value 6.0e-37
Match length 92
% identity 67

NCBI Description (AL035440) putative protein [Arabidopsis thaliana]

Seq. No. 19145

Contig ID 65301 1.R1040

5'-most EST LIB3107-033-Q1-K1-C7

Seq. No. 19146

Contig ID 65307\_1.R1040

5'-most EST LIB3107-033-Q1-K1-D2

Seq. No. 19147

Contig ID 65308 1.R1040 5'-most EST leu701149642.h1

Seq. No. 19148

Contig ID 65311 1.R1040

5'-most EST LIB3170-082-Q1-J1-F5

Method BLASTN
NCBI GI g3599418
BLAST score 42
E value 3.0e-14
Match length 59
% identity 93

NCBI Description Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds

Seq. No. 19149

Contig ID 65315\_1.R1040 5'-most EST uaw700666037.h1

Seq. No. 19150

Contig ID 65319\_1.R1040

5'-most EST LIB3170-083-Q1-K1-G5

Seq. No. 19151



Contig ID 65319\_2.R1040 5'-most EST kl1701206460.h1

Seq. No. 19152

Contig ID 65320\_1.R1040

5'-most EST LIB3107-034-Q1-K1-C1

Seq. No. 19153

Contig ID 65324 1.R1040

5'-most EST LIB3109-009-Q1-K1-C12

Method BLASTX
NCBI GI g3646340
BLAST score 499
E value 3.0e-50
Match length 156
% identity 63

NCBI Description (AJ000763) MADS-box protein [Malus domestica]

Seq. No. 19154

Contig ID 65336 1.R1040

5'-most EST LIB3107-034-Q1-K1-D3

Seq. No. 19155

Contig ID 65341\_1.R1040 5'-most EST eep700864228.h1

Method BLASTX
NCBI GI g1931645
BLAST score 530
E value 7.0e-54
Match length 189
% identity 58

NCBI Description (U95973) Fe(II) transporter isolog [Arabidopsis thaliana]

Seq. No. 19156

Contig ID 65342\_1.R1040

5'-most EST LIB3107-034-Q1-K1-E10

Method BLASTX
NCBI GI g2791278
BLAST score 227
E value 1.0e-18
Match length 128
% identity 41

NCBI Description (Z69257) beta-xylosidase [Hypocrea jecorina]

Seq. No. 19157

Contig ID 65343 1.R1040

5'-most EST LIB3170-081-Q1-K1-H6

Seq. No. 19158

Contig ID 65348 1.R1040 5'-most EST kwa701015639.h1

Seq. No. 19159

Contig ID 65351 1.R1040

5'-most EST jC-gmro02910015f11a1

Seq. No. 19160



65351 2.R1040 Contig ID

uC-gmflminsoy028c09b1 5'-most EST

Method BLASTN NCBI GI q3821780 34 BLAST score 1.0e-09 E value Match length 34 59 % identity

NCBI Description Xenopus laevis cDNA clone 27A6-1

19161 Seq. No.

65353 1.R1040 Contig ID

LIB3170-083-Q1-K1-B6 5'-most EST

19162 Seq. No.

65354 1.R1040 Contig ID 5'-most EST ncj700976132.hl

Seq. No. 19163

65356 1.R1040 Contig ID

5'-most EST LIB3107-035-Q1-K1-D1

19164 Seq. No.

Contig ID 65364 1.R1040

LIB3107-035-Q1-K1-E10 5'-most EST

Method BLASTN NCBI GI g11554 181 BLAST score 2.0e-97 E value Match length 307 92 % identity

NCBI Description Broad bean chloroplast ndhF gene

>gi\_343641\_gb\_M36832\_VFACPNDHF V.faba chloroplast NADH
dehydrogenase (ndhF) DNA, complete cds

19165 Seq. No.

65381 1.R1040 Contig ID

LIB3107-035-Q1-K1-G4 5'-most EST

BLASTX Method NCBI GI q3367537 BLAST score 416 7.0e-41 E value Match length 135 % identity

(AC004392) Contains similarity to ANK repeat region of NCBI Description

Fowlpox virus BamHI-orf7 protein homolog C18F10.7 gi\_485107 from Caenorhabditis elegans cosmid gb\_U00049. This gene is continued from unannotated gene on BAC F19K23 gb\_AC000375.

[Arabid

19166 Seq. No.

65389 1.R1040 Contig ID

5'-most EST LIB3107-035-Q1-K1-H2

Method BLASTX g3123712 NCBI GI 324 BLAST score E value 1.0e-29



Match length 235 % identity 34

NCBI Description (D89051) ERD6 protein [Arabidopsis thaliana]

Seq. No. 19167

Contig ID 65394\_1.R1040

5'-most EST LIB3107-036-Q1-K1-A11

Seq. No. 19168

Contig ID 65397 1.R1040 5'-most EST pmv700891430.h1

Seq. No. 19169

Contig ID 65402 1.R1040

5'-most EST LIB3107-036-Q1-K1-G1

Seq. No. 19170

Contig ID 65409 1.R1040

5'-most EST LIB3107-036-Q1-K1-G5

Method BLASTX
NCBI GI g2462781
BLAST score 394
E value 4.0e-38
Match length 87
% identity 83

NCBI Description (U73175) carbamoyl phosphate synthetase small subunit

[Arabidopsis thaliana]

Seq. No. 19171

Contig ID 65417 1.R1040

5'-most EST LIB3107-036-Q1-K1-H4

Seq. No. 19172

Contig ID 65418 1.R1040 5'-most EST epx701105820.h1

Seq. No. 19173

Contig ID 65419 1.R1040

5'-most EST LIB3107-036-Q1-K1-H7

Method BLASTN
NCBI GI g12178
BLAST score 120
E value 9.0e-61
Match length 224
% identity 91

NCBI Description Pea chloroplast rpl36 (partial), rps11, rpoA, and petD

(partial) genes for ribosomal proteins L36 and S11, RNA polymerase alpha subunit, and cytochrome bf complex subunit

IV

Seq. No. 19174

Contig ID 65422\_1.R1040

5'-most EST LIB3107-037-Q1-K1-A1

Method BLASTX
NCBI GI g2914710
BLAST score 426
E value 6.0e-42



Match length 119 % identity 66

NCBI Description (AC003974) putative beta-D-galactosidase [Arabidopsis

thaliana]

Seq. No. 19175

Contig ID 65426 1.R1040

5'-most EST LIB3107-037-Q1-K1-A4

Method BLASTX
NCBI GI g3877655
BLAST score 231
E value 4.0e-19
Match length 109
% identity 42

NCBI Description (Z72511) possible zinc finger protein; cDNA EST EMBL:M89115

comes from this gene; cDNA EST EMBL:D71533 comes from this gene; cDNA EST EMBL:D72314 comes from this gene; cDNA EST

EMBL: D75164 comes from this gene; cDNA EST EMBL: C1

Seq. No. 19176

Contig ID 65431 1.R1040

5'-most EST LIB3109-034-Q1-K1-B4

Method BLASTX
NCBI GI g3859659
BLAST score 467
E value 9.0e-47
Match length 136
% identity 72

NCBI Description (AL031394) putative potassium transporter AtKT5p (AtKT5)

[Arabidopsis thaliana]

Seq. No. 19177

Contig ID 65433\_1.R1040

5'-most EST LIB3107-037-Q1-K1-B2

Seg. No. 19178

Contig ID 65445\_1.R1040

5'-most EST LIB3107-037-Q1-K1-H7

Seq. No. 19179

Contig ID 65449\_1.R1040

5'-most EST LIB3170-082-Q1-K1-C9

Seq. No. 19180

Contig ID 65453\_1.R1040 5'-most EST ncj700987208.h1

Seq. No. 19181

Contig ID 65453\_2.R1040 5'-most EST vzy700754173.h1

Seq. No. 19182

Contig ID 65457\_1.R1040 5'-most EST ssr700554559.h1

Method BLASTX NCBI GI g123530 BLAST score 157



```
E value 2.0e-10 Match length 108 % identity 3
```

NCBI Description HISTIDINE-RICH GLYCOPROTEIN PRECURSOR >gi 72400 pir KGZQHL

histidine-rich glycoprotein precursor - Plasmodium lophurae >gi\_9999 emb\_CAA25698\_ (X01469) histidine-rich protein [Plasmodium lophurae] >gi\_224316\_prf\_\_1101401A protein, His

rich [Plasmodium sp.]

Seq. No. 19183

Contig ID 65472 1.R1040

5'-most EST LIB3107-038-Q1-K1-D9

Seq. No. 19184

Contig ID 65477\_1.R1040 5'-most EST rca700999774.h1

Method BLASTX
NCBI GI g3063453
BLAST score 274
E value 6.0e-24
Match length 58
% identity 79

NCBI Description (AC003981) F22013.15 [Arabidopsis thaliana]

Seq. No. 19185

Contig ID 65479\_1.R1040 5'-most EST hyd700729211.h1

Seq. No. 19186

Contig ID 65480\_1.R1040

5'-most EST LIB3170-084-Q1-K1-D11

Seq. No. 19187

Contig ID 65482 1.R1040

5'-most EST LIB3107-039-Q1-K1-E8

Seq. No. 19188

Contig ID 65483 1.R1040

5'-most EST LIB3107-039-Q1-K1-E9

Method BLASTX
NCBI GI g4204095
BLAST score 461
E value 8.0e-46
Match length 185
% identity 48

NCBI Description (AF030260) CYP94A1 [Vicia sativa]

Seq. No. 19189

Contig ID 65488\_1.R1040

5'-most EST LIB3107-039-Q1-K1-F7

Method BLASTX
NCBI GI g3319342
BLAST score 263
E value 7.0e-23
Match length 75
% identity 65

NCBI Description (AF077407) similar to mitochondrial carrier proteins (Pfam:



mit\_carr.hmm, score: 79.74 and 42.50) [Arabidopsis thaliana]

Seq. No. 19190

Contig ID 65493 1.R1040

5'-most EST LIB3170-082-Q1-K1-A11

Seq. No. 19191

Contig ID 65497 1.R1040

5'-most EST jC-gmst02400029d06a1

Method BLASTX
NCBI GI g2952545
BLAST score 173
E value 5.0e-12
Match length 247
% identity 6

NCBI Description (AF051898) coronin binding protein [Dictyostelium

discoideum]

Seq. No. 19192

Contig ID 65503 1.R1040

5'-most EST LIB3170-083-Q1-K1-B11

Seq. No. 19193

Contig ID 65523 1.R1040

5'-most EST LIB3107-040-Q1-K1-B9

Method BLASTX
NCBI GI g2289790
BLAST score 264
E value 5.0e-23
Match length 126
% identity 44

NCBI Description (D88750) beta-galactosidase [Bacillus circulans]

Seq. No. 19194

Contig ID 65536 1.R1040

5'-most EST LIB3107-041-Q1-K1-B10

Seq. No. 19195

Contig ID 65539 1.R1040

5'-most EST LIB3107-041-Q1-K1-B6

Seq. No. 19196

Contig ID 65548 1.R1040

5'-most EST LIB3107-041-Q1-K1-C6

Seq. No. 19197

Contig ID 65549 1.R1040

5'-most EST LIB3107-041-Q1-K1-C7

Method BLASTN
NCBI GI g533301
BLAST score 37
E value 3.0e-11
Match length 45
% identity 96

NCBI Description Beta trigyna chloroplast DNA for cytochrome b6/f complex

subunit 5, Trp-tRNA, Pro-tRNA



Seq. No. Contig ID 5'-most EST 19198

65557 1.R1040 LIB3107-041-Q1-K1-D4

Seq. No.

19199

65558 1.R1040 Contig ID LIB3107-041-Q1-K1-D5 5'-most EST

Seq. No. Contig ID

19200

65560 1.R1040

LIB3107-041-Q1-K1-E1 5'-most EST

Seq. No.

19201 65570 1.R1040

Contig ID LIB3107-042-Q1-K1-C3 5'-most EST

Seq. No. Contig ID

5'-most EST

19202 65573 1.R1040  $asn70\overline{1}139812.h1$ 

Seq. No. Contig ID 19203

65583 1.R1040

5'-most EST

LIB3107-042-Q1-K1-E4

Seq. No.

19204

65586 1.R1040 Contig ID 5'-most EST

LIB3107-042-Q1-K1-E8

Seq. No.

19205

65588 1.R1040 Contig ID

5'-most EST

LIB3170-086-Q1-J1-B3

Seq. No.

19206

65596 1.R1040 Contig ID

LIB3167-010-P1-K1-B3 5'-most EST

BLASTX Method q2706544 NCBI GI 1236 BLAST score 1.0e-136 E value 287 Match length

84 % identity

NCBI Description (Y15899) Sig1 [Sinapis alba]

19207 Seq. No.

65599 1.R1040 Contig ID

LIB3109-010-Q1-K1-H5 5'-most EST

BLASTX Method q4567309 NCBI GI 450 BLAST score 2.0e-44 E value 245 Match length

(AC005956) hypothetical protein [Arabidopsis thaliana] % identity NCBI Description

19208 Seq. No.

65602\_1.R1040 Contig ID



```
LIB3107-042-Q1-K1-G9
5'-most EST
                  19209
Seq. No.
                  65608 1.R1040
Contig ID
5'-most EST
                  LIB3170-086-Q1-K1-B3
                  19210
Seq. No.
Contig ID
                  65609 1.R1040
5'-most EST
                  zsg701122501.h1
Method
                  BLASTN
NCBI GI
                  q881440
BLAST score
                  80
E value
                  6.0e-37
Match length
                  168
                  87
% identity
NCBI Description
                  Lupinus luteus NADH-plastoquinone oxidoreductase (ndhC)
                  gene, chloroplast gene encoding chloroplast protein,
                  complete cds
Seq. No.
                  19211
Contig ID
                  65610 1.R1040
                  LIB3170-085-Q1-K1-H3
5'-most EST
                  19212
Seq. No.
Contig ID
                  65615 1.R1040
5'-most EST
                  LIB3107-044-Q1-K1-B1
                  19213
Seq. No.
Contig ID
                  65618 1.R1040
5'-most EST
                  LIB3139-072-P1-N1-D5
Seq. No.
                  19214
                  65619 1.R1040
Contig ID
                  LIB3107-044-Q1-K1-H1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g4056437
BLAST score
                  252
                  3.0e-28
E value
Match length
                  130
% identity
                  45
NCBI Description (AC005990) Strong similarity to PFAM PF 00069 Eukaryotic
                  protein kinase domain. [Arabidopsis thaliana]
Seq. No.
                  19215
                  65621 1.R1040
Contig ID
5'-most EST
                  fC-gmf1700905635a1
Method
                  BLASTX
NCBI GI
                  q4102600
BLAST score
                  973
E value
                  1.0e-105
Match length
                  527
% identity
                  69
```

Contig ID 65621\_2.R1040

5'-most EST jC-gmst02400025g03a1

NCBI Description (AF013467) ARF6 [Arabidopsis thaliana]



Method BLASTX
NCBI GI g4102600
BLAST score 294
E value 4.0e-42
Match length 124
% identity 81

NCBI Description (AF013467) ARF6 [Arabidopsis thaliana]

Seq. No. 19217

Contig ID 65625 1.R1040

5'-most EST LIB3170-076-Q1-J1-B5

Method BLASTX
NCBI GI g3283026
BLAST score 157
E value 8.0e-21
Match length 101
% identity 55

NCBI Description (AF051562) putative transposase [Arabidopsis thaliana]

Seq. No. 19218

Contig ID 65629 1.R1040

5'-most EST LIB3107-044-Q1-K1-H9

Seq. No. 19219

Contig ID 65631\_1.R1040 5'-most EST zsg701129542.hl

Method BLASTX
NCBI GI g3128192
BLAST score 157
E value 2.0e-10
Match length 160
% identity 31

NCBI Description (AC004521) axi 1-like protein [Arabidopsis thaliana]

Seq. No. 19220

Contig ID 65633 1.R1040 5'-most EST sat701012026.h1

Seq. No. 19221

Contig ID 65640\_1.R1040

5'-most EST LIB3107-048-Q1-K1-B9

Method BLASTX
NCBI GI g2618686
BLAST score 208
E value 4.0e-34
Match length 94
% identity 81

NCBI Description (AC002510) hypothetical protein [Arabidopsis thaliana]

Seq. No. 19222

Contig ID 65642 1.R1040

5'-most EST LIB3107-048-Q1-K1-C11

Seq. No. 19223

Contig ID 65644 1.R1040

5'-most EST LIB3107-048-Q1-K1-C9



Contig ID 65645\_1.R1040

5'-most EST LIB3107-048-Q1-K1-D11

Seq. No. 19225

Contig ID 65645\_2.R1040 5'-most EST fde700873943.h1

Seq. No. 19226

Contig ID 65649 1.R1040 5'-most EST hrw701062991.h1

Method BLASTX
NCBI GI g1360088
BLAST score 350
E value 9.0e-33
Match length 76
% identity 78

% identity 78 NCBI Description (X97947) Zn finger protein [Nicotiana tabacum]

Seq. No. 19227

Contig ID 65649\_2.R1040 5'-most EST uxk700670518.h1

Seq. No. 19228

Contig ID 65653\_1.R1040

5'-most EST LIB3107-048-Q1-K1-G12

Seq. No. 19229

Contig ID 65670\_1.R1040 5'-most EST sat701009911.h2

Seq. No. 19230

Contig ID 65670\_2.R1040 5'-most EST hrw701059779.h1

Seq. No. 19231

Contig ID 65679\_1.R1040

5'-most EST LIB3107-050-Q1-K1-B4

Seq. No. 19232

Contig ID 65686\_1.R1040

5'-most EST LIB3107-050-Q1-K1-C3

Seq. No. 19233

Contig ID 65686\_2.R1040 5'-most EST uxk700669560.h1

Seq. No. 19234

Contig ID 65697\_1.R1040

5'-most EST LIB3109-036-Q1-K1-C8

Method BLASTX
NCBI GI g4538993
BLAST score 608
E value 6.0e-63
Match length 213
% identity 52

NCBI Description (AL049481) putative host response protein [Arabidopsis



## thaliana]

Seq. No. 19235 Contig ID 65698\_1.R1040 5'-most EST bth700844561.h1

Seq. No. 19236

Contig ID 65703 1.R1040

5'-most EST LIB3107-050-Q1-K1-E12

Seq. No. 19237

Contig ID 65709 1.R1040

5'-most EST LIB3107-050-Q1-K1-E6

Method BLASTX
NCBI GI g3645899
BLAST score 162
E value 4.0e-11
Match length 100
% identity 54

NCBI Description (U68408) 5' end not determined experimentally [Zea mays]

Seq. No. 19238

Contig ID 65710 1.R1040

5'-most EST LIB3107-050-Q1-K1-E7

Method BLASTX
NCBI GI g3947735
BLAST score 220
E value 6.0e-18
Match length 66
% identity 58

NCBI Description (AJ009720) NL27 [Solanum tuberosum]

Seq. No. 19239

Contig ID 65731\_1.R1040 5'-most EST uC-gmropic059c10b1

Method BLASTX
NCBI GI g2598575
BLAST score 426
E value 6.0e-42
Match length 120
% identity 68

NCBI Description (Y15293) MtN21 [Medicago truncatula]

Seq. No. 19240

Contig ID 65736 1.R1040

5'-most EST jC-gmro02910040d07a1

Seq. No. 19241

Contig ID 65746\_1.R1040

5'-most EST uC-gmflminsoy042d04b1

Seq. No. 19242

Contig ID 65746\_2.R1040

5'-most EST LIB3109-033-Q1-K1-H8

Seq. No. 19243

Contig ID 65750 1.R1040

Contig ID

19250

65812 1.R1040



```
5'-most EST
                  jC-gmf102220082a09a1
Method
                  BLASTX
                  g4455323
NCBI GI
BLAST score
                  419
                  3.0e-41
E value
Match length
                  146
% identity
                  62
NCBI Description (AL035525) aminopeptidase-like protein [Arabidopsis
                  thaliana]
Seq. No.
                  19244
Contig ID
                  65770 1.R1040
5'-most EST
                  vwf700676478.hl
Method
                  BLASTX
NCBI GI
                  g3746594
BLAST score
                  323
                  5.0e-30
E value
Match length
                  124
                  50
% identity
NCBI Description (AF064611) RNA polymerase II subunit 2 [Periploca graeca]
                  19245
Seq. No.
                  65775 1.R1040
Contig ID
5'-most EST
                  gsv701051369.hl
                  19246
Seq. No.
                  65775 2.R1040
Contig ID
5'-most EST
                  leu701152273.h1
                  19247
Seq. No.
                  65775 3.R1040
Contig ID
5'-most EST
                  uC-gmropic008c08b1
Method
                  BLASTN
                  g3097320
NCBI GI
BLAST score
                  66
E value
                  2.0e-28
Match length
                  250
% identity
NCBI Description Glycine max gene for Bd 30K, complete cds
Seq. No.
                  19248
                  65790 1.R1040
Contig ID
5'-most EST
                  LIB3107-056-Q1-K1-A9
Method
                  BLASTN
NCBI GI
                  g19504
BLAST score
                  43
E value
                  6.0e-15
Match length
                  79
% identity
                  90
NCBI Description L.polyphyllus pPLZ25 mRNA
Seq. No.
                  19249
                  65809 1.R1040
Contig ID
5'-most EST
                  uC-gmropic016d02b1
```



```
5'-most EST
                   LIB3107-056-Q1-K1-D6
Seq. No.
                   19251
                   65816 1.R1040
Contig ID
                  uC-gmropic066b07b1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g2346974
                  331
BLAST score
E value
                  2.0e-30
                  120
Match length
                   55
% identity
NCBI Description (AB006599) ZPT2-12 [Petunia x hybrida]
                  19252
Seq. No.
                   65831 1.R1040
Contig ID
5'-most EST
                  LIB3107-059-Q1-K1-B4
Seq. No.
                   19253
Contig ID
                   65833 1.R1040
5'-most EST
                   crh700850076.h1
Method
                  BLASTX
                  g2961377
NCBI GI
BLAST score
                   458
                   7.0e-46
E value
Match length
                  105
                   86
% identity
                  (AL022141) putative receptor protein kinase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   19254
                   65835 1.R1040
Contig ID
5'-most EST
                   pmv700891850.hl
Method
                   BLASTX
NCBI GI
                   g3335378
BLAST score
                   446
E value
                   1.0e-77
                   266
Match length
% identity
                   62
                  (AC003028) Myb-related transcription activator [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   19255
Contig ID
                   65848 1.R1040
5'-most EST
                   zsq701120287.hl
Method
                   BLASTX
NCBI GI
                   q4262148
BLAST score
                   833
E value
                   2.0e-89
Match length
                   232
% identity
                   68
NCBI Description (AC005275) predicted protein of unknown function
                   [Arabidopsis thaliana]
```

65852 1.R1040 Contig ID zhf700961696.h1 5'-most EST

Method BLASTX



NCBI GI g629561 BLAST score 863 E value 8.0e-93 Match length 280 % identity 59

NCBI Description SRG1 protein - Arabidopsis thaliana

>gi 479047 emb CAA55654 (X79052) SRG1 [Arabidopsis

thaliana]

Seq. No. 19257

Contig ID 65855\_1.R1040

5'-most EST LIB3107-059-Q1-K1-E5

Seq. No. 19258

Contig ID 65858\_1.R1040

5'-most EST LIB3107-059-Q1-K1-H5

Seq. No. 19259

Contig ID 65862 1.R1040

5'-most EST LIB3107-059-Q1-K1-F4

Method BLASTX
NCBI GI g3152605
BLAST score 271
E value 1.0e-23
Match length 86
% identity 63

NCBI Description (AC004482) hypothetical protein [Arabidopsis thaliana]

Seq. No. 19260

Contig ID 65880 1.R1040

5'-most EST LIB3107-063-Q1-K1-G4

Seq. No. 19261

Contig ID 65883\_1.R1040

5'-most EST jC-gmf102220052e06d1

Seq. No. 19262

Contig ID 65885 1.R1040

5'-most EST LIB3109-037-Q1-K1-F1

Seq. No. 19263

Contig ID 65896\_1.R1040

5'-most EST LIB3107-064-Q1-K1-B11

Method BLASTX
NCBI GI g1813489
BLAST score 206
E value 3.0e-16
Match length 87
% identity 54

NCBI Description (U64312) amidase [Bacillus firmus]

Seq. No. 19264

Contig ID 65914\_1.R1040 5'-most EST eep700865915.h1

Method BLASTX NCBI GI g2911052 BLAST score 1432



```
E value 1.0e-159
Match length 396
% identity 72
NCBI Description (AL021961) putative protein [Arabidopsis thaliana]
Seg. No. 19265
```

 Seq. No.
 19265

 Contig ID
 65924\_1.R1040

 5'-most EST
 LIB3139-051-P1-N1-B5

 Method
 BLASTX

 NCBI GI
 g3641838

NCBI GI g3641838 BLAST score 994 E value 1.0e-108 Match length 268 % identity 72

NCBI Description (AL023094) putative protein (fragment) [Arabidopsis

thaliana

Seq. No. 19266

Contig ID 65968 1.R1040

5'-most EST jC-gmle01810070f10a1

Seq. No. 19267

Contig ID 65968 2.R1040

5'-most EST LIB3107-070-Q1-K1-A2

Seq. No. 19268

Contig ID 65993 1.R1040

5'-most EST LIB3107-078-Q1-K1-C6

Method BLASTN
NCBI GI g1419732
BLAST score 221
E value 1.0e-121
Match length 326
% identity 91

NCBI Description P.sativum mitochondrial DNA for 18S rRNA gene

Seq. No. 19269

Contig ID 65997 1.R1040

5'-most EST LIB3107-078-Q1-K1-F6

Method BLASTN
NCBI GI g295119
BLAST score 183
E value 2.0e-98
Match length 387
% identity 87

NCBI Description Spinach chloroplast RNA polymerase (rpoB and rpoCl) genes,

complete cds, Cys-tRNA gene and rps2 gene, partial cds

Seq. No. 19270

Contig ID 65999\_1.R1040

5'-most EST LIB3107-078-Q1-K1-H5

Seq. No. 19271

Contig ID 66000\_1.R1040

5'-most EST LIB3107-079-Q1-K1-A12

Method BLASTN NCBI GI g168685



```
BLAST score
E value
                  1.0e-167
Match length
                  418
% identity
                  88
NCBI Description Maize 22 kd (Mw=26.99 kd) zein protein 3, mRNA
Seq. No.
                  19272
                  66051 1.R1040
Contig ID
5'-most EST
                  LIB3107-024-Q1-K1-F6
                  19273
Seq. No.
Contig ID
                  66075 1.R1040
                  LIB3107-030-Q1-K1-D9
5'-most EST
                  19274
Seq. No.
Contig ID
                  66079 1.R1040
5'-most EST
                  LIB3107-079-Q1-K1-A7
Method
                  BLASTX
NCBI GI
                  q4038043
                  204
BLAST score
                  8.0e-16
E value
Match length
                  134
% identity
                  32
NCBI Description (AC005936) putative DNA-binding protein [Arabidopsis
                  thaliana]
                  19275
Seq. No.
Contig ID
                  66080 1.R1040
5'-most EST
                  LIB3107-031-Q1-K1-H11
                  BLASTX
Method
NCBI GI
                  g1001311
BLAST score
                  194
E value
                  1.0e-14
                  56
Match length
% identity
                  64
NCBI Description (D64006) hypothetical protein [Synechocystis sp.]
                  19276
Seq. No.
                  66083 1.R1040
Contig ID
5'-most EST
                  LIB3170-083-Q1-K1-C4
Seq. No.
                  19277
Contig ID
                  66105 1.R1040
5'-most EST
                  LIB3107-053-Q1-K1-F7
                  19278
Seq. No.
                  66108 1.R1040
Contig ID
```

5'-most EST LIB3107-053-Q1-K1-G10

Seq. No. 19279

66118 1.R1040 Contig ID 5'-most EST q5753395

Method BLASTX NCBI GI q4049350 231 BLAST score 6.0e-19 E value Match length 88



% identity 47
NCBI Description (AL034567) putative protein [Arabidopsis thaliana]
Seq. No. 19280
Contig ID 66126\_1.R1040
5'-most EST LIB3107-055-Q1-K1-E1
Seq. No. 19281

Contig ID 66138\_1.R1040
5'-most EST leu701156445.h1
Method BLASTX
NCBI GI g4539008
BLAST score 200
E value 1.0e-15

BLAST score 200 E value 1.0e Match length 107 % identity 47

NCBI Description (AL049481) lipase-like protein [Arabidopsis thaliana]

Seq. No. 19282

Contig ID 66142\_1.R1040

5'-most EST LIB3107-055-Q1-K1-F9

Seq. No. 19283

Contig ID 66148\_1.R1040

5'-most EST jC-gmf102220055b12a1

Seq. No. 19284

Contig ID 66156\_1.R1040

5'-most EST LIB3139-055-P1-N1-C12

Method BLASTX
NCBI GI g1737218
BLAST score 545
E value 5.0e-56
Match length 132
% identity 67

NCBI Description (U79959) vacuolar sorting receptor homolog [Arabidopsis

thaliana]

Seq. No. 19285

Contig ID 66188\_1.R1040

5'-most EST LIB3107-058-Q1-K1-G4

Seq. No. 19286

Contig ID 66192\_1.R1040 5'-most EST zpv700761869.h1

Seq. No. 19287

Contig ID 66214\_1.R1040 5'-most EST asn701135308.h1

Method BLASTX
NCBI GI g3874214
BLAST score 265
E value 4.0e-23
Match length 151
% identity 40

NCBI Description (Z83217) Similarity to Yeast E1-E2 ATPase YEL031W

(SW:YED1\_YEAST); cDNA EST EMBL:D27574 comes from this gene;

% identity



cDNA EST EMBL:D33757 comes from this gene; cDNA EST EMBL:D34256 comes from this gene; cDNA EST EMBL:D37288 comes from

19288 Seq. No. 66215 1.R1040 Contig ID 5'-most EST LIB3107-061-Q1-K1-E1 Method BLASTX NCBI GI q100226 BLAST score 248 9.0e-21 E value Match length 112 % identity 47 NCBI Description hypothetical protein - tomato >gi\_19275\_emb\_CAA78112\_ (Z12127) protein of unknown function [Lycopersicon esculentum] >gi 445619 prf 1909366A Leu zipper protein [Lycopersicon esculentum] Seq. No. 19289 Contig ID 66223 1.R1040 5'-most EST LIB3107-061-Q1-K1-F10 19290 Seq. No. Contig ID 66229 1.R1040 5'-most EST LIB3107-061-Q1-K1-F5 BLASTX Method NCBI GI q3293031 BLAST score 418 E value 5.0e-41 110 Match length 73 % identity NCBI Description (AJ007574) amino acid carrier [Ricinus communis] Seq. No. 19291 66236 1.R1040 Contig ID LIB3139-081-P1-N1-D5 5'-most EST Method BLASTX NCBI GI q4220534 BLAST score 841 2.0e-90 E value Match length 241 67 % identity NCBI Description (AL035356) putative protein [Arabidopsis thaliana] 19292 Seq. No. 66281 1.R1040 Contig ID 5'-most EST wvk700683104.h1 Method BLASTX NCBI GI g1172761 BLAST score 712 E value 2.0e-75 Match length 187

NCBI Description ADENYLOSUCCINATE LYASE (ADENYLOSUCCINASE) (ASL) >gi\_1573637 (U32747) adenylosuccinate lyase (purB) [Haemophilus

influenzae Rd]



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Seq. No. 19293
Contig ID 66286_1.R1040
5'-most EST fua701043303.h1
Seq. No. 19294
```

Contig ID 66290\_1.R1040
5'-most EST k11701207829.h1
Method BLASTX
NCBI GI g3193285

NCBI GI g3193285 BLAST score 417 E value 1.0e-40 Match length 134 % identity 55

NCBI Description (AF069298) T14P8.18 gene product [Arabidopsis thaliana]

Seq. No. 19295

Contig ID 66298\_1.R1040 5'-most EST fC-gmst700649030g1

Seq. No. 19296

Contig ID 66306\_1.R1040
5'-most EST g5509381
Method BLASTX
NCBI GI g4467147
BLAST score 1089

E value 1.0e-119
Match length 290
% identity 73

NCBI Description (AL035540) putative protein [Arabidopsis thaliana]

Seq. No. 19297

Contig ID 66331 1.R1040

5'-most EST LIB3107-067-Q1-K1-F11

Seq. No. 19298

Contig ID 66333\_1.R1040 5'-most EST fde700873187.h1

Method BLASTX
NCBI GI g3236235
BLAST score 286
E value 2.0e-25
Match length 95
% identity 51

NCBI Description (AC004684) unknown protein [Arabidopsis thaliana]

>gi 4056501 (AC005896) unknown protein [Arabidopsis

thaliana]

Seq. No. 19299

Contig ID 66349 1.R1040

5'-most EST LIB3107-067-Q1-K1-H8
Method BLASTN
NCBI GI g18660

BLAST score 210 E value 1.0e-114 Match length 310 % identity 92

NCBI Description G.max hsp22 gene for low MW heat shock protein



19300 Seq. No. Contia ID

66351 1.R1040 LIB3107-069-Q1-K1-A1 5'-most EST

19301 Seq. No.

66365 1.R1040 Contig ID hyd700725277.hl 5'-most EST

BLASTX Method g2914703 NCBI GI 619 BLAST score 3.0e-64 E value 278 Match length 54

NCBI Description (AC003974) unknown protein [Arabidopsis thaliana]

19302 Seq. No.

66371 1.R1040 Contig ID rlr700898640.hl 5'-most EST

19303 Seq. No.

66379 1.R1040 Contig ID

uC-gmflminsoy027e07b1 5'-most EST

BLASTX Method q1929056 NCBI GI 222 BLAST score 2.0e-18 E value 58 Match length 79 % identity

(Y12090) putative 3,4-dihydroxy-2-butanone kinase NCBI Description

[Lycopersicon esculentum]

19304 Seq. No.

66387 1.R1040 Contig ID

LIB3107-071-Q1-K1-A1 5'-most EST

19305 Seq. No.

66392 1.R1040 Contig ID

LIB3107-071-Q1-K1-B1 5'-most EST

19306 Seq. No.

66396 1.R1040 Contig ID

LIB3107-071-Q1-K1-B3 5'-most EST

19307 Seq. No.

66404\_1.R1040 Contig ID

jC-gmst02400059h02a1 5'-most EST

BLASTX Method g3062806 NCBI GI 424 BLAST score 8.0e-42 E value 120 Match length % identity 71

(D86198) dolichol-phosphate-mannose synthase [Homo sapiens] NCBI Description

>gi\_4503363\_ref\_NP\_003850.1\_pDPM1\_ UNKNOWN

19308 Seq. No.

3126



Contig ID 66406\_1.R1040

5'-most EST LIB3107-071-Q1-K1-D5

Method BLASTX
NCBI GI g3892050
BLAST score 349
E value 1.0e-32
Match length 118
% identity 63

NCBI Description (AC002330) hypothetical protein [Arabidopsis thaliana]

Seq. No. 19309

Contig ID 66410\_1.R1040

5'-most EST LIB3107-072-Q1-K1-C2

Method BLASTX
NCBI GI g464900
BLAST score 298
E value 7.0e-27
Match length 169
% identity 37

NCBI Description PUTATIVE KINASE-LIKE PROTEIN TMKL1 PRECURSOR

>gi 539008 pir S39476 kinase-like transmembrane protein

TMKL1 precursor - Arabidopsis thaliana

>gi 313190 emb\_CAA51385\_ (X72863) TMKL1 [Arabidopsis

thaliana]

Seq. No. 19310

Contig ID 66442\_1.R1040 5'-most EST uC-gmropic110a12b1

Method BLASTN
NCBI GI g2062705
BLAST score 36
E value 1.0e-10
Match length 36
% identity 38

NCBI Description Human butyrophilin (BTF5) mRNA, complete cds

Seq. No. 19311

Contig ID 66442\_2.R1040 5'-most EST g5058028

Seq. No. 19312

Contig ID 66443 1.R1040

5'-most EST LIB3107-074-Q1-K1-A5

Seq. No. 19313

Contig ID 66453\_1.R1040 5'-most EST zsg701126084.h1

Seq. No. 19314

Contig ID 66467 1.R1040 5'-most EST asn701136004.h1

Seq. No. 19315

Contig ID 66484\_1.R1040

5'-most EST LIB3107-075-Q1-K1-D9

Seq. No. 19316



```
Contig ID
                  66491 1.R1040
                  uC-gmflminsoy098g11b1
5'-most EST
Method
                  BLASTX
                  q2341042
NCBI GI
BLAST score
                  313
                  8.0e-29
E value
Match length
                  89
% identity
                  70
NCBI Description (AC000104) F19P19.26 [Arabidopsis thaliana]
Seq. No.
                  19317
                  66500 1.R1040
Contig ID
5'-most EST
                  LIB3107-075-Q1-K1-F9
                  19318
Seq. No.
Contig ID
                  66501 1.R1040
5'-most EST
                  sat701006236.h2
Method
                  BLASTX
NCBI GI
                  q2887500
BLAST score
                  441
E value
                  1.0e-43
Match length
                  107
                  82
% identity
                  (AC002339) putative AP2 domain-containing protein
NCBI Description
                  [Arabidopsis thaliana]
                  19319
Seq. No.
Contia ID
                  66513 1.R1040
5'-most EST
                  LIB3107-076-Q1-K1-A1
                  19320
Seq. No.
Contig ID
                  66525 1.R1040
                  LIB3109-037-Q1-K1-H10
5'-most EST
Method
                  BLASTX
NCBI GI
                  a2275199
BLAST score
                  520
                  7.0e-53
E value
Match length
                  188
% identity
NCBI Description
                 (AC002337) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  19321
Contig ID
                   66531 1.R1040
                  smc700747426.hl
5'-most EST
Method
                  BLASTX
NCBI GI
                  q3980413
BLAST score
                  752
E value
                  9.0e-80
Match length
                  166
% identity
```

NCBI Description

Contig ID 66531\_3.R1040 5'-most EST fC-gmst700891365d3

Seq. No. 19323

(AC004561) pumilio-like protein [Arabidopsis thaliana]



```
Contig ID 66531_4.R1040
5'-most EST sat701009683.h1
Method BLASTX
NCBI GI q3980417
```

NCBI GI g3980417 BLAST score 279 E value 1.0e-24 Match length 99 % identity 51

NCBI Description (AC004561) pumilio-like protein [Arabidopsis thaliana]

Seq. No. 19324

Contig ID 66532\_1.R1040

5'-most EST LIB3109-028-Q1-K1-B8

Seq. No. 19325

Contig ID 66540 1.R1040

5'-most EST LIB3107-077-Q1-K1-E5

Seq. No. 19326

Contig ID 66543 1.R1040 5'-most EST fua701040634.h1

Seq. No. 19327

Contig ID 66546 1.R1040

5'-most EST LIB3107-077-Q1-K1-F12

Seq. No. 19328

Contig ID 66550 1.R1040

5'-most EST LIB3107-077-Q1-K1-G2

Seq. No. 19329

Contig ID 66557\_1.R1040 5'-most EST zzp700829641.h1

Seq. No. 19330

Contig ID 66575\_1.R1040

5'-most EST LIB3107-079-Q1-K1-C12

Method BLASTX
NCBI GI g2462741
BLAST score 249
E value 3.0e-21
Match length 56
% identity 79

NCBI Description (AC002292) Highly similar to auxin-induced protein (aldo/keto reductase family) [Arabidopsis thaliana]

Seq. No. 19331

Contig ID 66578 1.R1040

5'-most EST jC-gmst02400074d07a1

Method BLASTX
NCBI GI g4521249
BLAST score 526
E value 2.0e-53
Match length 135
% identity 76

NCBI Description (AB013912) DNA helicase [Mus musculus]



Contig ID 66579 1.R1040

5'-most EST jC-gmst02400055b01d1

19333 Seq. No.

66592 1.R1040 Contig ID 5'-most EST dpv701102750.h1

19334 Seq. No.

Contig ID 66612\_1.R1040

5'-most EST LIB3107-080-Q1-K1-E8

Method BLASTX NCBI GI g4102600 BLAST score 312 E value 2.0e-28 Match length 142 % identity 55

NCBI Description (AF013467) ARF6 [Arabidopsis thaliana]

Seq. No. 19335

66615 1.R1040 Contig ID

5'-most EST LIB3107-080-Q1-K1-F11

19336 Seq. No.

Contig ID 66626 1.R1040

5'-most EST LIB3107-080-Q1-K1-G7

19337 Seq. No.

66628 1.R1040 Contig ID

5'-most EST uC-gmflminsoy080h05b1

Method BLASTX g3252866 NCBI GI BLAST score 440 2.0e-43 E value Match length 138

% identity 62

NCBI Description (AF033535) putative zinc transporter [Arabidopsis thaliana]

19338 Seq. No.

Contig ID 66629 1.R1040

5'-most EST LIB3107-080-Q1-K1-H7

Method BLASTX NCBI GI q3763917 BLAST score 1049 1.0e-114 E value Match length 271 % identity 73

NCBI Description (AC004450) hypothetical protein [Arabidopsis thaliana]

>gi\_4531438\_gb\_AAD22123.1 AC006224 5 (AC006224)

hypothetical protein [Arabidopsis thaliana]

Seq. No. 19339

66630 1.R1040 Contig ID

5'-most EST LIB3107-080-Q1-K1-H8

Method BLASTX NCBI GI q3250693 BLAST score 286



E value 1.0e-25
Match length 98
% identity 51

NCBI Description (AL024486) lectin like protein [Arabidopsis thaliana]

Seq. No. 19340

Contig ID 66636\_1.R1040

5'-most EST LIB3170-079-Q1-J1-E9

Seq. No. 19341

Contig ID 66643\_1.R1040

5'-most EST LIB3107-082-Q1-K1-G3

Method BLASTX
NCBI GI g3876103
BLAST score 418
E value 7.0e-41
Match length 207
% identity 48

NCBI Description (Z54271) similar to phosphoacetylglucosamine mutase; cDNA EST EMBL: Z14378 comes from this gene; cDNA EST EMBL: D32979

comes from this gene; cDNA EST EMBL: D35696 comes from this

gene; cDNA EST yk254c11.3 comes from this gene; cDN

Seq. No. 19342

Contig ID 66644\_1.R1040

5'-most EST LIB3107-082-Q1-K1-G5

Seq. No. 19343

Contig ID 66648\_1.R1040 5'-most EST leu701156734.h1

Method BLASTX
NCBI GI g2500963
BLAST score 150
E value 2.0e-09
Match length 94
% identity 39

NCBI Description ALANYL-TRNA SYNTHETASE (ALANINE--TRNA LIGASE) (ALARS)

>gi\_2118343\_pir\_\_D64370 alanine--tRNA ligase (EC 6.1.1.7) Methanococcus jannaschii >gi\_1591270 (U67505) alanyl-tRNA

synthetase (alaS) [Methanococcus jannaschii]

Seq. No. 19344

Contig ID 66654\_1.R1040

5'-most EST jC-gmf102220057g03a1

Method BLASTX
NCBI GI g4432823
BLAST score 457
E value 7.0e-45
Match length 303
% identity 40

NCBI Description (AC006593) hypothetical protein [Arabidopsis thaliana]

Seq. No. 19345

Contig ID 66654\_2.R1040 5'-most EST uC-gmropic006g03b1

Seq. No. 19346



Contig ID 66663\_1.R1040 5'-most EST gsv701046674.h1

Seq. No. 19347

Contig ID 66679\_1.R1040

5'-most EST LIB3170-037-Q1-K1-E9

Method BLASTX
NCBI GI g4165089
BLAST score 188
E value 5.0e-14
Match length 119
% identity 36

NCBI Description (AF084480) Williams-Beuren syndrome deletion transcript 9

homolog [Mus musculus]

Seq. No. 19348

Contig ID 66685 1.R1040

5'-most EST LIB3170-081-Q1-K1-A10

Seq. No. 19349

Contig ID 66688 1.R1040

5'-most EST LIB3107-038-Q1-K1-E10

Method BLASTX
NCBI GI g3779026
BLAST score 120
E value 5.0e-12
Match length 70
% identity 45

NCBI Description (AC005171) putative retrotransposon [Arabidopsis thaliana]

Seq. No. 19350

Contig ID 66694\_1.R1040

5'-most EST LIB3107-039-Q1-K1-B4

Seq. No. 19351

Contig ID 66696 1.R1040

5'-most EST LIB3139-063-P1-N1-D10

Method BLASTX
NCBI GI g3892059
BLAST score 233
E value 5.0e-19
Match length 121
% identity 48

NCBI Description (AC002330) predicted protein of unknown function

[Arabidopsis thaliana]

Seq. No. 19352

Contig ID 66699 1.R1040

5'-most EST LIB3170-085-Q1-K1-A1

Seq. No. 19353

Contig ID 66705\_1.R1040

5'-most EST LIB3109-030-Q1-K1-G12

Seq. No. 19354

Contig ID 66711 1.R1040

5'-most EST LIB3107-012-Q1-K1-C11



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Seq. No.
                  19355
Contig ID
                  66724 1.R1040
5'-most EST
                  LIB3107-015-Q1-K1-A8
Method
                  BLASTX
NCBI GI
                  g2494076
BLAST score
                  556
E value
                  3.0e-57
Match length
                  123
% identity
                  85
NCBI Description NADP-DEPENDENT GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE
                  (NON-PHOSPHORYLATING GLYCERALDEHYDE 3-PHOSPHATE
                  DEHYDROGENASE) (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE
                  (NADP+)) (TRIOSEPHOSPHATE DEHYDROGENASE) >gi_1842115
                   (U87848) non-phosphorylating glyceraldehyde dehydrogenase
                  [Nicotiana plumbaginifolia]
Seq. No.
                  19356
                  66735 1.R1040
Contig ID
5'-most EST
                  uC-gmropic054a05b1
Method
                  BLASTX
NCBI GI
                  q4454480
BLAST score
                  260
                  3.0e-22
E value
                  73
Match length
                  62
% identity
NCBI Description
                  (AC006234) putative (1-4)-beta-mannan endohydrolase
                  [Arabidopsis thaliana]
Seq. No.
                  19357
Contig ID
                  66741 1.R1040
                  LIB3107-052-Q1-K1-F5
5'-most EST
                  BLASTX
Method
NCBI GI
                  a4049401
BLAST score
                  352
E value
                  2.0e-33
Match length
                  91
% identity
                  69
NCBI Description (AJ131580) glutathione transferase AtGST 10 [Arabidopsis
                  thaliana]
                  19358
Seq. No.
                  66742 1.R1040
Contig ID
5'-most EST
                  LIB3107-052-Q1-K1-F7
Method
                  BLASTN
NCBI GI
                  q4206101
BLAST score
                  269
E value
                  1.0e-150
Match length
                  365
% identity
                  93
NCBI Description Glycine max retroelement diaspora gag-pol polyprotein
                  (gag-pol) pseudogene, partial sequence
```

66744 1.R1040 Contig ID

5'-most EST LIB3107-052-Q1-K1-F9



Seq. No. 19360 Contig ID 66746 1.R1040

Contig ID 66746\_1.R1040 5'-most EST LIB3107-052-Q1-K1-G10

Seq. No. 19361

Contig ID 66751\_1.R1040 5'-most EST pmv700893648.h1

Seq. No. 19362

Contig ID 66760\_1.R1040

5'-most EST LIB3138-051-Q1-N1-B4

Method BLASTX
NCBI GI g2245144
BLAST score 351
E value 3.0e-33
Match length 90
% identity 76

% identity 76
NCBI Description (Y10846) O-acetylserine(thiol) lyase [Brassica juncea]

Seq. No. 19363

Contig ID 66792\_1.R1040 5'-most EST leu701152962.h1

Method BLASTX
NCBI GI g2832241
BLAST score 340
E value 9.0e-32
Match length 176
% identity 51

NCBI Description (AF030864) nonphototropic hypocotyl 1 [Arabidopsis

thaliana]

Seq. No. 19364

Contig ID 66794\_1.R1040

5'-most EST LIB3107-056-Q1-K1-F4

Seq. No. 19365

Contig ID 66808\_1.R1040

5'-most EST LIB3107-057-Q1-K1-A11

Seq. No. 19366

Contig ID 66819\_1.R1040 5'-most EST wvk700684113.h1

Method BLASTN
NCBI GI g3687388
BLAST score 185
E value 1.0e-99
Match length 473
% identity 85

NCBI Description Lycopersicon esculentum mRNA for putative cullin protein

Seq. No. 19367

Contig ID 66856\_1.R1040

5'-most EST LIB3109-016-Q1-K3-A7

Seq. No. 19368

Contig ID 66885\_1.R1040 5'-most EST xpa700795209.h1

NCBI Description

thaliana]



```
19369
Seq. No.
                  66900 1.R1040
Contig ID
                  zsg701118046.h2
5'-most EST
                  BLASTX
Method
                  g2497281
NCBI GI
                  274
BLAST score
                  1.0e-23
E value
                  111
Match length
                  48
% identity
                  TRANSLATION INITIATION FACTOR IF-2
NCBI Description
                  >gi_1651769_dbj_BAA16696_ (D90900) initiation factor IF-2
                   [Synechocystis sp.]
                   19370
Seq. No.
                   66900 2.R1040
Contig ID
                  LIB3167-010-P1-K1-A8
5'-most EST
                   19371
Seq. No.
                   66913 1.R1040
Contig ID
                   pxt700943888.hl
5'-most EST
                   19372
Seq. No.
                   66921_1.R1040
Contig ID
                   jC-gmro02800033d07d1
5'-most EST
                   BLASTX
Method
                   g532703
NCBI GI
                   182
BLAST score
                   2.0e-13
E value
                   43
Match length
                   70
% identity
NCBI Description (U13180) unknown [Glycine max]
                   19373
Seq. No.
                   66922 1.R1040
Contig ID
5'-most EST
                   zsq701124560.hl
                   BLASTX
Method
                   g2245030
NCBI GI
                   265
BLAST score
                   7.0e-28
E value
                   78
Match length
                   78
 % identity
                   (Z97341) apetala2 domain TINY homolog [Arabidopsis
NCBI Description
                   thaliana]
                   19374
 Seq. No.
                   66923 1.R1040
 Contig ID
                   awf700837201.hl
 5'-most EST
                   BLASTX
 Method
                   q3822225
 NCBI GI
                   343
 BLAST score
                   2.0e-31
 E value
                   170
 Match length
                    42
 % identity
```

(AF079183) RING-H2 finger protein RHG1a [Arabidopsis



```
19375
Seq. No.
                  66927 1.R1040
Contig ID
                  LIB3107-070-Q1-K1-B1
5'-most EST
Seq. No.
                  19376
                  66932 1.R1040
Contig ID
                  ssr700560161.hl
5'-most EST
                  BLASTX
Method
                  g1946371
NCBI GI
                  282
BLAST score
                  1.0e-24
E value
                  124
Match length
                  50
% identity
                  (U93215) regulatory protein Viviparous-1 isolog
NCBI Description
                   [Arabidopsis thaliana]
                  19377
Seq. No.
                  66939 1.R1040
Contig ID
                  LIB3107-070-Q1-K1-C6
5'-most EST
Seq. No.
                  19378
                  66954 1.R1040
Contig ID
                  LIB3107-070-Q1-K1-E12
5'-most EST
                  BLASTX
Method
                  g3024708
NCBI GI
BLAST score
                  117
                   2.0e-13
E value
                   69
Match length
                   62
% identity
                  TRANSCRIPTION INITIATION FACTOR TFIID 20/15 KD SUBUNITS
NCBI Description
                   (TAFII-20/TAFII-15) (TAFII20/TAFII15)
                   >gi_2135937_pir__JC4676 PolII transcription factor TFTIID
                   chain TAFII20 - human >gi_791055_emb_CAA58826_ (X84002)
                   PolII transcription factor TFTIID [Homo sapiens]
                   >gi_1345404_dbj_BAA09112_ (D50544) TFIID subunit p22 [Homo
                   sapiens] >gi 1373377 (U57693) TAF20 [Homo sapiens]
                   19379
Seq. No.
                   66964 1.R1040
Contig ID
5'-most EST
                   taw700656837.hl
                   BLASTX
Method
                   g170131
NCBI GI
                   244
BLAST score
                   1.0e-20
E value
Match length
                   57
                   77
% identity
NCBI Description (M55322) ribosomal protein 30S subunit [Spinacia oleracea]
Seq. No.
                   19380
                   66966 1.R1040
Contig ID
                   LIB3107-070-Q1-K1-F8
 5'-most EST
                   BLASTX
Method
```

q3193324

274 4.0e-24

100

42

NCBI GI BLAST score

E value Match length

% identity



NCBI Description (AF069299) contains similarity to WD domains, G-beta repeats (Pfam: G-beta.hmm, score: 22.80 and 35.84) [Arabidopsis thaliana]

Seq. No. 19381

Contig ID 66973 1.R1040

5'-most EST LIB3107-080-Q1-K1-F5

Method BLASTN
NCBI GI g516853
BLAST score 83
E value 2.0e-38
Match length 323
% identity 60

NCBI Description Soybean SUBI-2 gene for ubiquitin, complete cds

Seq. No. 19382

Contig ID 66975\_1.R1040 5'-most EST kl1701204247.h2

Method BLASTX
NCBI GI g2864610
BLAST score 252
E value 3.0e-21
Match length 108
% identity 46

NCBI Description (AL021811) putative protein [Arabidopsis thaliana]

>gi\_4049336\_emb\_CAA22561\_ (AL034567) putative protein

[Arabidopsis thaliana]

Seq. No. 19383

Contig ID 66997 1.R1040

5'-most EST LIB3109-016-Q1-K2-H5

Method BLASTX
NCBI GI g3386596
BLAST score 594
E value 1.0e-61
Match length 136
% identity 78

NCBI Description (AC004665) unknown protein [Arabidopsis thaliana]

>gi\_3702346 (AC005397) unknown protein [Arabidopsis

thaliana]

Seq. No. 19384

Contig ID 66997\_2.R1040 5'-most EST hyd700725113.h1

Method BLASTX
NCBI GI g3386596
BLAST score 160
E value 2.0e-11
Match length 33
% identity 88

NCBI Description (AC004665) unknown protein [Arabidopsis thaliana]

>gi 3702346 (AC005397) unknown protein [Arabidopsis

thaliana]

Seq. No. 19385

Contig ID 66998 1.R1040 5'-most EST g5677602



```
19386
Seq. No.
                  66999 1.R1040
Contig ID
5'-most EST
                  LIB3109-016-Q1-K3-H8
Method
                  BLASTX
NCBI GI
                  g4262239
BLAST score
                  162
                  4.0e-11
E value
Match length
                  105
                  35
% identity
NCBI Description (AC006200) putative membrane transporter [Arabidopsis
                  thaliana]
                  19387
Seq. No.
Contig ID
                  67017 1.R1040
5'-most EST
                  LIB3109-016-Q1-K3-C7
Method
                  BLASTX
NCBI GI
                  q4325342
BLAST score
                  354
                  2.0e-33
E value
Match length
                  98
                  72
% identity
NCBI Description (AF128393) No definition line found [Arabidopsis thaliana]
                  19388
Seq. No.
Contig ID
                  67031 1.R1040
5'-most EST
                  LIB3109-016-Q1-K1-F7
                  19389
Seq. No.
Contig ID
                  67032 1.R1040
5'-most EST
                  bth700845995.h1
                  19390
Seq. No.
Contig ID
                  67034 1.R1040
5'-most EST
                  LIB3109-016-Q1-K3-G3
Seq. No.
                  19391
                  67040 1.R1040
Contig ID
5'-most EST
                  LIB3109-016-Q1-K1-H3
Method
                  BLASTX
NCBI GI
                  g3702327
BLAST score
                  169
E value
                  5.0e-12
                  37
Match length
% identity
NCBI Description (AC005397) unknown protein [Arabidopsis thaliana]
                  19392
Seq. No.
                  67049 1.R1040
Contig ID
5'-most EST
                  LIB3109-017-Q1-K2-B7
                  19393
Seq. No.
```

Contig ID 67051\_1.R1040

5'-most EST LIB3109-017-Q1-K1-B7

Seq. No. 19394

Contig ID 67055 1.R1040



```
jC-gmle01810002d11d1
5'-most EST
                  19395
Seq. No.
                  67061 1.R1040
Contig ID
                  LIB3109-021-Q1-K2-D3
5'-most EST
                  19396
Seq. No.
                  67064 1.R1040
Contig ID
                  bth700845189.h1
5'-most EST
                  BLASTX
Method
                  g2914703
NCBI GI
                  604
BLAST score
                  1.0e-62
E value
                  178
Match length
                  47
% identity
                  (AC003974) unknown protein [Arabidopsis thaliana]
NCBI Description
                  19397
Seq. No.
                   67068 1.R1040
Contig ID
                   jC-gmst02400074c03a1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q2511715
                   399
BLAST score
                   7.0e-39
E value
                   105
Match length
                   76
% identity
                  (AF019380) putative phosphatidylinositol-4-phosphate
NCBI Description
                   5-kinase [Arabidopsis thaliana]
                   19398
Seq. No.
                   67068 2.R1040
Contig ID
                   LIB3109-021-Q1-K2-E11
5'-most EST
                   BLASTX
Method
                   q2511715
NCBI GI
                   416
BLAST score
                   8.0e-41
E value
                   104
Match length
                   73
% identity
                  (AF019380) putative phosphatidylinositol-4-phosphate
NCBI Description
                   5-kinase [Arabidopsis thaliana]
Seq. No.
                   19399
                   67071 1.R1040
Contig ID
5'-most EST
                   LIB3109-021-Q1-K2-E5
                   19400
Seq. No.
                   67072 1.R1040
Contig ID
                   LIB3167-050-P1-K1-A9
5'-most EST
                   BLASTX
Method
                   g3093294
NCBI GI
                   363
BLAST score
E value
                   1.0e-34
                   156
Match length
                   57
 % identity
NCBI Description (Y12782) putative villin [Arabidopsis thaliana]
```



Contig ID 67087\_1.R1040 5'-most EST LIB3109-021-Q1-K1-F9

Seq. No. 19402

Contig ID 67088\_1.R1040 5'-most EST pcp700993734.h1

Seq. No. 19403

Contig ID 67089\_1.R1040

5'-most EST LIB3109-021-Q1-K1-G10

Seq. No. 19404

Contig ID 67093\_1.R1040

5'-most EST jC-gmro02910038g09a1

Method BLASTX
NCBI GI g2088650
BLAST score 306
E value 7.0e-28
Match length 103
% identity 37

NCBI Description (AF002109) peroxisomal ATP/ADP carrier protein isolog

[Arabidopsis thaliana]

Seq. No. 19405

Contig ID 67097\_1.R1040

5'-most EST LIB3109-021-Q1-K1-H10

Seq. No. 19406

Contig ID 67134\_1.R1040

5'-most EST LIB3109-041-Q1-K1-H3

Method BLASTX
NCBI GI g2738752
BLAST score 522
E value 2.0e-56
Match length 152
% identity 72

NCBI Description (AF016306) sulfate permease [Zea mays]

Seq. No. 19407

Contig ID 67136\_1.R1040

5'-most EST uC-gmflminsoy071f12b2

Method BLASTN
NCBI GI g549972
BLAST score 54
E value 2.0e-21
Match length 122
% identity 86

NCBI Description Arabidopsis thaliana Col-O casein kinase I-like protein

mRNA, complete cds

Seq. No. 19408

Contig ID 67138\_1.R1040 5'-most EST leu701156502.h1

Seq. No. 19409

Contig ID 67156\_1.R1040 5'-most EST vzy700755014.h1



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19410
Seq. No.
                  67166 1.R1040
Contig ID
                  uC-gmropic074e09b1
5'-most EST
                  BLASTX
Method
                  g3482918
NCBI GI
                   682
BLAST score
                   6.0e-72
E value
                  151
Match length
                   89
% identity
                  (AC003970) Similar to ATP-citrate-lyase [Arabidopsis
NCBI Description
                   thaliana]
                   19411
Seq. No.
                   67172 1.R1040
Contig ID
                   LIB3109-010-Q1-K1-H7
5'-most EST
                   19412
Seq. No.
                   67172 2.R1040
Contig ID
                   kmv700737936.hl
5'-most EST
                   19413
Seq. No.
                   67182 1.R1040
Contig ID
                   LIB3109-001-Q1-K2-C12
5'-most EST
                   19414
Seq. No.
                   67187 1.R1040
Contig ID
                   LIB3170-070-Q1-K2-F3
5'-most EST
                   BLASTX
Method
                   q4115377
NCBI GI
                   242
BLAST score
                   3.0e-30
E value
                   116
Match length
                   63
 % identity
NCBI Description (AC005967) unknown protein [Arabidopsis thaliana]
                   19415
 Seq. No.
                   67190 1.R1040
 Contig ID
                   LIB3109-001-Q1-K2-D5
 5'-most EST
                    19416
 Seq. No.
                    67193 1.R1040
 Contig ID
                   LIB3109-001-Q1-K2-E11
 5'-most EST
                    19417
 Seq. No.
                    67203 1.R1040
 Contig ID
                    LIB31\overline{0}9-001-Q1-K2-G6
 5'-most EST
                    BLASTX
 Method
                    q3928095
 NCBI GI
                    407
 BLAST score
                    7.0e-40
 E value
                    108
 Match length
 % identity
 NCBI Description (AC005770) putative protein kinase [Arabidopsis thaliana]
```

Contig ID 67210\_1.R1040



5'-most EST LIB3109-001-Q1-K4-H6

Method BLASTX NCBI GI g1742959 BLAST score 222 E value 4.0e-18 Match length 71 % identity

(Z71450) CLC-d chloride channel protein [Arabidopsis NCBI Description

thaliana]

19419 Seq. No.

Contig ID 67212 1.R1040 5'-most EST asn701140763.h1

Seq. No. 19420

67220 1.R1040 Contig ID

5'-most EST jC-gmf102220088a09a1

Method BLASTX NCBI GI q3281861 430 BLAST score 3.0e-42 E value 100 Match length % identity 78

NCBI Description (AL031004) putative protein [Arabidopsis thaliana]

Seq. No. 19421

67220 2.R1040 Contig ID 5'-most EST uaw700661045.h1

BLASTX Method g3281861 NCBI GI BLAST score 644 E value 1.0e-67 Match length 139 % identity 81

NCBI Description (AL031004) putative protein [Arabidopsis thaliana]

Seq. No. 19422

67230 1.R1040 Contig ID

5'-most EST LIB3109-002-Q1-K3-B9

Seq. No. 19423

Contig ID 67232 1.R1040

5'-most EST uC-gmflminsoy023a10b1

Method BLASTX NCBI GI g2622714 BLAST score 289 E value 2.0e-29 Match length 137

% identity

(AE000918) phosphonopyruvate decarboxylase NCBI Description

[Methanobacterium thermoautotrophicum]

19424 Seq. No.

67232 2.R1040 Contig ID

5'-most EST LIB3109-002-Q1-K3-C11

Seq. No. 19425



```
Contig ID
                   67233 1.R1040
5'-most EST
                  LIB3109-002-Q1-K1-C12
                  19426
Seq. No.
Contig ID
                  67235 1.R1040
5'-most EST
                  uC-qmrominsoy058d06b1
Method
                  BLASTX
NCBI GI
                  q3004555
BLAST score
                  291
E value
                  7.0e-26
Match length
                  163
% identity
                  (AC003673) similar to salt inducible protein [Arabidopsis
NCBI Description
Seq. No.
                  19427
                   67237 1.R1040
Contig ID
                  LIB3109-002-Q1-K2-C5
5'-most EST
                  BLASTX
Method
                  q1263160
NCBI GI
                  190
BLAST score
                  2.0e-14
E value
Match length
                  88
% identity
                   9
                  (X89226) leucine-rich repeat/receptor protein kinase [Oryza
NCBI Description
                   19428
Seq. No.
                   67240 1.R1040
Contig ID
                  LIB3109-002-Q1-K2-C8
5'-most EST
Method
                   BLASTX
                   g4539452
NCBI GI
                   550
BLAST score
                   1.0e-56
E value
Match length
                   138
                   67
% identity
                   (AL049500) putative phosphoribosylanthranilate transferase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   19429
                   67241 1.R1040
Contig ID
5'-most EST
                   dpv701102705.h1
                   BLASTX
Method
NCBI GI
                   g1731181
BLAST score
                   154
E value
                   4.0e-10
Match length
                   45
                   62
% identity
                  HYPOTHETICAL 75.5 KD PROTEIN C14A4.3 IN CHROMOSOME II
NCBI Description
                   >qi 3874230 emb CAA90107 (Z49909) weak similarity with a
```

B. Flavum translocation protein (Swiss Prot accession number P38376); cDNA EST yk220e10.5 comes from this gene

[Caenorhabditis elegans]

19430 Seq. No.

67249 1.R1040 Contig ID

LIB3139-020-P1-N1-C7 5'-most EST



 Seq. No.
 19431

 Contig ID
 67254\_1.R1040

 5'-most EST
 hyd700728812.h1

Seq. No. 19432 Contig ID 67269\_1.R1040

5'-most EST epx701108529.h1

Seq. No. 19433

Contig ID 67273 1.R1040 5'-most EST gsv701045803.h1

Method BLASTX
NCBI GI g416758
BLAST score 1140
E value 1.0e-125
Match length 303
% identity 69

% identity 69
NCBI Description SERINE CARBOXYPEPTIDASE PRECURSOR >gi 166674 (M81130)

carboxypeptidase Y-like protein [Arabidopsis thaliana] >gi\_445120\_prf\_\_1908426A carboxypeptidase Y [Arabidopsis

tha $\overline{l}$ iana]

Seq. No. 19434

Contig ID 67289\_1.R1040

5'-most EST LIB3109-002-Q1-K2-G2

Method BLASTX
NCBI GI g3522956
BLAST score 401
E value 2.0e-46
Match length 132
% identity 69

NCBI Description (AC004411) putative pectinacetylesterase precursor

[Arabidopsis thaliana]

Seq. No. 19435

Contig ID 67299\_1.R1040 5'-most EST vzy700752637.h1

Method BLASTX
NCBI GI g2252843
BLAST score 189
E value 9.0e-14
Match length 269
% identity 37

NCBI Description (AF013293) No definition line found [Arabidopsis thaliana]

Seq. No. 19436

Contig ID 67302\_1.R1040

5'-most EST LIB3109-002-Q1-K3-H7

Seq. No. 19437

Contig ID 67307\_1.R1040

5'-most EST LIB31 $\overline{0}$ 9-044-Q1-K1-D8

Method BLASTX
NCBI GI g4454042
BLAST score 279
E value 1.0e-24



Match length 129 % identity 43

NCBI Description (AL035394) putative protein [Arabidopsis thaliana]

Seq. No. 19438

Contig ID 67307\_2.R1040 5'-most EST uC-gmropic116g11b1

Seq. No. 19439

Contig ID 67310\_1.R1040 5'-most EST zhf700955273.h1

Seq. No. 19440

Contig ID 67314\_1.R1040

5'-most EST LIB3170-071-Q1-K1-A1

Seq. No. 19441

Contig ID 67317\_1.R1040

5'-most EST LIB3170-056-Q1-K1-E9

Method BLASTX
NCBI GI g3308971
BLAST score 213
E value 3.0e-20
Match length 181
% identity 33

NCBI Description (AB002111) peroxisome assembly factor-3 (PAF-3) [Rattus

norvegicus]

Seq. No. 19442

Contig ID 67345 1.R1040

5'-most EST LIB3109-003-Q1-K1-C1

 Method
 BLASTX

 NCBI GI
 g1346769

 BLAST score
 268

 E value
 9.0e-24

 Match length
 96

% identity 57

NCBI Description PROLYL ENDOPEPTIDASE (POST-PROLINE CLEAVING ENZYME) (PE)

>gi\_558596\_emb\_CAA52605\_ (X74496) prolyl oligopeptidase
[Homo sapiens] >gi\_1585155\_prf\_\_2124300A Pro oligopeptidase
[Homo sapiens] >gi\_4506043\_ref\_NP\_002717.1\_pPREP\_ prolyl

endopeptidase

Seq. No. 19443

Contig ID 67349 1.R1040 5'-most EST dpv701100848.h1

Method BLASTN
NCBI GI g2264309
BLAST score 58
E value 2.0e-23
Match length 318
% identity 85

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MJJ3, complete sequence [Arabidopsis thaliana]

Seq. No. 19444

Contig ID 67349\_2.R1040



```
ncj700979814.h2
5'-most EST
                  19445
Seq. No.
Contig ID
                  67355 1.R1040
5'-most EST
                  asn701132071.h1
                  19446
Seq. No.
                  67357 1.R1040
Contig ID
                  rca701001540.hl
5'-most EST
Seq. No.
                  19447
                  67380 1.R1040
Contig ID
                  LIB3109-005-Q1-K1-C6
5'-most EST
                  BLASTN
Method
                  q4190975
NCBI GI
BLAST score
                  180
                  1.0e-96
E value
Match length
                  312
                  89
% identity
NCBI Description Vigna radiata mRNA for cytokinin-specific binding protein,
                  complete cds
                   19448
Seq. No.
                   67404 1.R1040
Contig ID
                  LIB3109-005-Q1-K1-E8
5'-most EST
                   19449
Seq. No.
                   67405 1.R1040
Contig ID
                   pmv700891796.hl
5'-most EST
                   BLASTX
Method
                   q2621189
NCBI GI
                   287
BLAST score
                   1.0e-25
E value
                   104
Match length
                   52
 % identity
                  (AE000803) conserved protein [Methanobacterium
NCBI Description
                   thermoautotrophicum]
                   19450
Seq. No.
                   67406 1.R1040
 Contig ID
                   LIB3139-045-P1-N1-H8
 5'-most EST
                   BLASTX
Method
                   g2160170
 NCBI GI
                   578
 BLAST score
                   2.0e-59
 E value
                   199
 Match length
                   65
 % identity
NCBI Description (AC000132) No definition line found [Arabidopsis thaliana]
                   19451
 Seq. No.
                   67407 1.R1040
```

Contig ID

 $LIB31\overline{0}9-005-Q1-K1-F12$ 5'-most EST

BLASTX Method g3075392 NCBI GI BLAST score 532 2.0e-54 E value Match length 132



% identity 75

NCBI Description (AC004484) putative steroid dehydrogenase [Arabidopsis

thaliana]

Seq. No. 19452

Contig ID 67435\_1.R1040 5'-most EST asn701134620.h2

Method BLASTX
NCBI GI g1495366
BLAST score 1728
E value 0.0e+00
Match length 473
% identity 66

NCBI Description (Z69370) nitrite transporter [Cucumis sativus]

Seq. No. 19453

Contig ID 67436\_1.R1040

5'-most EST LIB3109-044-Q1-K1-C4

Seq. No. 19454

Contig ID 67437 1.R1040 5'-most EST gsv701054938.h1

Seq. No. 19455

Contig ID 67445\_1.R1040

5'-most EST LIB3109-006-Q1-K1-G6

Method BLASTX
NCBI GI g4218991
BLAST score 173
E value 2.0e-12
Match length 90
% identity 43

NCBI Description (AF098632) subtilisin-like protease [Arabidopsis thaliana]

Seq. No. 19456

Contig ID 67448\_1.R1040

5'-most EST LIB3109-043-Q1-K1-D6

Seq. No. 19457

Contig ID 67462\_1.R1040

5'-most EST LIB3109-007-Q1-K1-A2

Method BLASTX
NCBI GI g1083342
BLAST score 281
E value 6.0e-25
Match length 84
% identity 62

NCBI Description GPI-anchor biosynthesis protein PIG-A - mouse

>gi\_577723\_dbj\_BAA05047\_ (D26047) Pig-a precursor [Mus
musculus] >gi\_1402592\_dbj\_BAA06663\_ (D31863) PIG-A protein

[Mus musculus]

Seq. No. 19458

Contig ID 67471 1.R1040

5'-most EST LIB3109-007-Q1-K1-G6

Method BLASTX NCBI GI g3493131



BLAST score 2.0e-14 E value Match length 50 72 % identity

(AF081570) thymidylate kinase [Arabidopsis thaliana] NCBI Description

19459 Seq. No.

67475 1.R1040 Contig ID hrw701057441.h1 5'-most EST

Method BLASTN g292442 NCBI GI 279 BLAST score 1.0e-156 E value 279 Match length % identity 100

Homo sapiens ribosomal protein S20 (RPS20) mRNA, complete NCBI Description

cds >qi 4506696 ref NM 001023.1\_RPS20\_ Homo sapiens

ribosomal protein S20 (RPS20) mRNA

19460 Seq. No.

Contig ID 67480 1.R1040

LIB3109-009-Q1-K1-A10 5'-most EST

BLASTX Method g2104689 NCBI GI 195 BLAST score 8.0e-30 E value 239 Match length 39 % identity

NCBI Description (U92793) alpha glucosidase II, alpha subunit [Mus musculus]

19461 Seq. No.

67482 1.R1040 Contig ID uaw700666619.h1 5'-most EST

BLASTX Method NCBI GI q2129854 180 BLAST score 7.0e-24 E value Match length 129 45 % identity

NCBI Description early nodulin 8 precursor - alfalfa >gi\_304037 (L18899)

early nodulin [Medicago sativa]

19462 Seq. No.

Contig ID 67490 1.R1040 5'-most EST k11701204820.h1

19463 Seq. No.

67491 1.R1040 Contig ID

5'-most EST LIB3109-057-Q1-K1-C9

BLASTX Method NCBI GI g3122914 BLAST score 702 1.0e-141 E value Match length 303 76 % identity

VALYL-TRNA SYNTHETASE (VALINE--TRNA LIGASE) (VALRS) NCBI Description



## thaliana]

Seq. No. 19464 Contig ID 67495 1.R1040 5'-most EST LIB3109-009-Q1-K1-B7

Seq. No. 19465

67499 1.R1040 Contig ID 5'-most EST  $hrw70\overline{1}058616.h1$ 

Seq. No. 19466

Contig ID 67499 2.R1040 hrw701059874.h1 5'-most EST

Seq. No. 19467

Contig ID 67501 1.R1040

5'-most EST LIB3109-009-Q1-K1-C2

Method BLASTX g2160166 NCBI GI 147 BLAST score 2.0e-09 E value Match length 87

% identity 39

NCBI Description (AC000132) No definition line found [Arabidopsis thaliana]

Seq. No. 19468

67503 1.R1040 Contig ID 5'-most EST  $jex70\overline{0}906349.h1$ 

19469 Seq. No.

Contig ID 67509 1.R1040

5'-most EST LIB3109-009-Q1-K1-D1

Method BLASTX NCBI GI q4263824 BLAST score 155 E value 1.0e-19 Match length 84 % identity 58

NCBI Description (AC006067) unknown protein [Arabidopsis thaliana]

19470 Seq. No.

67510 1.R1040 Contig ID 5'-most EST leu701147215.h1

19471 Seq. No.

67510 2.R1040 Contig ID 5'-most EST  $ncj70\overline{0}976834.h1$ 

Seq. No. 19472

67510 4.R1040 Contig ID

5'-most EST jC-gmf102220136b02a1

19473 Seq. No.

67510 5.R1040 Contig ID

5'-most EST LIB3167-031-P1-K1-G7



Contig ID 67514\_1.R1040 5'-most EST LIB3109-010-Q1-K1-A5

Seq. No. 19475

Contig ID 67522 1.R1040

5'-most EST LIB3109-010-Q1-K1-B2

Seq. No. 19476

Contig ID 67523\_1.R1040 5'-most EST hyd700728822.h1

Method BLASTX
NCBI GI g1351856
BLAST score 1226
E value 1.0e-135
Match length 260
% identity 89

NCBI Description ACONITATE HYDRATASE, CYTOPLASMIC (CITRATE HYDRO-LYASE)

(ACONITASE) >gi\_868003\_dbj\_BAA06108\_ (D29629) aconitase

[Cucurbita sp.]

Seq. No. 19477

Contig ID 67533\_1.R1040

5'-most EST LIB3109-010-Q1-K1-C3

Seq. No. 19478

Contig ID 67541\_1.R1040

5'-most EST LIB3109-021-Q1-K3-A10

Seq. No. 19479

Contig ID 67544\_1.R1040

5'-most EST LIB3109-010-Q1-K1-D5

Method BLASTX
NCBI GI g3122334
BLAST score 270
E value 6.0e-24
Match length 110
% identity 46

NCBI Description PUTATIVE 3-ISOPROPYLMALATE DEHYDRATASE LARGE SUBUNIT

(ISOPROPYLMALATE ISOMERASE) (ALPHA-IPM ISOMERASE) (IPMI) >gi\_2648576 (AE000967) aconitase (acn) [Archaeoglobus

fulgidus]

Seq. No. 19480

Contig ID 67548 1.R1040

5'-most EST LIB3109-010-Q1-K1-D9

Method BLASTX
NCBI GI g1360084
BLAST score 194
E value 2.0e-14
Match length 89
% identity 53

NCBI Description (X97945) In finger protein [Nicotiana tabacum]

Seq. No. 19481

Contig ID 67548\_2.R1040 5'-most EST g5753583 Method BLASTX

```
NCBI GI
                   q3341468
BLAST score
                   150
E value
                   2.0e-09
Match length
                   70
% identity
                   57
NCBI Description
                   (AJ009594) Dof zinc finger protein [Nicotiana tabacum]
Seq. No.
                   19482
Contiq ID
                   67553 1.R1040
5'-most EST
                   zhf70\overline{0}958717.h1
Method
                   BLASTX
NCBI GI
                   q4558665
BLAST score
                   242
E value
                   2.0e-20
Match length
                   102
% identity
                   53
NCBI Description
                   (AC007063) putative white protein [Arabidopsis thaliana]
                   19483
Seq. No.
Contig ID
                   67559 1.R1040
5'-most EST
                   dpv70\overline{1}101215.h1
Method
                   BLASTX
NCBI GI
                   q2529678
BLAST score
                   305
E value
                   2.0e-27
Match length
                   132
% identity
                   23
NCBI Description
                   (AC002535) unknown protein [Arabidopsis thaliana]
Seq. No.
                   19484
Contig ID
                   67564 1.R1040
5'-most EST
                   LIB3139-091-P1-N1-F6
Method
                   BLASTX
NCBI GI
                   g4127461
BLAST score
                   593
E value
                   3.0e-61
Match length
                   212
% identity
                   54
NCBI Description
                   (AJ011674) receptor-like protein kinase, RLK3 [Arabidopsis
                   thaliana]
Seq. No.
                   19485
                   67566 1.R1040
Contig ID
5'-most EST
                   LIB3109-011-Q1-K1-D11
                   19486
Seq. No.
                   67571_1.R1040
Contig ID
5'-most EST
                   LIB3109-011-Q1-K1-D5
Method
                   BLASTX
                   q285741
                   229
                   9.0e-19
```

NCBI GI BLAST score E value Match length 177 % identity 38

NCBI Description (D14550) EDGP precursor [Daucus carota]



Contig ID 67583\_1.R1040 5'-most EST LIB3109-046-Q1-K1-D10

Seq. No. 19488

Contig ID 67597\_1.R1040 5'-most EST smc700747255.h1

Seq. No. 19489

Contig ID 67620\_1.R1040 5'-most EST uC-gmropic089a06b1

Method BLASTX
NCBI GI g3176690
BLAST score 241
E value 5.0e-25
Match length 248
% identity 36

NCBI Description (AC003671) Similar to ubiquitin ligase gb\_D63905 from S.

cerevisiae. EST gb R65295 comes from this gene.

[Arabidopsis thaliana]

Seq. No. 19490

Contig ID 67626 1.R1040

5'-most EST LIB3109-005-Q1-K1-H1

Method BLASTX
NCBI GI g4455293
BLAST score 288
E value 1.0e-25
Match length 115
% identity 61

NCBI Description (AL035528) putative protein [Arabidopsis thaliana]

Seq. No. 19491

Contig ID 67626\_2.R1040 5'-most EST ncj700985431.h1

Method BLASTX
NCBI GI g4455293
BLAST score 164
E value 2.0e-11
Match length 35
% identity 89

NCBI Description (AL035528) putative protein [Arabidopsis thaliana]

Seq. No. 19492

Contig ID 67631 1.R1040

5'-most EST jC-gmf102220076g07a1

Seq. No. 19493

Contig ID 67636\_1.R1040 5'-most EST dpv701098416.h1

Seq. No. 19494

Contig ID 67639 1.R1040

5'-most EST LIB3109-043-Q1-K1-E10

Method BLASTX
NCBI GI g4538911
BLAST score 248
E value 4.0e-21

3152



Match length 81 % identity 60

NCBI Description (AL049482) hypothetical protein [Arabidopsis thaliana]

Seq. No. 19495

Contig ID 67640 1.R1040 5'-most EST uxk700670028.h1

Method BLASTX
NCBI GI g3859591
BLAST score 225
E value 3.0e-18
Match length 99
% identity 45

NCBI Description (AF104919) No definition line found [Arabidopsis thaliana]

Seq. No. 19496

Contig ID 67648 1.R1040

5'-most EST LIB3109-013-Q1-K1-B8

Method BLASTX
NCBI GI g3341696
BLAST score 406
E value 1.0e-39
Match length 97
% identity 81

NCBI Description (AC003672) unknown protein [Arabidopsis thaliana]

Seq. No. 19497

Contig ID 67654\_1.R1040

5'-most EST LIB3109-013-Q1-K1-C4

Seq. No. 19498

Contig ID 67664 1.R1040

5'-most EST LIB3109-013-Q1-K1-D5

Seq. No. 19499

Contig ID 67664\_2.R1040 5'-most EST uC-gmropic038g12b1

Seq. No. 19500

Contig ID 67667 1.R1040

5'-most EST uC-gmrominsoy156b09b1

Method BLASTX
NCBI GI g4539452
BLAST score 891
E value 4.0e-96
Match length 277
% identity 59

NCBI Description (AL049500) putative phosphoribosylanthranilate transferase

[Arabidopsis thaliana]

Seq. No. 19501

Contig ID 67670 1.R1040

5'-most EST LIB3109-047-Q1-K1-A4

Seq. No. 19502

Contig ID 67671 1.R1040 5'-most EST jex700904685.h1



Method BLASTX
NCBI GI g3451463
BLAST score 383
E value 8.0e-37
Match length 130
% identity 52

NCBI Description (AL031349) hypothetical protein [Schizosaccharomyces pombe]

Seq. No. 19503

Contig ID 67675\_1.R1040

5'-most EST uC-gmflminsoy011b05b1

Seq. No. 19504

Contig ID 67682\_1.R1040

5'-most EST LIB3109-014-Q1-K1-D9

Method BLASTX
NCBI GI g1657619
BLAST score 232
E value 4.0e-26
Match length 135
% identity 44

NCBI Description (U72504) G5p [Arabidopsis thaliana] >gi\_3068710 (AF049236)

putative transmembrane protein G5p [Arabidopsis thaliana]

Seq. No. 19505

Contig ID 67691\_1.R1040

5'-most EST LIB3109-014-Q1-K1-E9

Seq. No. 19506

Contig ID 67692\_1.R1040 5'-most EST fde700872017.h1

Seq. No. 19507

Contig ID 67696\_1.R1040 5'-most EST sat701010016.h2

Method BLASTX
NCBI GI g1076289
BLAST score 303
E value 2.0e-27
Match length 127
% identity 46

NCBI Description amino acid permease AAP5 - Arabidopsis thaliana

>qi 608673 emb CAA54632\_ (X77501) amino acid permease

[Arabidopsis thaliana]

Seq. No. 19508

Contig ID 67711\_1.R1040

5'-most EST LIB3109-014-Q1-K1-G6

Method BLASTX
NCBI GI g2832700
BLAST score 245
E value 1.0e-20
Match length 86
% identity 56

NCBI Description (AL021713) unknown protein [Arabidopsis thaliana]



```
67717 1.R1040
Contig ID
                  LIB3109-015-Q1-K1-E12
5'-most EST
Method
                  BLASTX
NCBI GI
                  q2582381
BLAST score
                  371
                  1.0e-35
E value
                  132
Match length
% identity
                  61
                  (AF021220) cation-chloride co-transporter [Nicotiana
NCBI Description
                  19510
Seq. No.
                  67728 1.R1040
Contig ID
5'-most EST
                  LIB3109-015-Q1-K1-F4
```

Method BLASTX q3738297 NCBI GI BLAST score 321 2.0e-29 E value 193 Match length G) % identity

NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]

19511 Seq. No. 67732 1.R1040 Contig ID 5'-most EST LIB3109-015-Q1-K1-F9 BLASTX Method

g1477480 NCBI GI 1297 BLAST score 1.0e-143 E value 325 Match length 43 % identity

(U40341) carbamoyl phosphate synthetase large chain NCBI Description

[Arabidopsis thaliana]

Seq. No. 19512

Contig ID 67744\_1.R1040

5'-most EST uC-gmrominsoy311g07b1

Method BLASTX q529707 NCBI GI BLAST score 308 8.0e-28 E value 157 Match length % identity 42

NCBI Description (U13070) No definition line found [Caenorhabditis elegans]

19513 Seq. No.

67763 1.R1040 Contig ID 5'-most EST ssr700555120.h1

Method BLASTX NCBI GI q4056482 BLAST score 841 2.0e-91 E value Match length 285 % identity 31

NCBI Description (AC005896) putative ABC transporter [Arabidopsis thaliana]



67771 1.R1040 Contig ID 5'-most EST jC-qmf102220069g07a1 Method BLASTX g2129604 NCBI GI 637 BLAST score 2.0e-66 E value Match length 151 % identity 78 NCBI Description GTP-binding protein 1 - Arabidopsis thaliana >gi\_2129607\_pir\_\_S71584 GTP-binding protein ATBG1 -Arabidopsis thaliana >gi\_1184981 (U46924) ATGB1 [Arabidopsis thaliana] 19515 Seq. No. 67780 1.R1040 Contig ID LIB3109-016-Q1-K3-D4 5'-most EST BLASTX Method NCBI GI q4432844 BLAST score 281 9.0e-25 E value Match length 118 50 % identity NCBI Description (AC006283) unknown protein [Arabidopsis thaliana] 19516 Seq. No. 67810 1.R1040 Contig ID 5'-most EST LIB3109-018-Q1-K1-A3 Seq. No. 19517 Contig ID 67823 1.R1040 5'-most EST LIB3109-018-Q1-K1-B5 19518 Seq. No. 67827 1.R1040 Contig ID 5'-most EST ncj700985818.h1 19519 Seq. No. 67832 1.R1040 Contig ID LIB3109-018-Q1-K1-D1 5'-most EST 19520 Seq. No. 67841 1.R1040 Contig ID LIB3109-018-Q1-K1-D7 5'-most EST 19521 Seq. No. 67865 1.R1040 Contig ID LIB3109-019-Q1-K1-D2 5'-most EST 19522 Seq. No. 67874 1.R1040 Contig ID

Seq. No. 19522
Contig ID 67874 1.R1040
5'-most EST fde700876716.h1
Method BLASTX
NCBI GI g1346875
BLAST score 357
E value 1.0e-33

112

58

Match length

% identity



NCBI Description PHOTOSYSTEM II REACTION CENTRE W PROTEIN

>gi 1185169 emb\_CAA91652\_ (Z67753) PSII, protein W, 13 kDa

[Odontella sinensis]

Seq. No. 19523

Contig ID 67877 1.R1040

5'-most EST LIB3109-045-Q1-K1-H8

Seq. No. 19524

Contig ID 67884\_1.R1040 5'-most EST wvk700683989.h1

Seq. No. 19525

Contig ID 67890\_1.R1040 5'-most EST zzp700835191.h1

Method BLASTX
NCBI GI g2493318
BLAST score 346
E value 3.0e-32
Match length 121
% identity 60

NCBI Description BLUE COPPER PROTEIN PRECURSOR >gi\_562779\_emb\_CAA80963\_

(Z25471) blue copper protein [Pisum sativum]

>gi 1098264 prf\_\_2115352A blue Cu protein [Pisum sativum]

Seq. No. 19526

Contig ID 67899 1.R1040

5'-most EST uC-gmronoir038c11b1

Method BLASTX
NCBI GI g2651303
BLAST score 475
E value 1.0e-47
Match length 111
% identity 82

NCBI Description (AC002336) putative potassium transporter [Arabidopsis

thaliana]

Seq. No. 19527

Contig ID 67903 1.R1040

5'-most EST LIB3109-019-Q1-K1-H10

Seq. No. 19528

Contig ID 67909 1.R1040 5'-most EST asn701131574.h1

Method BLASTX
NCBI GI g1402890
BLAST score 341
E value 1.0e-31
Match length 120
% identity 56

NCBI Description (X98130) unknown [Arabidopsis thaliana]

Seq. No. 19529

Contig ID 67913\_1.R1040

5'-most EST LIB3109-020-Q1-K1-E4



Contig ID 67917\_1.R1040 5'-most EST sat701012764.h1

Method BLASTX
NCBI GI g4567281
BLAST score 195
E value 7.0e-15
Match length 70
% identity 59

NCBI Description (AC006841) unknown protein [Arabidopsis thaliana]

Seq. No. 19531

Contig ID 67917\_2.R1040

5'-most EST LIB3109-020-Q1-K1-E9

Method BLASTX
NCBI GI g4567281
BLAST score 186
E value 7.0e-14
Match length 70
% identity 57

NCBI Description (AC006841) unknown protein [Arabidopsis thaliana]

Seq. No. 19532

Contig ID 67927 1.R1040

5'-most EST LIB3109-020-Q1-K1-G1

Seq. No. 19533

Contig ID 67928 1.R1040

5'-most EST LIB3109-016-Q1-K1-F9

Method BLASTX
NCBI GI g112800
BLAST score 171
E value 4.0e-12
Match length 144
% identity 31

NCBI Description 4-COUMARATE--COA LIGASE 1 (4CL) >gi\_82059\_pir\_\_S01667 4-coumarate--CoA ligase (EC 6.2.1.12) (clone pc4CL-1) -

parsley >gi 20432 emb CAA31696 (X13324) 4-coumarate:CoA

ligase Pc4Cl-1 (AA 1-544) [Petroselinum crispum]

Seq. No. 19534

Contig ID 67987\_1.R1040 5'-most EST gsv701052052.h1

Method BLASTX
NCBI GI g3046821
BLAST score 713
E value 3.0e-75
Match length 204
% identity 72

NCBI Description (AB004785) homeobox gene [Nicotiana tabacum]

Seq. No. 19535

Contig ID 67995\_1.R1040 5'-most EST hyd700728779.h1

Method BLASTX
NCBI GI g3290209
BLAST score 572
E value 7.0e-59



Match length 149 % identity 75

NCBI Description (U78947) MADS-box protein 1 [Malus domestica]

Seq. No. 19536

Contig ID 68009\_1.R1040 5'-most EST fde700877202.h1

Seq. No. 19537

Contig ID 68026\_1.R1040 5'-most EST pmv700889988.h1

Method BLASTN
NCBI GI 94454587
BLAST score 34
E value 1.0e-09
Match length 209
% identity 88

NCBI Description Arabidopsis thaliana BAC F21A20 from chromosome V near 61

cM, complete sequence [Arabidopsis thaliana]

Seq. No. 19538

Contig ID 68027 1.R1040

5'-most EST LIB3138-008-Q1-N1-D2

Method BLASTX
NCBI GI g3668089
BLAST score 384
E value 4.0e-38
Match length 122
% identity 70

NCBI Description (AC004667) unknown protein [Arabidopsis thaliana]

Seq. No. 19539

Contig ID 68036 1.R1040

5'-most EST LIB3109-027-Q1-K1-B12

Method BLASTX
NCBI GI g3850108
BLAST score 259
E value 3.0e-31
Match length 181
% identity 43

NCBI Description (AL033388) putative calcium-transporting atpase

[Schizosaccharomyces pombe]

Seq. No. 19540

Contig ID 68038\_1.R1040 5'-most EST gsv701047339.h1

Method BLASTX
NCBI GI g3702352
BLAST score 197
E value 4.0e-15
Match length 55
% identity 75

NCBI Description (AC005397) putative mitochondrial carrier protein

[Arabidopsis thaliana]

Seq. No. 19541

Contig ID 68054 1.R1040



seb700648582.h1 5'-most EST BLASTX Method g4218991 NCBI GI BLAST score 824 2.0e-90 E value 363 Match length 49 % identity (AF098632) subtilisin-like protease [Arabidopsis thaliana] NCBI Description 19542 Seq. No. 68059 1.R1040 Contig ID LIB3109-028-Q1-K1-B5 5'-most EST BLASTX Method g4104931 NCBI GI BLAST score 735 3.0e-78 E value 158 Match length 87 % identity (AF042196) auxin response factor 8 [Arabidopsis thaliana] NCBI Description 19543 Seq. No. 68077 1.R1040 Contia ID LIB3109-028-Q1-K1-D10 5'-most EST 19544 Seq. No. 68077 2.R1040 Contig ID  $asn70\overline{1}136040.h1$ 5'-most EST 19545 Seq. No. 68078 1.R1040 Contig ID kl1701206359.h1 5'-most EST BLASTX Method g4262229 NCBI GI 499 BLAST score 2.0e-50 E value 153 Match length % identity (AC006200) unknown protein [Arabidopsis thaliana] NCBI Description 19546 Seq. No. 68092 1.R1040 Contig ID awf700837647.h1 5'-most EST BLASTX Method g2281093 NCBI GI 1651 BLAST score 0.0e+00E value 345 Match length 86 % identity NCBI Description (AC002333) beta transducin isolog [Arabidopsis thaliana] Seq. No. 19547 68092 2.R1040 Contig ID

gsv701055204.h1 5'-most EST

BLASTX Method NCBI GI g2281093 BLAST score 188 2.0e-14 E value



Match length 52 % identity 71

NCBI Description (AC002333) beta transducin isolog [Arabidopsis thaliana]

Seq. No. 19548

Contig ID 68096\_1.R1040 5'-most EST fua701038773.h1

Method BLASTX
NCBI GI g1351438
BLAST score 237
E value 8.0e-20
Match length 131
% identity 44

NCBI Description XANTHINE DEHYDROGENASE (XD) (CONTAINS: XANTHINE OXIDASE (XO)) >gi\_2144325\_pir\_XOCHDH xanthine dehydrogenase (EC

(XO)) >g1\_2144325\_p1r\_\_XOCHDH Xanthine denydrogenase (16 1.1.1.204) - chicken >g1\_507880\_dbj\_BAA02502\_ (D13221)

xanthine dehydrogenase [Gallus gallus]

Seq. No. 19549

Contig ID 68103 1.R1040

5'-most EST LIB3109-029-Q1-K1-C4

Method BLASTX
NCBI GI g3738323
BLAST score 625
E value 7.0e-65
Match length 173
% identity 65

NCBI Description (AC005170) hypothetical protein [Arabidopsis thaliana]

Seq. No. 19550

Contig ID 68118\_1.R1040

5'-most EST jC-gmf102220114f05a1

Seq. No. 19551

Contig ID 68120\_1.R1040 5'-most EST ncj700985801.h1

Seq. No. 19552

Contig ID 68120\_2.R1040 5'-most EST smc700747093.h1

Seq. No. 19553

Contig ID 68124\_1.R1040 5'-most EST dpv701100312.h1

Seq. No. 19554

Contig ID 68126\_1.R1040 5'-most EST zhf700951917.h1

Method BLASTX
NCBI GI 94580455
BLAST score 326
E value 6.0e-56
Match length 248
% identity 56

NCBI Description (AC006081) unknown protein [Arabidopsis thaliana]



```
68127 1.R1040
Contig ID
                  LIB3109-029-Q1-K1-E6
5'-most EST
                  19556
Seq. No.
Contig ID
                   68130 1.R1040
                  LIB3109-029-Q1-K1-E9
5'-most EST
                  BLASTX
Method
                   q4263777
NCBI GI
BLAST score
                   378
                   2.0e-36
E value
Match length
                   105
% identity
                   (AC006068) putative serine carboxypeptidase II [Arabidopsis
NCBI Description
                   thaliana] >gi_4510391_gb_AAD21479.1_ (AC007017) putative
                   serine carboxypeptidase II [Arabidopsis thaliana]
                   19557
Seq. No.
                   68145 1.R1040
Contig ID
                   LIB3109-029-Q1-K1-G2
5'-most EST
                   19558
Seq. No.
                   68150 1.R1040
Contig ID
                   epx701110464.h1
5'-most EST
                   BLASTN
Method
                   g669095
NCBI GI
BLAST score
                   268
E value
                   1.0e-149
                   504
Match length
                   88
% identity
NCBI Description A.majus chloroplast psaB gene (wild type)
                   19559
Seq. No.
                   68151 1.R1040
Contig ID
                   LIB3109-031-Q1-K1-B8
5'-most EST
Seq. No.
                   19560
                   68159 1.R1040
Contig ID
                   LIB3109-031-Q1-K1-C6
5'-most EST
                   BLASTX
Method
                   g305323
NCBI GI
                   452
BLAST score
                   9.0e-45
E value
                   215
Match length
                   44
% identity
NCBI Description (L21171) malonyl CoA decarboxylase [Anser anser]
                   19561
Seq. No.
                    68161_1.R1040
Contig ID
                   sat70\overline{1}011094.h1
 5'-most EST
                   BLASTX
Method
                    g2213597
NCBI GI
BLAST score
                    258
                    3.0e-22
 E value
```

NCBI Description (AC000348) T7N9.17 [Arabidopsis thaliana]

83

61

Match length

% identity



Seq. No. 19562
Contig ID 68169 1.R1040
5'-most EST LIB3170-066-Q1-K1-F2
Seq. No. 19563
Contig ID 68170 1.R1040

Seq. No. 19564

5'-most EST

Contig ID 68179\_1.R1040 5'-most EST smc700747536.h1

Method BLASTX
NCBI GI g2829902
BLAST score 206
E value 1.0e-16
Match length 70
% identity 53

NCBI Description (AC002311) Putative sulphate transporter protein#protein

[Arabidopsis thaliana]

LIB3109-031-Q1-K1-D9

Seq. No. 19565

Contig ID 68179\_2.R1040

5'-most EST LIB3109-031-Q1-K1-E6

Method BLASTX
NCBI GI g2829902
BLAST score 291
E value 3.0e-26
Match length 106
% identity 67

NCBI Description (AC002311) Putative sulphate transporter protein#protein

[Arabidopsis thaliana]

Seq. No. 19566

Contig ID 68180 1.R1040

5'-most EST LIB3109-031-Q1-K1-E7

Method BLASTX
NCBI GI g3413719
BLAST score 212
E value 6.0e-17
Match length 128
% identity 47

NCBI Description (AC004747) unknown protein [Arabidopsis thaliana]

>gi 3643592 (AC005395) unknown protein [Arabidopsis

thaliana]

Seq. No. 19567

Contig ID 68186\_1.R1040 5'-most EST uC-gmropic015g05b1

Method BLASTX
NCBI GI g3451068
BLAST score 353
E value 2.0e-33
Match length 108
% identity 69

NCBI Description (AL031326) putative protein [Arabidopsis thaliana]



Contig ID 68190\_1.R1040 5'-most EST LIB3109-032-Q1-K1-C5

Seq. No. 19569

Contig ID 68192\_1.R1040

5'-most EST LIB3 $\overline{0}$ 9-032-Q1-K1-C7

Method BLASTX
NCBI GI g4337191
BLAST score 675
E value 6.0e-71
Match length 213
% identity 60

NCBI Description (AC006403) hypothetical protein [Arabidopsis thaliana]

Seq. No. 19570

Contig ID 68200\_1.R1040 5'-most EST fC-gmst700667092f4

Method BLASTX
NCBI GI g1174718
BLAST score 998
E value 1.0e-109
Match length 240
% identity 82

NCBI Description PUTATIVE RECEPTOR PROTEIN KINASE TMK1 PRECURSOR

>gi\_322579\_pir\_\_JQ1674 receptor protein kinase TMK1 (EC 2.7.1.-) precursor - Arabidopsis thaliana >gi\_166888

(L00670) protein kinase [Arabidopsis thaliana]

Seq. No. 19571

Contig ID 68217 1.R1040

5'-most EST LIB3109-032-Q1-K1-F12

Method BLASTX
NCBI GI g4115905
BLAST score 271
E value 4.0e-24
Match length 58
% identity 76

NCBI Description (AF072131) secondary xylem cellulose synthase [Populus

tremuloides]

Seq. No. 19572

Contig ID 68220\_1.R1040

5'-most EST LIB3109-056-Q1-K1-E1

Method BLASTX
NCBI GI g4455254
BLAST score 312
E value 1.0e-28
Match length 111
% identity 56

NCBI Description (AL035523) putative protein [Arabidopsis thaliana]

Seq. No. 19573

Contig ID 68221\_1.R1040 5'-most EST uaw700665929.h1

Method BLASTX
NCBI GI g2493910
BLAST score 513



```
3.0e-52
E value
Match length
                  140
% identity
                  69
NCBI Description CULLIN HOMOLOG 4B (CUL-4B) >gi 1381150 (U58091) Hs-CUL-4B
                  [Homo sapiens]
                  19574
Seq. No.
Contig ID
                  68231 1.R1040
5'-most EST
                  crh700855624.hl
                  BLASTX
Method
NCBI GI
                  q534982
BLAST score
                  154
E value
                  2.0e-10
Match length
                  107
% identity
NCBI Description (X75898) phosphoglucomutase [Spinacia oleracea]
                  19575
Seq. No.
                  68231 2.R1040
Contig ID
5'-most EST
                  LIB3109-050-Q1-K1-E8
                  19576
Seq. No.
Contig ID
                  68239 1.R1040
5'-most EST
                  dpv701103578.h1
Method
                  BLASTX
NCBI GI
                  g3914002
BLAST score
                  922
E value
                  1.0e-100
Match length
                  240
% identity
                  75
NCBI Description MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR >gi 2935279
                  (AF033862) Lon protease [Arabidopsis thaliana]
                  19577
Seq. No.
Contig ID
                  68241 1.R1040
5'-most EST
                  LIB3109-033-Q1-K1-E2
Seq. No.
                  19578
                  68250 1.R1040
Contig ID
5'-most EST
                  LIB3109-033-Q1-K1-F12
                  BLASTX
Method
NCBI GI
                  g1483150
BLAST score
                  599
                  3.0e-62
E value
Match length
                  145
                  78
% identity
NCBI Description (D84417) monodehydroascorbate reductase [Arabidopsis
                  thaliana]
                  19579
Seq. No.
Contig ID
                  68271 1.R1040
```

5'-most EST LIB3109-033-Q1-K1-H3

Method BLASTX
NCBI GI g731834
BLAST score 201
E value 2.0e-15
Match length 99



% identity 45

NCBI Description HYPOTHETICAL 41.9 KD PROTEIN IN SDS3-THS1 INTERGENIC REGION

>gi\_1077790\_pir\_\_S49797 hypothetical protein YIL083c yeast (Saccharomyces cerevisiae) >gi\_577131\_emb\_CAA86711.1\_

(Z46728) YI9910.13c, unknown orf, len: 365, CAI: 0.17

[Saccharomyces cerevisiae]

Seq. No. 19580

Contig ID 68271\_2.R1040 5'-most EST zsg701125806.h1

Seq. No. 19581

Contig ID 68291\_1.R1040 5'-most EST zhf700962583.h1

Method BLASTX
NCBI GI g4309760
BLAST score 473
E value 2.0e-47
Match length 105
% identity 88

NCBI Description (AC006217) unknown protein [Arabidopsis thaliana]

Seq. No. 19582

Contig ID 68293\_1.R1040 5'-most EST g5510276 Method BLASTX NCBI GI q4006886

BLAST score 800 E value 2.0e-85 Match length 259 % identity 60

NCBI Description (Z99708) putative protein [Arabidopsis thaliana]

Seq. No. 19583

Contig ID 68308\_1.R1040

5'-most EST LIB3109-035-Q1-K1-B3

Method BLASTX
NCBI GI g4512702
BLAST score 618
E value 2.0e-64
Match length 142
% identity 80

NCBI Description (AC006569) hypothetical protein [Arabidopsis thaliana]

Seq. No. 19584

Contig ID 68313 1.R1040

5'-most EST LIB3109-035-Q1-K1-C1

Seq. No. 19585

Contig ID 68315\_1.R1040 5'-most EST gsv701050261.h1

Seq. No. 19586

Contig ID 68316\_1.R1040 5'-most EST uxk700673288.h1



68324 1.R1040 Contig ID uC-gmronoir006g07b1 5'-most EST Method BLASTX g4539306 NCBI GI 765 BLAST score 2.0e-81 E value 257 Match length 21 % identity NCBI Description (AL049480) pumilio-like protein [Arabidopsis thaliana] 19588 Seq. No. 68327 1.R1040 Contig ID LIB31 $\overline{0}$ 9-035-Q1-K2-D7 5'-most EST 19589 Seq. No. 68327 2.R1040 Contig ID g4289589 5'-most EST Method BLASTX g4056506 NCBI GI BLAST score 146 4.0e-13 E value 101 Match length 35 % identity (ACO05896) nodulin-like protein [Arabidopsis thaliana] NCBI Description 19590 Seq. No. 68327 3.R1040 Contig ID rry700808468.hl 5'-most EST Method BLASTX q4056506 NCBI GI 258 BLAST score 1.0e-31 E value 126 Match length 51 % identity (AC005896) nodulin-like protein [Arabidopsis thaliana] NCBI Description 19591 Seq. No. 68329 1.R1040 Contig ID fde700877250.h1 5'-most EST BLASTX Method g2160189 NCBI GI 469 BLAST score 5.0e-77 E value 206 Match length 70 % identity (AC000132) Similar to A. thaliana receptor-like protein NCBI Description kinase (gb\_RLK5\_ARATH). ESTs gb\_ATTS0475,gb\_ATTS4362 come from this gene. [Arabidopsis thaliana] 19592 Seq. No. 68337 1.R1040 Contig ID

wvk700679960.h2 5'-most EST

BLASTX Method g2465923 NCBI GI 611 BLAST score E value 1.0e-63 147 Match length



% identity 79

NCBI Description (AF024648) receptor-like serine/threonine kinase [Arabidopsis thaliana]

Seq. No. 19593

Contig ID 68339\_1.R1040

5'-most EST LIB3109-035-Q1-K4-E5

Method BLASTX
NCBI GI g3776559
BLAST score 469
E value 4.0e-47
Match length 103
% identity 83

NCBI Description (AC005388) Strong similarity to gene F14J9.26 gi 3482933

cdc2 protein kinase homolog from A. thaliana BAC

gb\_AC003970. ESTs gb\_Z35332 and gb\_F19907 come from this

gene. [Arabidopsis thaliana]

Seq. No. 19594

Contig ID 68353 1.R1040

5'-most EST LIB3109-035-Q1-K2-G5

Seq. No. 19595

Contig ID 68355\_1.R1040

5'-most EST LIB31 $\overline{0}$ 9-042-Q1-K1-D7

Method BLASTX
NCBI GI g3757521
BLAST score 689
E value 2.0e-72
Match length 250
% identity 57

NCBI Description (AC005167) unknown protein [Arabidopsis thaliana]

Seq. No. 19596

Contig ID 68359 1.R1040

5'-most EST LIB3109-035-Q1-K1-H3

Method BLASTX
NCBI GI g4567265
BLAST score 470
E value 3.0e-47
Match length 117
% identity 78

NCBI Description (AC006841) putative kinesin protein [Arabidopsis thaliana]

Seq. No. 19597

Contig ID 68410\_1.R1040 5'-most EST uC-gmropic111e09b1

Method BLASTX
NCBI GI g462147
BLAST score 1516
E value 1.0e-169
Match length 349
% identity 82

NCBI Description GLUCOSE-6-PHOSPHATE ISOMERASE, CYTOSOLIC (GPI)

(PHOSPHOGLUCOSE ISOMERASE) (PGI) (PHOSPHOHEXOSE ISOMERASE) (PHI) >gi\_541866\_pir\_\_S41808\_glucose-6-phosphate\_isomerase

(EC 5.3.1.9) - Arabidopsis thaliana



>gi\_415923\_emb\_CAA48940\_ (X69195) glucose-6-phosphate
isomerase [Arabidopsis thaliana]

Seq. No. 19598

Contig ID 68422 1.R1040

5'-most EST LIB3109-035-Q1-K6-G11

Seq. No. 19599

Contig ID 68487 1.R1040

5'-most EST uC-gmrominsoy226e02b1

Seq. No. 19600

Contig ID 68494 1.R1040

5'-most EST LIB3109-036-Q1-K1-F3

Method BLASTX
NCBI GI g3540186
BLAST score 405
E value 6.0e-39
Match length 178
% identity 53

NCBI Description (AC004122) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 19601

Contig ID 68500\_1.R1040 5'-most EST xpa700795132.h1

Seq. No. 19602

Contig ID 68501 1.R1040

5'-most EST LIB3109-036-Q1-K1-G12

Method BLASTX
NCBI GI g4376873
BLAST score 155
E value 7.0e-15
Match length 127
% identity 45

NCBI Description (AE001642) Pseudouridylate Synthase I [Chlamydia

pneumoniae]

Seq. No. 19603

Contig ID 68502\_1.R1040

5'-most EST LIB3109-036-Q1-K1-G3

Method BLASTX
NCBI GI g2224911
BLAST score 1110
E value 1.0e-122
Match length 247
% identity 85

NCBI Description (U93048) somatic embryogenesis receptor-like kinase [Daucus

carota]

Seq. No. 19604

Contig ID 68512 1.R1040 5'-most EST jsh70\overline{1}068376.h1

Seq. No. 19605

Contig ID 68519 1.R1040

5'-most EST uC-gmflminsoy001d10b1

NCBI Description



```
19606
Seq. No.
                  68519 2.R1040
Contig ID
                  ssr700559713.hl
5'-most EST
Method
                  BLASTX
                  q4454452
NCBI GI
                  436
BLAST score
                  7.0e-43
E value
                  138
Match length
                   62
% identity
                  (AC006234) unknown protein [Arabidopsis thaliana]
NCBI Description
                   19607
Seq. No.
                   68519 3.R1040
Contig ID
                   uC-gmronoir0001f04b1
5'-most EST
                   19608
Seq. No.
                   68522 1.R1040
Contig ID
                   zhf700961774.h1
5'-most EST
                   BLASTX
Method
                   g3402757
NCBI GI
                   321
BLAST score
                   2.0e-29
E value
                   156
Match length
                   41
% identity
                   (AL031187) receptor-like serine/threonine protein kinase
NCBI Description
                   ARK3 [Arabidopsis thaliana]
                   19609
Seq. No.
                   68526 1.R1040
Contig ID
                   jC-gmro02910017a12a1
5'-most EST
                   19610
Seq. No.
                   68528 1.R1040
Contig ID
                   LIB3170-072-Q1-J1-G10
5'-most EST
                   BLASTX
Method
                   q4415922
NCBI GI
                   131
BLAST score
                   1.0e-12
E value
                   105
Match length
                   41
 % identity
                   (AC006282) putative glucosyl transferase [Arabidopsis
 NCBI Description
                   thaliana]
                   19611
 Seq. No.
 Contig ID
                   68530 1.R1040
                   LIB3109-028-Q1-K1-A10
 5'-most EST
                   BLASTX
 Method
 NCBI GI
                   q140474
                   156
 BLAST score
 E value
                   2.0e-10
                   55
 Match length
                    49
 % identity
                   HYPOTHETICAL 69.2 KD PROTEIN IN HSP30-PMP1 INTERGENIC
```

YCR023c - yeast (Saccharomyces cerevisiae)

REGION >gi\_83212\_pir\_\_S19434 probable transport protein

>gi\_1907167\_emb\_CAA42315\_ (X59720) YCR023c, len:611



## [Saccharomyces cerevisiae]

```
19612
Seq. No.
Contig ID
                  68550 1.R1040
5'-most EST
                  jC-qmro02910006a10a1
Method
                  BLASTX
                  q3953465
NCBI GI
BLAST score
                  443
                  1.0e-43
E value
                  210
Match length
% identity
                  55
                  (AC002328) F20N2.10 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   19613
                   68563 1.R1040
Contig ID
5'-most EST
                   sat701015306.hl
Method
                  BLASTX
NCBI GI
                   g1351630
BLAST score
                   328
                   2.0e-30
E value
                   170
Match length
% identity
                   41
                   PROBABLE RNA 3'-TERMINAL PHOSPHATE CYCLASE
NCBI Description
                   (RNA-3'-PHOSPHATE CYCLASE) (RNA CYCLASE)
                   >gi 2130253_pir___S62537 hypothetical protein SPAC12G12.06c
                   - fission yeast (Schizosaccharomyces pombe)
                   >gi_1052524_emb_CAA91501_ (Z66568) SPAC12G12.06c, unknown,
                   len: 363 [Schizosaccharomyces pombe]
                   19614
Seq. No.
                   68567 1.R1040
Contig ID
                   LIB3109-038-Q1-K1-B6
5'-most EST
                   BLASTX
Method
                   g4335739
NCBI GI
                   203
BLAST score
                   1.0e-15
E value
                   106
Match length
                   42
% identity
                  (AC006248) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   19615
Seq. No.
                   68573 1.R1040
Contig ID
                   LIB3109-038-Q1-K1-C2
5'-most EST
                   BLASTX
Method
                   g3540184
NCBI GI
BLAST score
                   818
                   9.0e-88
E value
                   210
Match length
% identity
                  (AC004122) Similar to endoxylanases [Arabidopsis thaliana]
NCBI Description
                   19616
Seq. No.
```

Contig ID 68584 1.R1040

5'-most EST LIB3 $\overline{10}$ 9-041-Q1-K1-B9

Method BLASTX NCBI GI g1076414 BLAST score 199



3.0e-15 E value Match length 107 % identity 45

NCBI Description subtilisin-like proteinase (EC 3.4.21.-) - Arabidopsis thaliana (fragment) >gi\_757534\_emb\_CAA59963\_ (X85974)

subtilisin-like protease [Arabidopsis thaliana]

Seq. No. 19617

Contig ID 68585\_1.R1040

5'-most EST LIB3109-041-Q1-K1-C10

Method BLASTX NCBI GI g2961373 BLAST score 278 E value 2.0e-24 Match length 189 37 % identity

NCBI Description (AL022141) putative disease resistance protein [Arabidopsis

thaliana]

Seq. No. 19618

68588 1.R1040 Contig ID 5'-most EST  $zhf70\overline{0}961917.h1$ 

Method BLASTX NCBI GI g4539347 BLAST score 215 E value 5.0e-17 Match length 82 50 % identity

(AL035539) putative growth regulator protein [Arabidopsis NCBI Description

thaliana]

19619 Seq. No.

Contig ID 68588 2.R1040 5'-most EST g5606092

Seq. No. 19620

Contig ID 68592 1.R1040 5'-most EST leu701154687.h1

Seq. No. 19621

68595 1.R1040 Contig ID

5'-most EST LIB3109-041-Q1-K1-E12

Seq. No. 19622

68597 1.R1040 Contig ID 5'-most EST ssr700558855.hl

Method BLASTX NCBI GI g1946361 BLAST score 360 E value 4.0e-34 Match length 107 62 % identity

(U93215) C3HC4 zinc finger protein isolog [Arabidopsis NCBI Description

thaliana]

19623 Seq. No.

Contig ID 68605 1.R1040



```
uC-gmflminsoy011c04b1
5'-most EST
Seq. No.
                  19624
                  68618 1.R1040
Contig ID
                  uC-gmropic112f05b1
5'-most EST
                  BLASTX
Method
                  g3402699
NCBI GI
                  883
BLAST score
                  4.0e-95
E value
                  313
Match length
                  61
% identity
                  (AC004261) unknown protein [Arabidopsis thaliana]
NCBI Description
                  19625
Seq. No.
                  68623 1.R1040
Contig ID
                  sat701004935.hl
5'-most EST
                  BLASTX
Method
                  q4544412
NCBI GI
                  217
BLAST score
                   6.0e-17
E value
Match length
                  164
                   30
% identity
                  (AC006955) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   19626
Seq. No.
                   68623 2.R1040
Contig ID
                   rry700808322.h1
5'-most EST
                   19627
Seq. No.
                   68627 1.R1040
Contig ID
                   LIB3109-042-Q1-K1-B9
5'-most EST
                   BLASTN
Method
                   g3176077
NCBI GI
                   328
BLAST score
                   0.0e+00
E value
                   536
Match length
% identity
NCBI Description Medicago sativa mRNA for protein phosphatase 1, epsilon
                   subunit
                   19628
Seq. No.
                   68631 1.R1040
Contig ID
                   LIB3109-042-Q1-K1-H8
5'-most EST
                   19629
Seq. No.
                   68636 1.R1040
Contig ID
                   crh700852831.h1
 5'-most EST
                   19630
 Seq. No.
                   68636 2.R1040
 Contig ID
 5'-most EST
                   awf700840962.h1
```

19631 Seq. No.

68644 1.R1040 Contig ID

LIB3109-043-Q1-K1-B11 5'-most EST

BLASTX Method g2335097 NCBI GI

3173



```
BLAST score
                   1.0e-106
E value
Match length
                   252
% identity
                   19
                  (AC002339) putative receptor-like protein kinase
NCBI Description
                   [Arabidopsis thaliana]
                   19632
Seq. No.
                   68650 1.R1040
Contig ID
                   LIB31\overline{0}9-043-Q1-K1-C1
5'-most EST
                   BLASTX
Method
                   q3860264
NCBI GI
                   188
BLAST score
                   4.0e-14
E value
                   45
Match length
% identity
                   71
NCBI Description (AC005824) unknown protein [Arabidopsis thaliana]
                   19633
Seq. No.
                   68657 1.R1040
Contig ID
                   fde700873255.hl
5'-most EST
                   BLASTX
Method
                   g3273097
NCBI GI
                   209
BLAST score
                   2.0e-16
E value
Match length
                   160
                   35
% identity
NCBI Description (Y17040) recA/RAD51 family protein [Mus musculus]
                   19634
Seq. No.
                    68658 1.R1040
Contig ID
                    zhf70\overline{0}962518.h1
5'-most EST
                   BLASTX
Method
                    g4558673
NCBI GI
                    230
BLAST score
                    9.0e-19
E value
                    117
Match length
                    33
% identity
NCBI Description (AC007063) hypothetical protein [Arabidopsis thaliana]
                    19635
Seq. No.
                    68672 1.R1040
Contig ID
```

LIB3109-043-Q1-K1-E2 5'-most EST

19636 Seq. No.

68685 1.R1040 Contig ID

LIB3139-092-P1-N1-C6 5'-most EST

BLASTX Method NCBI GI g2281102 348 BLAST score E value 1.0e-32 139 Match length % identity

(AC002333) SF16 isolog [Arabidopsis thaliana] NCBI Description

19637 Seq. No.

68698\_1.R1040 Contig ID

Match length

NCBI Description

% identity

91

thaliana]



```
5'-most EST
                  LIB3109-044-Q1-K1-E10
                  19638
Seq. No.
                  68701 1.R1040
Contig ID
5'-most EST
                  LIB3170-033-Q1-K1-A9
Method
                  BLASTX
NCBI GI
                  q4210451
BLAST score
                  603
                  1.0e-62
E value
Match length
                  169
% identity
                  (AB016472) ARR2 protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  19639
Contig ID
                   68704 1.R1040
5'-most EST
                  jC-gmro02910010f08a1
                  19640
Seq. No.
                   68706 1.R1040
Contig ID
5'-most EST
                  LIB3109-044-Q1-K1-F1
                   19641
Seq. No.
Contig ID
                   68712 1.R1040
5'-most EST
                  LIB3109-044-Q1-K1-H4
                   19642
Seq. No.
Contig ID
                   68715 1.R1040
5'-most EST
                  gsv701046534.hl
Seq. No.
                   19643
                   68723 1.R1040
Contig ID
5'-most EST
                   sat701003664.hl
Method
                  BLASTX
                   g3859659
NCBI GI
BLAST score
                   869
E value
                   2.0e-93
Match length
                   279
% identity
                   63
                  (AL031394) putative potassium transporter AtKT5p (AtKT5)
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   19644
                   68740 1.R1040
Contig ID
5'-most EST
                   LIB3109-045-Q1-K1-F2
                   19645
Seq. No.
                   68746 1.R1040
Contig ID
5'-most EST
                   LIB3109-045-Q1-K1-F9
Method
                   BLASTX
                   g3894193
NCBI GI
BLAST score
                   154
E value
                   2.0e-12
```

(AC005662) putative strictosidine synthase [Arabidopsis



Seq. No. 19646

Contig ID 68753\_1.R1040 5'-most EST hrw701058472.h1

Method BLASTX
NCBI GI 94415942
BLAST score 1311
E value 1.0e-145
Match length 397
% identity 66

NCBI Description (AC006418) hypothetical protein [Arabidopsis thaliana]

Seq. No. 19647

Contig ID 68753\_2.R1040 5'-most EST ncj700984982.h1 Method BLASTX

Method BLASTX
NCBI GI g4415942
BLAST score 148
E value 9.0e-10
Match length 34
% identity 79

NCBI Description (AC006418) hypothetical protein [Arabidopsis thaliana]

Seq. No. 19648

Contig ID 68771\_1.R1040 5'-most EST zhf700963253.h1

Method BLASTX
NCBI GI g4262235
BLAST score 466
E value 3.0e-46
Match length 164
% identity 55

NCBI Description (AC006200) putative transcription factor [Arabidopsis

thaliana]

Seq. No. 19649

Contig ID 68774\_1.R1040 5'-most EST pmv700889519.h1

Seq. No. 19650

Contig ID 68775 1.R1040

5'-most EST LIB3109-046-Q1-K1-A5

Seq. No. 19651

Contig ID 68784\_1.R1040 5'-most EST ssr700553552.h1

Method BLASTX
NCBI GI g2760830
BLAST score 328
E value 1.0e-30
Match length 85
% identity 75

NCBI Description (AC003105) putative beta-ketoacyl-CoA synthase [Arabidopsis

thaliana]

Seq. No. 19652

Contig ID 68800 1.R1040 5'-most EST zhf700961686.h1

Method

NCBI GI

E value

BLAST score

BLASTX

233

q4455309

2.0e-19



```
19653
Seq. No.
                  68810 1.R1040
Contig ID
                  eep700867996.hl
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3947735
BLAST score
                  259
E value
                  7.0e-22
Match length
                  241
% identity
                  32
NCBI Description (AJ009720) NL27 [Solanum tuberosum]
                  19654
Seq. No.
Contig ID
                  68814 1.R1040
5'-most EST
                  LIB3109-045-Q1-K1-E11
Method
                  BLASTX
NCBI GI
                  g3327196
BLAST score
                  460
E value
                  9.0e-46
Match length
                  147
% identity
                   62
                  (AB014591) KIAA0691 protein [Homo sapiens]
NCBI Description
                  19655
Seq. No.
Contig ID
                  68814 2.R1040
5'-most EST
                  uC-gmflminsoy018f09b1
                  BLASTX
Method
                  g3327196
NCBI GI
BLAST score
                   504
                   5.0e-51
E value
Match length
                  164
% identity
                   60
NCBI Description
                  (AB014591) KIAA0691 protein [Homo sapiens]
Seq. No.
                   19656
                   68819 1.R1040
Contig ID
5'-most EST
                  pcp700994038.h1
                  19657
Seq. No.
                   68833 1.R1040
Contig ID
5'-most EST
                  LIB3109-047-Q1-K1-H8
Seq. No.
                  19658
Contig ID
                   68848 1.R1040
5'-most EST
                  art700605356.h2
Seq. No.
                   19659
                   68848 2.R1040
Contig ID
5'-most EST
                  LIB3109-048-Q1-K1-B12
                  19660
Seq. No.
                   68852 1.R1040
Contig ID
5'-most EST
                  zsg701121257.hl
```

3177



Match length 89 % identity 56

NCBI Description (AL035528) hypothetical protein [Arabidopsis thaliana]

Seq. No. 19661

Contig ID 68852\_2.R1040 5'-most EST xpa700793868.h1

Method BLASTN
NCBI GI g4097879
BLAST score 54
E value 1.0e-21
Match length 106
% identity 88

NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein

gene, complete cds

Seq. No. 19662

Contig ID 68860 1.R1040 5'-most EST fua701039462.h1

Method BLASTX
NCBI GI g2739168
BLAST score 270
E value 1.0e-23
Match length 121
% identity 47

NCBI Description (AF032386) aldose-1-epimerase-like protein [Nicotiana

tabacum]

Seq. No. 19663

Contig ID 68860\_2.R1040

5'-most EST LIB3109-048-Q1-K1-C4

Seq. No. 19664

Contig ID 68863\_1.R1040

5'-most EST LIB3109-048-Q1-K1-C7

Seq. No. 19665

Contig ID 68877 1.R1040

5'-most EST LIB3109-050-Q1-K1-B8

Seq. No. 19666

Contig ID 68893\_1.R1040 5'-most EST uC-gmropic090c02b1

Method BLASTX
NCBI GI g2827637
BLAST score 196
E value 7.0e-15
Match length 104
% identity 38

NCBI Description (AL021636) putative protein [Arabidopsis thaliana]

Seq. No. 19667

Contig ID 68922 1.R1040

5'-most EST LIB3109-052-Q1-K1-D6

Method BLASTX
NCBI GI g4508069
BLAST score 503



E value 5.0e-51 Match length 142 % identity 61

NCBI Description (AC005882) 12246 [Arabidopsis thaliana]

Seq. No. 19668

Contig ID 68935 1.R1040

5'-most EST LIB3139-034-P1-N1-D9

Seq. No. 19669

Contig ID 68939 1.R1040

5'-most EST LIB3109-052-Q1-K1-F5

Seq. No. 19670

Contig ID 68942\_1.R1040

5'-most EST LIB3 $\overline{109}$ -052-Q1-K1-F9

Seq. No. 19671

Contig ID 68944\_1.R1040 5'-most EST kl1701213119.h1

Seq. No. 19672

Contig ID 68951\_1.R1040

5'-most EST LIB3109-056-Q1-K1-H1

Method BLASTX
NCBI GI g1652217
BLAST score 176
E value 1.0e-12
Match length 55
% identity 56

NCBI Description (D90903) hypothetical protein [Synechocystis sp.]

Seq. No. 19673

Contig ID 68951\_2.R1040 5'-most EST kmv700740647.h1

Method BLASTX
NCBI GI g1652217
BLAST score 327
E value 3.0e-30
Match length 133
% identity 50

NCBI Description (D90903) hypothetical protein [Synechocystis sp.]

Seq. No. 19674

Contig ID 68955\_1.R1040

5'-most EST LIB3109-052-Q1-K1-H6

Method BLASTX
NCBI GI g2499466
BLAST score 158
E value 3.0e-10
Match length 91
% identity 38

NCBI Description PHOSPHOENOLPYRUVATE CARBOXYLASE (PEPCASE)

>gi\_1086118\_pir\_\_S37072 phosphoenolpyruvate carboxylase (EC
4.1.1.31) - Flaveria australasica >gi\_397915\_emb\_CAA81072\_

(Z25853) phosphoenolpyruvate carboxylase [Flaveria

australasica]



19675 Seq. No. Contig ID 68965 1.R1040 uC-gmropic009c03b1 5'-most EST 19676 Seq. No. 68974 1.R1040 Contig ID dpv701097132.hl 5'-most EST BLASTX Method g4455359 NCBI GI 608 BLAST score 3.0e-63 E value 165 Match length 74 % identity (AL035524) putative protein [Arabidopsis thaliana] NCBI Description 19677 Seq. No. 68974 2.R1040 Contig ID LIB3109-054-Q1-K1-B7 5'-most EST BLASTN Method g2656031 NCBI GI BLAST score 59 3.0e-24 E value 115 Match length 88 % identity Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MXC20 19678 Seq. No. 68976 1.R1040 Contig ID LIB3109-054-Q1-K1-B9 5'-most EST BLASTX Method g4262234 NCBI GI 227 BLAST score 1.0e-18 E value Match length 63 70 % identity (AC006200) unknown protein [Arabidopsis thaliana] NCBI Description 19679 Seq. No. 68981 1.R1040 Contig ID LIB3109-054-Q1-K1-C2 5'-most EST 19680 Seq. No. 68992 1.R1040 Contig ID g5126989 5'-most EST BLASTX Method

Contig ID 68992\_1.R1040
5'-most EST g5126989
Method BLASTX
NCBI GI g4557060
BLAST score 844
E value 1.0e-90

Match length 271 % identity 76

NCBI Description (AC007154) putative chromosome-associated polypeptide, 5'

partial [Arabidopsis thaliana]

Seq. No. 19681

Contig ID 68995\_1.R1040



zpv700762911.h1 5'-most EST 19682 Seq. No. Contig ID 69005 1.R1040 5'-most EST fde700872722.h1 19683 Seq. No. 69006 1.R1040 Contig ID crh700850315.h15'-most EST BLASTX Method NCBI GI g1369852 731 BLAST score 2.0e-77 E value 239 Match length % identity NCBI Description (L46702) kinesin heavy chain-like protein [Solanum tuberosum] 19684 Seq. No. Contig ID 69015 1.R1040 uC-gmronoir045f06b1 5'-most EST 19685 Seq. No. 69016 1.R1040 Contig ID LIB3109-054-Q1-K1-G9 5'-most EST Seq. No. 19686 69053 1.R1040 Contig ID 5'-most EST pxt700944748.hl 19687 Seq. No. Contig ID 69063 1.R1040 LIB3109-056-Q1-K1-B5 5'-most EST 19688 Seq. No. 69066\_1.R1040 Contig ID uC-gmrominsoy294a02b1 5'-most EST BLASTX Method g4056493 NCBI GI 351 BLAST score 5.0e-33 E value 188 Match length 40 % identity NCBI Description (AC005896) unknown protein [Arabidopsis thaliana] 19689 Seq. No. 69072 1.R1040 Contig ID LIB3109-057-Q1-K1-B3 5'-most EST BLASTX Method g4262225 NCBI GI BLAST score 232 3.0e-19 E value 88 Match length 48 % identity (AC006200) putative phosphatidic acid phosphatase NCBI Description

[Arabidopsis thaliana]



Seq. No. 19690

Contig ID 69075\_1.R1040

5'-most EST jC-gmle01810077e11a1

Seq. No. 19691

Contig ID 69094 1.R1040 5'-most EST fde700876954.h1

Method BLASTX
NCBI GI g3850583
BLAST score 197
E value 3.0e-15
Match length 52
% identity 71

NCBI Description (AC005278) Contains similarity to transcription initiation

factor IIE, alpha subunit gb\_X63468 from Homo sapiens.

[Arabidopsis thaliana]

Seq. No. 19692

Contig ID 69099\_1.R1040

5'-most EST LIB3139-036-P1-N1-G6

Method BLASTX
NCBI GI g2827700
BLAST score 110
E value 6.0e-13
Match length 62
% identity 69

NCBI Description (AL021684) DEAD box ATP dependent helicase protein

[Arabidopsis thaliana]

Seq. No. 19693

Contig ID 69108\_1.R1040

5'-most EST LIB3109-016-Q1-K1-D12

Seq. No. 19694

Contig ID 69110\_1.R1040 5'-most EST leu701145604.h1

Method BLASTX
NCBI GI g3047124
BLAST score 562
E value 2.0e-57
Match length 235
% identity 51

NCBI Description (AF058919) No definition line found [Arabidopsis thaliana]

Seq. No. 19695

Contig ID 69110\_2.R1040

5'-most EST jC-gmro02910066f10a1

Method BLASTX
NCBI GI g3047101
BLAST score 369
E value 5.0e-35
Match length 162
% identity 46

NCBI Description (AF058919) Similar to protein kinase; coded for by A.

thaliana cDNA H36947; coded for by A. thaliana cDNA H37158

[Arabidopsis thaliana]



Seq. No. 19696

Contig ID 69110\_3.R1040

5'-most EST jC-gmle01810045c11d1

Seq. No. 19697

Contig ID 69111\_1.R1040

5'-most EST LIB3109-057-Q1-K1-G1

Seq. No. 19698

Contig ID 69115\_1.R1040

5'-most EST LIB3109-057-Q1-K1-G4

Method BLASTX
NCBI GI g2252847
BLAST score 291
E value 2.0e-29
Match length 98
% identity 73

NCBI Description (AF013293) No definition line found [Arabidopsis thaliana]

Seq. No. 19699

Contig ID 69127\_1.R1040

5'-most EST LIB3109-048-Q1-K1-A4

Seq. No. 19700

Contig ID 69136\_1.R1040

5'-most EST LIB3109-011-Q1-K1-C12

Method BLASTN
NCBI GI g3255942
BLAST score 171
E value 6.0e-91
Match length 454
% identity 85

NCBI Description Catharanthus roseus mRNA for type 2A Ser/Thr protein

phosphatase

Seq. No. 19701

Contig ID 69144\_1.R1040

5'-most EST LIB3109-035-Q1-K4-B10

Seq. No. 19702

Contig ID 69155\_1.R1040

5'-most EST LIB3109-001-Q1-K4-E5

Method BLASTX
NCBI GI 94455304
BLAST score 289
E value 6.0e-26
Match length 97
% identity 61

NCBI Description (AL035528) hypothetical protein [Arabidopsis thaliana]

Seq. No. 19703

Contig ID 69163\_1.R1040

5'-most EST LIB3109-001-Q1-K4-F4

Method BLASTX
NCBI GI g2244876
BLAST score 473
E value 1.0e-47



Match length 77 % identity

NCBI Description (Z97338) hypothetical protein [Arabidopsis thaliana]

Seq. No. Contig ID

19704 69182 1.R1040

5'-most EST

LIB3109-001-Q1-K4-H2

Seq. No.

19705

Contig ID

69187 1.R1040

5'-most EST

LIB3109-001-Q1-K2-A2

Method NCBI GI BLASTX g2598575 231

BLAST score E value

6.0e-19 145

Match length % identity

33

NCBI Description (Y15293) MtN21 [Medicago truncatula]

Seq. No.

19706

Contig ID

69210 1.R1040

5'-most EST

LIB3109-001-Q1-K4-D8

Seq. No.

19707

Contig ID

69255 1.R1040

5'-most EST

LIB3109-002-Q1-K3-G9

Seq. No.

19708

Contig ID

69369 1.R1040

5'-most EST

LIB3170-031-Q1-J1-C9

Seq. No.

19709

Contig ID

69369\_2.R1040

5'-most EST Method

q5509340 BLASTN

NCBI GI

g3241927

BLAST score E value

40 4.0e-13

Match length

128

% identity

88

NCBI Description

Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:

MTE17, complete sequence [Arabidopsis thaliana]

Seq. No.

19710

Contig ID 5'-most EST 69377 1.R1040 zsg701126406.hl

Seq. No.

19711

Contig ID

69377 2.R1040

5'-most EST

jC-gmf102220060g10a1

Seq. No.

19712

932

Contig ID

69381 1.R1040

5'-most EST

jC-gmro02910051h11a1

Method

BLASTX

NCBI GI

BLAST score

g3242789



E value 1.0e-106 Match length 288 % identity 64

NCBI Description (AF055357) respiratory burst oxidase protein D [Arabidopsis

thaliana]

Seq. No. 19713

Contig ID 69385\_1.R1040

5'-most EST LIB3109-005-Q1-K1-G4

Method BLASTX
NCBI GI g2781363
BLAST score 201
E value 3.0e-15
Match length 148
% identity 40

NCBI Description (AC003113) F2401.19 [Arabidopsis thaliana]

Seq. No. 19714

Contig ID 69386\_1.R1040 5'-most EST smc700746318.h1

Method BLASTX
NCBI GI g2924509
BLAST score 724
E value 1.0e-76
Match length 216
% identity 64

NCBI Description (AL022023) subtilisin proteinase - like [Arabidopsis

thaliana]

Seq. No. 19715

Contig ID 69391 1.R1040 5'-most EST fua701041082.h1

Seq. No. 19716

Contig ID 69405\_2.R1040

5'-most EST LIB3138-123-Q1-N1-E1

Method BLASTX
NCBI GI g1617274
BLAST score 471
E-value 3.0e-47
Match length 127
% identity 69

NCBI Description (Z72152) AMP-binding protein [Brassica napus]

Seq. No. 19717

Contig ID 69412\_1.R1040 5'-most EST zsg701126292.h1

Seq. No. 19718

Contig ID 69433 1.R1040

5'-most EST LIB3109-007-Q1-K1-A4

Method BLASTX
NCBI GI g3885339
BLAST score 390
E value 1.0e-37
Match length 141
% identity 52



NCBI Description (AC005623) putative bzip protein [Arabidopsis thaliana]

Seq. No. 19719

Contig ID 69441 1.R1040

5'-most EST LIB3109-007-Q1-K1-F12

Method BLASTN
NCBI GI g507251
BLAST score 129
E value 3.0e-66
Match length 229
% identity 99

NCBI Description Human ferritin heavy chain mRNA, complete cds

Seq. No. 19720

Contig ID 69450\_1.R1040 5'-most EST zsg701120628.h1

Method BLÄSTX
NCBI GI g2129755
BLAST score 591
E value 4.0e-61
Match length 175
% identity 70

NCBI Description tryptophan synthase (EC 4.2.1.20) alpha chain - Arabidopsis

thaliana >gi\_619753 (U18993) tryptophan synthase alpha chain [Arabidopsis thaliana] >gi\_1585768\_prf\_\_2201482A Trp

synthase:SUBUNIT=alpha [Arabidopsis thaliana]

Seq. No. 19721

Contig ID 69456 1.R1040

5'-most EST LIB3109-007-Q1-K1-D4

Seq. No. 19722

Contig ID 69465\_1.R1040 5'-most EST pxt700943173.h1

Method BLASTX
NCBI GI g3327868
BLAST score 303
E value 2.0e-27
Match length 122
% identity 58

NCBI Description (AB012912) COP1-Interacting Protein 7 (CIP7) [Arabidopsis

thaliana]

Seq. No. 19723

Contig ID 69475\_1.R1040 5'-most EST vwf700678492.h1

Method BLASTX
NCBI GI g4185129
BLAST score 353
E value 2.0e-33
Match length 165
% identity 47

NCBI Description (AC005724) unknown protein [Arabidopsis thaliana]

>gi\_4218012 (AC006135) unknown protein [Arabidopsis

thaliana]

Seq. No. 19724



```
Contig ID
                  69476 1.R1040
5'-most EST
                  LIB3109-007-Q1-K1-F8
                  BLASTX
Method
NCBI GI
                  q1931645
BLAST score
                  697
E value
                  2.0e-73
Match length
                  162
                  83
% identity
NCBI Description (U95973) Fe(II) transporter isolog [Arabidopsis thaliana]
                  19725
Seq. No.
                  69493 1.R1040
Contig ID
5'-most EST
                  LIB3109-009-Q1-K1-F1
Seq. No.
                  19726
Contig ID
                  69496 1.R1040
5'-most EST
                  LIB3109-009-Q1-K1-F2
Method
                  BLASTX
                  q3451474
NCBI GI
BLAST score
                  647
E value
                  1.0e-67
Match length
                  258
% identity
                  50
                 (AL031349) conserved hypothetical protein
NCBI Description
                  [Schizosaccharomyces pombe]
                  19727
Seq. No.
Contig ID
                  69504 1.R1040
5'-most EST
                  uC-gmrominsoy169c09b1
                  19728
Seq. No.
                  69508 1.R1040
Contig ID
5'-most EST
                  LIB3138-084-P1-N1-A7
Method
                  BLASTN
NCBI GI
                  g218327
BLAST score
                  435
E value
                  0.0e+00
Match length
                  882
% identity
                  87
NCBI Description Vigna angularis mRNA for peroxidase basic isozyme
                  (monomer), complete cds
Seq. No.
                  19729
                  69508 2.R1040
Contig ID
5'-most EST
                  q5687832
Method
                  BLASTN
NCBI GI
                  g218327
BLAST score
                  154
E value
                  4.0e-81
Match length
                  379
% identity
NCBI Description Vigna angularis mRNA for peroxidase basic isozyme
                  (monomer), complete cds
```

Seq. No. 19730

Contig ID 69509\_1.R1040 5'-most EST uC-gmropic064e01b1



19731 Seq. No. Contig ID 69523 1.R1040 5'-most EST rca700998774.hl Method BLASTX NCBI GI g2213907 BLAST score 307 E value 9.0e-28 Match length 221

NCBI Description (AF004837) putative vacuolar protein sorting homolog

[Aspergillus fumigatus]

Seq. No. 19732

Contig ID 69533\_1.R1040 5'-most EST uC-gmropic071f04b1

37

Method BLASTX
NCBI GI g2789434
BLAST score 381
E value 1.0e-36
Match length 98
% identity 70

NCBI Description (AB001389) CLB1 [Lycopersicon esculentum]

Seq. No.

% identity

Contig ID 69536\_1.R1040 5'-most EST zpv700758841.h1

19733

Method BLASTX
NCBI GI g1170619
BLAST score 405
E value 5.0e-39
Match length 243
% identity 47

NCBI Description KINESIN-LIKE PROTEIN A >gi\_479594\_pir\_ S34830

kinesin-related protein katA - Arabidopsis thaliana >qi 303502 dbj BAA01972 (D11371) kinesin-like motor

protein heavy chain [Arabidopsis thaliana]

>gi\_2911084\_emb\_CAA17546\_ (AL021960) kinesin-related

protein katA [Arabidopsis thaliana]

Seq. No. 19734

Contig ID 69548\_2.R1040 5'-most EST sat701005288.h1

Seq. No. 19735

Contig ID 69549\_1.R1040 5'-most EST pxt700946470.h1

Seq. No. 19736

Contig ID 69553\_1.R1040

5'-most EST LIB3109-011-Q1-K1-A6

Method BLASTX
NCBI GI g1730616
BLAST score 324
E value 1.0e-29
Match length 151
% identity 44



HYPOTHETICAL 32.4 KD PROTEIN IN TAF40-ERV25 INTERGENIC NCBI Description REGION >gi\_1084919\_pir\_\_S55105 hypothetical protein YML014w - yeast (Saccharomyces cerevisiae) >gi\_854476\_emb\_CAA89938\_

(Z49810) unknown [Saccharomyces cerevisiae]

Seq. No. 19737

69567 1.R1040 Contig ID 5'-most EST hrw701060783.hl

Method BLASTX NCBI GI q3928099 BLAST score 352 4.0e-33 E value 199 Match length 20 % identity

NCBI Description (AC005770) unknown protein [Arabidopsis thaliana]

Seq. No. 19738

Contig ID 69588 1.R1040 5'-most EST zzp700833171.h1

Method BLASTX NCBI GI q3914359 BLAST score 983 1.0e-111 E value 234 Match length % identity 84

PHOSPHOLIPASE D PRECURSOR (PLD) (CHOLINE PHOSPHATASE) NCBI Description

(PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D)

>gi\_1928979 (U92656) phospholipase D [Vigna unguiculata]

Seq. No. 19739

69590 1.R1040 Contig ID

5'-most EST jC-qmro02910038e09a1

Method BLASTX NCBI GI g2499872 185 BLAST score E value 3.0e-13 223 Match length 30 % identity

TRIPEPTIDYL-PEPTIDASE II (TPP II) (TRIPEPTIDYL NCBI Description

AMINOPEPTIDASE) >gi\_2137836\_pir\_\_I48855

tripeptidyl-peptidase II (EC 3.4.14.10) - mouse

>gi\_575955 emb\_CAA57103 (X81323) tripeptidyl-peptidase ii

[Mus musculus]

19740 Seq. No.

Contig ID 69590 2.R1040 5'-most EST zpv700758176.hl

Method BLASTX NCBI GI g136107 BLAST score 194 E value 8.0e-22 Match length 359 % identity 27

NCBI Description TRIPEPTIDYL-PEPTIDASE II (TPP II) (TRIPEPTIDYL

AMINOPEPTIDASE) >gi\_1082875\_pir\_\_S54376 tripeptidyl-peptidase II (EC 3.4.14.10) - human >gi\_339880

(M73047) tripeptidyl peptidase II [Homo sapiens]



>gi 4507657 ref NP 003282.1 pTPP2 tripeptidyl peptidase II

19741 Seq. No.

Contig ID 69592 1.R1040

5'-most EST LIB3109-012-Q1-K1-B8

Seq. No.

19742

Contig ID

69607 1.R1040

5'-most EST

LIB3109-012-Q1-K1-D6

Method BLASTX NCBI GI q416873 BLAST score 324 E value 1.0e-29 Match length 159 48

% identity

NCBI Description

3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR (HIBADH)

>gi\_111295\_pir\_\_A32867 3-hydroxyisobutyrate dehydrogenase (EC 1.1.1.31) precursor - rat (fragment) >gi 556389 (J04628) 3-hydroxyisobutyrate dehydrogenase [Rattus

norvegicus]

Seq. No. 19743

Contig ID

69621 1.R1040

5'-most EST LIB3138-065-Q1-N1-C2

Seq. No.

19744

Contig ID

69627 1.R1040

LIB3109-013-Q1-K1-E4 5'-most EST

Seq. No. 19745

Contig ID 69628 1.R1040 5'-most EST asn701133480.hl

Seq. No. 19746

69642 1.R1040 Contig ID 5'-most EST  $eep70\overline{0}866849.h1$ 

BLASTX Method NCBI GI q2499710 BLAST score 781 E value 1.0e-136 Match length 361

% identity 61

PHOSPHOLIPASE D PRECURSOR (PLD) (CHOLINE PHOSPHATASE) NCBI Description

(PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D)

>gi 1438075 (L33686) phospholipase D [Ricinus communis]

19747 Seq. No.

Contig ID 69643 1.R1040 5'-most EST ncj700978815.hl

Method BLASTX NCBI GI g3024371 BLAST score 156 E value 3.0e-10 Match length 114 38 % identity

PEROXIN-12 >gi\_1938367 (U91521) peroxin 12 [Homo sapiens] NCBI Description

>gi 1938369 (U91522) peroxin 12 [Homo sapiens]



>gi\_3308973\_dbj\_BAA31559\_ (AB004546) peroxisome assembly

factor-3 (PAF-3) [Homo sapiens]

>gi\_4505721\_ref\_NP\_000277.1\_pPEX12\_ peroxisomal biogenesis

factor

Seq. No. 19748

Contig ID 69666 1.R1040

5'-most EST LIB3109-014-Q1-K1-B2

Seq. No. 19749

Contig ID 69677 1.R1040

5'-most EST LIB3109-014-Q1-K1-H11

Seq. No. 19750

Contig ID 69680\_1.R1040

5'-most EST uC-gmflminsoy089c06b1

Method BLASTX
NCBI GI g114974
BLAST score 287
E value 9.0e-26
Match length 79
% identity 63

NCBI Description NON-CYANOGENIC BETA-GLUCOSIDASE PRECURSOR

>gi 67491 pir GLJY31 beta-glucosidase (EC 3.2.1.21)

precursor (clone TRE361) - white clover

>gi\_21955\_emb\_CAA40058.1 (X56734) beta-glucosidase

[Trifolium repens]

Seq. No. 19751

Contig ID 69681\_1.R1040

5'-most EST LIB3109-014-Q1-K1-H5

Method BLASTX
NCBI GI g3928862
BLAST score 142
E value 1.0e-08
Match length 87
% identity 38

NCBI Description (AF089710) disease resistance protein RPP8 [Arabidopsis

thaliana]

Seq. No. 19752

Contig ID 69698\_1.R1040

5'-most EST LIB3109-015-Q1-K1-B11

Method BLASTX
NCBI GI g1477468
BLAST score 141
E value 1.0e-08
Match length 108
% identity 33

NCBI Description (U35244) vacuolar protein sorting homolog r-vps33a [Rattus

norvegicus]

Seq. No. 19753

Contig ID 69699\_1.R1040 5'-most EST pxt700941011.h1

Seq. No. 19754



Contig ID 69706 1.R1040 5'-most EST LIB3109-015-Q1-K1-B9

Seq. No. 19755

Contig ID 69716 1.R1040

5'-most EST LIB3138-050-Q1-N1-C8

Method BLASTX
NCBI GI g2914700
BLAST score 1689
E value 0.0e+00
Match length 366
% identity 91

NCBI Description (AC003974) tRNA-processing protein SEN3-like [Arabidopsis

thaliana]

Seq. No. 19756

Contig ID 69724 1.R1040

5'-most EST jC-gmle01810016h03a1

Seq. No. 19757

Contig ID 69746 1.R1040

5'-most EST LIB3109-016-Q1-K1-D11

Method BLASTN
NCBI GI g4519187
BLAST score 41
E value 1.0e-13
Match length 116
% identity 88

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:

K1G2, complete sequence

Seq. No. 19758

Contig ID 69764 1.R1040

5'-most EST LIB3109-016-Q1-K1-F2

Seq. No. 19759

Contig ID 69776\_1.R1040 5'-most EST wvk700684868.h1

Method BLASTX
NCBI GI g2943792
BLAST score 567
E value 3.0e-58
Match length 144
% identity 76

NCBI Description (AB006809) PV72 [Cucurbita sp.]

Seq. No. 19760

Contig ID 69776 2.R1040 5'-most EST gsv701054481.hl

Seq. No. 19761

Contig ID 69787 1.R1040

5'-most EST LIB3109-017-Q1-K1-D7

Seq. No. 19762

Contig ID 69789 1.R1040

5'-most EST LIB3109-017-Q1-K1-D9



Method BLASTX
NCBI GI g4454470
BLAST score 191
E value 3.0e-14
Match length 85
% identity 56

NCBI Description (AC006234) putative sugar transporter [Arabidopsis

thaliana]

Seq. No. 19763

Contig ID 69790 1.R1040

5'-most EST LIB3109-017-Q1-K1-E1

Seq. No. 19764

Contig ID 69793 1.R1040

5'-most EST LIB3139-012-P1-N1-E8

Seq. No. 19765

Contig ID 69795\_1.R1040 5'-most EST crh700851675.h1

Method BLASTN
NCBI GI g2246441
BLAST score 178
E value 3.0e-95
Match length 556
% identity 85

NCBI Description Pisum sativum farnesyltransferase alpha subunit mRNA,

complete cds

Seq. No. 19766

Contig ID 69795\_2.R1040

5'-most EST LIB3109-017-Q1-K2-E8

Method BLASTN
NCBI GI g2246441
BLAST score 198
E value 1.0e-107
Match length 518
% identity 85

NCBI Description Pisum sativum farnesyltransferase alpha subunit mRNA,

complete cds

Seq. No. 19767

Contig ID 69807\_1.R1040

5'-most EST LIB3109-017-Q1-K1-F6

Method BLASTX
NCBI GI g4455213
BLAST score 287
E value 4.0e-29
Match length 124
% identity 64

NCBI Description (AL035440) glutamine amidotransferase/cyclase [Arabidopsis

thaliana]

Seq. No. 19768

Contig ID 69809\_1.R1040

5'-most EST jC-gmro02910007e03a1

Method BLASTX

```
NCBI GI
                   g4490309
BLAST score
                  503
                  8.0e-51
E value
                  145
Match length
% identity
                  67
NCBI Description
                  (AL035678) peroxidase ATP17a-like protein [Arabidopsis
                  thaliana]
                  19769
Seq. No.
Contig ID
                  69810 1.R1040
```

5'-most EST LIB3109-017-Q1-K1-G11 Seq. No. 19770

 Seq. No.
 19770

 Contig ID
 69821\_1.R1040

 5'-most EST
 LIB3109-017-Q1-K2-H7

 Seq. No.
 19771

 Contig ID
 69830\_1.R1040

 5'-most EST
 uC-gmflminsoy067a03b1

 Method
 BLASTX

 NCBL CL
 24455335

Method BLASTX
NCBI GI 94455335
BLAST score 346
E value 2.0e-32
Match length 176
% identity 47

NCBI Description (AL035525) putative protein [Arabidopsis thaliana]

Seq. No. 19772

Contig ID 69832\_1.R1040

5'-most EST uC-gmrominsoy127e12b1

Seq. No. 19773

Contig ID 69846\_1.R1040 5'-most EST uC-gmropic062d11b1

Method BLASTX
NCBI GI g4539335
BLAST score 239
E value 1.0e-20
Match length 78
% identity 55

NCBI Description (AL035539) putative protein [Arabidopsis thaliana]

Seq. No. 19774

Contig ID 69857 1.R1040 5'-most EST dpv701099707.h1

Method BLASTX
NCBI GI g2467088
BLAST score 197
E value 3.0e-15
Match length 75
% identity 52

NCBI Description (AJ001911) putative Ckc2 [Arabidopsis thaliana]

Seq. No. 19775

Contig ID 69860 1.R1040

5'-most EST LIB3109-019-Q1-K1-A6



Seq. No. 19776

Contig ID 69892\_1.R1040

5'-most EST LIB3138-120-Q1-N1-F6

Seq. No. 19777

Contig ID 69893 1.R1040 5'-most EST asn701138050.h1

Seq. No. 19778

Contig ID 69901\_1.R1040 5'-most EST zpv700758490.h1

Method BLASTX
NCBI GI 94220515
BLAST score 280
E value 9.0e-25
Match length 120
% identity 51

NCBI Description (AL035356) putative protein [Arabidopsis thaliana]

Seq. No. 19779

Contig ID 69909\_1.R1040

5'-most EST uC-gmrominsoy035c06b1

Method BLASTX
NCBI GI g2244765
BLAST score 153
E value 1.0e-09
Match length 159
% identity 21

NCBI Description (Z97335) hypothetical protein [Arabidopsis thaliana]

Seq. No. 19780

Contig ID 69910\_1.R1040 5'-most EST ssr700559508.h1

Method BLASTX
NCBI GI g3450842
BLAST score 516
E value 2.0e-53
Match length 201
% identity 57

NCBI Description (AF080436) mitogen activated protein kinase kinase [Oryza

sativa]

Seq. No. 19781

Contig ID 69924\_1.R1040

5'-most EST LIB3109-021-Q1-K1-A12

Seq. No. 19782

Contig ID 69935\_1.R1040

5'-most EST jC-gmst02400075d07a1

Method BLASTX
NCBI GI g3559805
BLAST score 1259
E value 1.0e-139
Match length 270
% identity 79

NCBI Description (AJ006787) putative phytochelatin synthetase [Arabidopsis

thaliana]



```
19783
Seq. No.
                  69936_1.R1040
Contig ID
                  LIB3109-021-Q1-K2-B6
5'-most EST
Method
                  BLASTX
                  g3335361
NCBI GI
                  573
BLAST score
                  3.0e-59
E value
                  126
Match length
                  84
% identity
NCBI Description (AC003028) putative acyltransferase [Arabidopsis thaliana]
                  19784
Seq. No.
                  69939 1.R1040
Contig ID
5'-most EST
                  LIB3109-021-Q1-K1-B9
                  19785
Seq. No.
                  69944 1.R1040
Contig ID
                  jC-gmf102220083c03a1
5'-most EST
                  19786
Seq. No.
                   69947 1.R1040
Contia ID
                  LIB3109-021-Q1-K2-D1
5'-most EST
                   BLASTN
Method
                   g2920665
NCBI GI
BLAST score
                   123
                   1.0e-62
E value
Match length
                   139
                   97
% identity
NCBI Description Glycine max 2,4-D inducible glutathione S-transferase
                   (GSTa) mRNA, complete cds
                   19787
Seq. No.
                   69949 1.R1040
Contig ID
                   hrw701060710.h1
5'-most EST
                   19788
Seq. No.
                   69979 1.R1040
Contig ID
                   bth700844892.h1
 5'-most EST
Method
                   BLASTX
                   q3522933
NCBI GI
                   681
BLAST score
                   2.0e-71
E value
                   225
Match length
 % identity
                   (AC004411) putative anion exchange protein 3 [Arabidopsis
NCBI Description
                   thaliana]
                   19789
 Seq. No.
 Contig ID
                   69989 1.R1040
                   cle700967704.h1
```

5'-most EST

BLASTX Method q2961357 NCBI GI 818 BLAST score 9.0e-88 E value Match length 189 % identity 80

3196



NCBI Description (AL022140) putative protein [Arabidopsis thaliana]

Seq. No. 19790

Contig ID 70015 1.R1040

5'-most EST uC-gmflminsoy001c04b1

Method BLASTX
NCBI GI g4240169
BLAST score 154
E value 6.0e-10
Match length 163
% identity 11

NCBI Description (AB020647) KIAA0840 protein [Homo sapiens]

Seq. No. 19791

Contig ID 70025\_1.R1040 5'-most EST uC-gmropic099f07b1

Method BLASTX
NCBI GI g4103635
BLAST score 242
E value 3.0e-21
Match length 137
% identity 42

NCBI Description (AF026538) ABA-responsive protein [Hordeum vulgare]

Seq. No.

Contig ID 70026\_1.R1040

5'-most EST uC-gmronoir076d12b1

19792

Seq. No. 19793

Contig ID 70032\_1.R1040 5'-most EST pcp700992064.h1

Method BLASTX
NCBI GI g4006914
BLAST score 1195
E value 1.0e-132
Match length 286
% identity 78

NCBI Description (Z99708) serine C-palmitoyltransferase like protein

[Arabidopsis thaliana]

Seq. No. 19794

Contig ID 70042\_1.R1040

5'-most EST LIB3109-027-Q1-K1-F10

Seg. No. 19795

Contig ID 70044\_1.R1040 5'-most EST trc700563856.h1

Method BLASTX
NCBI GI g2253583
BLAST score 223
E value 2.0e-18
Match length 61
% identity 74

NCBI Description (U78721) hypothetical protein [Arabidopsis thaliana]

Seq. No. 19796

Contig ID 70061 1.R1040



5'-most EST LIB3109-027-Q1-K1-H4 Method BLASTN NCBI GI g2398665 BLAST score 82 3.0e-38 E value Match length 294 % identity 82

NCBI Description Lupinus albus mRNA for PR protein class

19797 Seq. No.

Contig ID 70063 1.R1040 5'-most EST seb700651578.hl

Method BLASTX g4371293 NCBI GI BLAST score 239 E value 4.0e-20 106 Match length % identity 48

NCBI Description (AC006260) hypothetical protein [Arabidopsis thaliana]

19798 Seq. No.

70079 1.R1040 Contig ID 5'-most EST gsv701044790.hl

19799 Seq. No.

Contig ID 70088 1.R1040 5'-most EST leu701156317.h1

Method BLASTX g4455293 NCBI GI 223 BLAST score E value 5.0e-18 Match length 90 % identity 52

NCBI Description (AL035528) putative protein [Arabidopsis thaliana]

Seq. No. 19800

Contig ID 70089 1.R1040

5'-most EST LIB3109-028-Q1-K1-G4

19801 Seq. No.

70089 2.R1040 Contig ID 5'-most EST wvk700685417.hl

19802 Seq. No.

70090 1.R1040 Contig ID

LIB3109-028-Q1-K1-G5 5'-most EST

BLASTX Method NCBI GI g3928543 BLAST score 376 E value 5.0e-36 Match length 172 % identity 53

NCBI Description (AB016819) UDP-glucose glucosyltransferase [Arabidopsis

thaliana]

Seq. No. 19803

Contig ID 70092 1.R1040



leu701148404.h1 5'-most EST

Method BLASTX NCBI GI a3377810 BLAST score 505 E value 4.0e-51 Match length 183 % identity

NCBI Description (AF076275) contains similarity to glutaredoxins

[Arabidopsis thaliana]

Seq. No. 19804

Contig ID 70096 1.R1040 5'-most EST uC-gmropic018b12b1

19805 Seq. No.

70097 1.R1040 Contig ID

5'-most EST LIB3109-028-Q1-K1-H11

Seq. No. 19806

70129 1.R1040 Contig ID 5'-most EST zzp700832851.hl

BLASTX Method NCBI GI q1169863 \_BLAST score 149 E value 3.0e-11 Match length 73 identity 60

\*NCBI Description

G-BOX BINDING FACTOR 4 >gi\_403418 (U01823) GBF4 [Arabidopsis thaliana] >gi\_4204292 (AC003027) lcl\_prt\_seq 1

No definition line found [Arabidopsis thaliana]

Seq. No. 19807

Contig ID 70140 1.R1040 5 most EST sat701009966.h2

19808 Seq. No.

70148 1.R1040 Contig ID leu701155953.h1 5 most EST

Method BLASTX NCB¶ GI q4056432 BLAST score 733 E value 8.0e-78 Match length 194 % identity 72

(AC005990) Similar to gi 2245014 glucosyltransferase NCBI Description

homolog from Arabidopsis thaliana chromosome 4 contig gb Z97341. ESTs gb T20778 and gb AA586281 come from this

gene. [Arabidopsis thaliana]

19809 Seq. No.

70159 1.R1040 Contig ID  $ncj70\overline{0}986583.h1$ 5'-most EST

Method BLASTX g2702370 NCBI GI BLAST score 231 7.0e-19 E value Match length 85



% identity 47

NCBI Description (AF038604) contains similarity to Drosophila ovarian tumor

locus protein (GB:X13693) [Caenorhabditis elegans]

Seq. No. 19810

Contig ID 70164\_1.R1040

5'-most EST LIB3109-031-Q1-K1-A5

Seq. No. 19811

Contig ID 70180\_1.R1040 5'-most EST gsv701046275.h1

Seq. No. 19812

Contig ID 70194\_1.R1040 5'-most EST txt700733344.h1

Seq. No. 19813

Contig ID 70195 1.R1040

5'-most EST LIB3109-031-Q1-K1-H4

Method BLASTX
NCBI GI g3256068
BLAST score 486
E value 6.0e-49
Match length 119
% identity 76

NCBI Description (Y14068) Heat Shock Factor 3 [Arabidopsis thaliana]

Seq. No. 19814

Contig ID 70195\_2.R1040 5'-most EST fC-gmf1700909342a1

Method BLASTX
NCBI GI 9729775
BLAST score 267
E value 2.0e-23
Match length 75
% identity 67

NCBI Description HEAT SHOCK FACTOR PROTEIN HSF8 (HEAT SHOCK TRANSCRIPTION

FACTOR 8) (HSTF 8) (HEAT STRESS TRANSCRIPTION FACTOR) >gi\_100264\_pir\_\_ \$25481 heat shock transcription factor 8 - Peruvian tomato >gi 19492 emb CAA47869 (X67600) heat shock

transcription factor 8 [Lycopersicon peruvianum]

Seq. No. 19815

Contig ID 70204 1.R1040

5'-most EST LIB3109-032-Q1-K1-A7

Method BLASTX
NCBI GI 94468981
BLAST score 362
E value 2.0e-34
Match length 91
% identity 71

NCBI Description (AL035605) formamidase-like protein [Arabidopsis thaliana]

Seq. No. 19816

Contig ID 70205 1.R1040

5'-most EST LIB3109-032-Q1-K1-A4

Method BLASTX



NCBI GI g4510348 BLAST score 648 E value 1.0e-67 Match length 216 % identity 51

NCBI Description (AC006921) unknown protein [Arabidopsis thaliana]

Seq. No. 19817

Contig ID 70210\_1.R1040 5'-most EST kl1701206659.h1

Method BLASTX
NCBI GI g1531758
BLAST score 928
E value 1.0e-100
Match length 208
% identity 77

NCBI Description (X98772) AUX1 [Arabidopsis thaliana] >gi\_3335360 (AC003028)

unknown protein [Arabidopsis thaliana]

Seq. No. 19818

Contig ID 70210\_2.R1040 5'-most EST uC-gmropic027d05b1

Method BLASTX
NCBI GI g1531758
BLAST score 388
E value 1.0e-37
Match length 87
% identity 78

NCBI Description (X98772) AUX1 [Arabidopsis thaliana] >gi 3335360 (AC003028)

unknown protein [Arabidopsis thaliana]

Seq. No. 19819

Contig ID 70219\_1.R1040 5'-most EST leu701149925.h1

Method BLASTX
NCBI GI g2246380
BLAST score 323
E value 1.0e-29
Match length 144
% identity 59

NCBI Description (Z86095) peptidyl-prolyl cis-trans isomerase [Arabidopsis

thaliana]

Seq. No. 19820

Contig ID 70237 1.R1040

5'-most EST jC-gmro02800032a04a1

Seq. No. 19821

Contig ID 70241\_1.R1040 5'-most EST taw700654316.h1

Seq. No. 19822

Contig ID 70247\_1.R1040

5'-most EST LIB3109-033-Q1-K1-C11

Seq. No. 19823

Contig ID 70247 2.R1040

```
sat701003304.h1
5'-most EST
Seq. No.
                  19824
Contig ID
                  70249 1.R1040
5'-most EST
                  LIB3109-033-Q1-K1-C2
Seq. No.
                  19825
                  70252 1.R1040
Contig ID
5'-most EST
                  kmv700740832.hl
Method
                  BLASTX
NCBI GI
                  q1653089
BLAST score
                  236
E value
                  9.0e-20
Match length
                  66
% identity
NCBI Description (D90911) hypothetical protein [Synechocystis sp.]
                  19826
Seq. No.
                  70259 1.R1040
Contig ID
5'-most EST
                  LIB3109-033-Q1-K1-D12
                  BLASTX
Method
                  g1362017
NCBI GI
BLAST score
                  167
E value
                  2.0e-11
Match length
                  136
% identity
                  38
NCBI Description zinc finger protein 4 - Arabidopsis thaliana >gi_790679
                   (L39647) zinc finger protein [Arabidopsis thaliana]
                  19827
Seq. No.
Contig ID
                  70263 1.R1040
5'-most EST
                  LIB3109-033-Q1-K1-D5
                  19828
Seq. No.
                  70269 1.R1040
Contig ID
                  seb700653980.h1
5'-most EST
Method
                  BLASTX
                  g4512659
NCBI GI
BLAST score
                   430
                  2.0e-42
E value
Match length
                  168
% identity
                  55
NCBI Description
                  (AC006931) putative protein kinase [Arabidopsis thaliana]
                  >qi 4544465 qb AAD22372.1 AC006580 4 (AC006580) putative
```

protein kinase [Arabidopsis thaliana]

Seq. No. 19829

Contig ID 70272 1.R1040

LIB3109-034-Q1-K1-A9 5'-most EST

Method BLASTX NCBI GI g577301 BLAST score 380 3.0e-36 E value Match length 234 % identity 36

(D42044) The ha3523 gene product is related to S.cerevisiae NCBI Description gene product located in chromosome III. [Homo sapiens]



Seq. No. 19830

Contig ID 70276 1.R1040

5'-most EST LIB3109-034-Q1-K1-B2

Method BLASTX
NCBI GI g136140
BLAST score 209
E value 1.0e-16
Match length 117
% identity 36

NCBI Description PUTATIVE AC9 TRANSPOSASE >gi\_72973\_pir\_\_TQZMCA probable

transposase - maize transposon Ac9

Seq. No. 19831

Contig ID 70296 1.R1040

5'-most EST LIB3109-034-Q1-K1-D12

Method BLASTX
NCBI GI g2827715
BLAST score 473
E value 1.0e-47
Match length 133
% identity 24

NCBI Description (AL021684) receptor protein kinase - like protein

[Arabidopsis thaliana]

Seq. No. 19832

Contig ID 70302 1.R1040

5'-most EST jC-gmle01810040b06a1

Method BLASTX
NCBI GI g2191140
BLAST score 436
E value 8.0e-43
Match length 184
% identity 53

NCBI Description (AF007269) contains weak similarity to MYB-related proteins

[Arabidopsis thaliana]

Seq. No. 19833

70306 1.R1040 Contig ID 5'-most EST g4306317 Method BLASTX NCBI GI q1507699 BLAST score 205 E value 7.0e-16 Match length 78 % identity 50

NCBI Description (L81119) COL2 [Arabidopsis thaliana] >gi 1507701 (L81120)

COL2 [Arabidopsis thaliana]

Seq. No. 19834

Contig ID 70310 1.R1040

5'-most EST jC-gmle01810046f06a1

Method BLASTX
NCBI GI g2459412
BLAST score 211
E value 1.0e-22
Match length 183



% identity NCBI Description (AC002332) putative G9a protein [Arabidopsis thaliana] 19835 Seq. No. Contig ID 70317 1.R1040 uC-gmflminsoy072d08b1 5'-most EST Method BLASTX q2326372 NCBI GI BLAST score 570 6.0e-59 E value Match length 142 78 % identity NCBI Description (Y14404) putative arabinose kinase [Arabidopsis thaliana] 19836 Seq. No. Contig ID 70323 1.R1040 5'-most EST uC-gmflminsoy032g08b1 19837 Seq. No. 70406 1.R1040 Contig ID 5'-most EST LIB3109-035-Q1-K6-A11 Method BLASTX NCBI GI g4539401 BLAST score 486 E value 2.0e-48 Match length 231 % identity 48 NCBI Description (AL035526) putative protein [Arabidopsis thaliana] 19838 Seq. No. 70418 1.R1040 Contig ID 5'-most EST ssr700559817.hl 19839 Seq. No. 70438 1.R1040 Contig ID LIB3109-035-Q1-K6-H9 5'-most EST BLASTX Method NCBI GI g2829897 BLAST score 145 E value 4.0e-09 Match length 51 % identity 53 NCBI Description (AC002311) Unknown protein [Arabidopsis thaliana] Seq. No. 19840 Contig ID 70470 1.R1040 5'-most EST LIB3139-106-P1-N1-E5 19841 Seq. No. 70489 1.R1040 Contig ID 5'-most EST wrg700787588.h1 Method BLASTX

Contig ID 70489 1.R1040
5'-most EST wrg700787588
Method BLASTX
NCBI GI g2494266
BLAST score 528
E value 1.0e-53
Match length 130

% identity 83



NCBI Description GTP-BINDING PROTEIN LEPA >gi\_1653961\_dbj\_BAA18871\_ (D90917) LepA [Synechocystis sp.]

Seq. No. 19842

Contig ID 70496 1.R1040

5'-most EST LIB3109-036-Q1-K1-D4

Method BLASTX
NCBI GI g3878264
BLAST score 160
E value 1.0e-10
Match length 66
% identity 45

NCBI Description (Z75712) Similarity to some prokaryotic esterases; cDNA EST

EMBL: D71448 comes from this gene; cDNA EST EMBL: D74156

comes from this gene [Caenorhabditis elegans]

Seq. No. 19843

Contig ID 70501\_1.R1040 5'-most EST gsv701056012.h1

Seq. No. 19844

Contig ID 70504\_1.R1040 5'-most EST kmv700738941.h1

Method BLASTX
NCBI GI g461812
BLAST score 264
E value 5.0e-23
Match length 83
% identity 57

NCBI Description CYTOCHROME P450 72 (CYPLXXII) (PROBABLE

GERANIOL-10-HYDROXYLASE) (GE10H) >gi\_167484 (L10081)

Cytochrome P-450 protein [Catharanthus roseus]

>gi\_445604\_prf\_\_1909351A cytochrome P450 [Catharanthus

roseus]

Seq. No. 19845

Contig ID 70521 1.R1040

5'-most EST jC-gmro02800031a02a1

Method BLASTX
NCBI GI g4415910
BLAST score 292
E value 9.0e-26
Match length 337
% identity 29

NCBI Description (AC006282) hypothetical protein [Arabidopsis thaliana]

Seq. No. 19846

Contig ID 70525 1.R1040

5'-most EST LIB3109-037-Q1-K1-D2

Seq. No. 19847

Contig ID 70531\_1.R1040 5'-most EST leu701150836.h1

Seq. No. 19848

Contig ID 70533\_1.R1040

5'-most EST LIB3109-037-Q1-K1-E12



```
BLASTX
Method
NCBI GI
                   g4490756
BLAST score
                   252
                   1.0e-21
E value
                  79
Match length
                   61
% identity
                   19849
Seq. No.
Contig ID
```

NCBI Description (AL035708) hypothetical protein [Arabidopsis thaliana]

70533 2.R1040 5'-most EST  $1eu70\overline{1}156582.h1$ 

BLASTX Method NCBI GI q4490756 BLAST score 348 E value 7.0e-33 Match length 105 % identity

NCBI Description (AL035708) hypothetical protein [Arabidopsis thaliana]

19850 Seq. No.

70537 1.R1040 Contig ID

5'-most EST uC-gmrominsoy053a09b1

BLASTX Method NCBI GI g1732363 BLAST score 301 6.0e-27 E value Match length 188 % identity 40

NCBI Description (U80270) early fruit mRNA [Malus domestica]

19851 Seq. No.

70541 1.R1040 Contig ID 5'-most EST uC-gmropic037a11b1

BLASTX Method NCBI GI g3242785 BLAST score 237 E value 1.0e-19 Match length 146 42 % identity

(AF055355) respiratory burst oxidase protein C [Arabidopsis NCBI Description

thaliana]

Seq. No. 19852

70541 2.R1040 Contig ID

LIB3109-037-Q1-K1-E9 5'-most EST

19853 Seq. No.

70553 1.R1040 Contig ID

5'-most EST LIB3109-037-Q1-K1-G1

Method BLASTX g3786008 NCBI GI BLAST score 238 E value 9.0e-20 Match length 152 % identity 45

NCBI Description (AC005499) unknown protein [Arabidopsis thaliana]



```
19854
Seq. No.
                   70554 1.R1040
Contig ID
                   LIB3109-037-Q1-K1-G11
5'-most EST
                   19855
Seq. No.
                   70565 1.R1040
Contig ID
5'-most EST
                   jex700906266.hl
Method
                   BLASTX
NCBI GI
                   q3928084
BLAST score
                   410
E value
                   5.0e-40
Match length
                   161
% identity
                   62
```

NCBI Description (AC005770) retrotransposon-like protein [Arabidopsis

thaliana]

Seq. No. 19856

Contig ID 70567 1.R1040

LIB3109-038-Q1-K1-E3 5'-most EST

BLASTX Method g2181180 NCBI GI BLAST score 452 1.0e-44 E value Match length 257 % identity 39

NCBI Description (Z84377) xylosidase [Aspergillus niger]

19857 Seq. No.

Contig ID 70570 1.R1040 5'-most EST pxt700942542.h1

Method BLASTX NCBI GI g3243033 BLAST score 107 E value 2.0e-09 Match length 122 33 % identity

(AF069765) signal recognition particle 72 [Homo sapiens] NCBI Description

>gi 3335650 (AF077019) signal recognition particle 72 [Homo

sapiens]

Seq. No. 19858

Contig ID 70576 1.R1040

5'-most EST jC-qmle01810090e04a1

Method BLASTX NCBI GI q1168759 BLAST score 156 4.0e-10 E value Match length 146 29 % identity

PHOSPHOENOLPYRUVATE CARBOXYLASE (PEPCASE) (PEPC) NCBI Description

> >gi\_1075143\_pir\_\_I64133 phosphoenolpyruvate carboxylase (ppc) homolog - Haemophilus influenzae (strain Rd KW20) >gi\_1574482 (U32836) phosphoenolpyruvate carboxylase (ppc)

[Haemophilus influenzae Rd]

19859 Seq. No.

70588 1.R1040 Contig ID

% identity

70



```
5'-most EST
                  LIB3109-038-Q1-K1-G3
Method
                  BLASTX
NCBI GI
                   q4544451
BLAST score
                  307
E value
                  7.0e-28
Match length
                  187
                  47
% identity
NCBI Description (AC006592) unknown protein [Arabidopsis thaliana]
Seq. No.
                  19860
Contig ID
                  70614 2.R1040
5'-most EST
                  sat701006217.h2
Method
                  BLASTX
NCBI GI
                  q1172494
BLAST score
                  197
E value
                  2.0e-15
Match length
                  97
% identity
                  37
NCBI Description
                  PTERIN-4-ALPHA-CARBINOLAMINE DEHYDRATASE (PHS)
                   (4-ALPHA-HYDROXY-TETRAHYDROPTERIN DEHYDRATASE)
                   (PHENYLALANINE HYDROXYLASE-STIMULATING PROTEIN) (PCD)
                  >gi 476742 (M88627) phenylalanine hydroxylase [Pseudomonas
                  aeruginosa]
Seq. No.
                  19861
Contig ID
                  70616 1.R1040
5'-most EST
                  sat701014480.h1
Method
                  BLASTX
NCBI GI
                  q3548802
BLAST score
                  498
E value
                  3.0e-50
Match length
                  181
% identity
                  56
NCBI Description
                  (AC005313) axi 1-like protein [Arabidopsis thaliana]
                  >gi 4335769 gb AAD17446 (AC006284) putative axi1 protein
                   [Nicotiana tabacum] [Arabidopsis thaliana]
Seq. No.
                  19862
Contig ID
                  70634 1.R1040
5'-most EST
                  rlr700901126.h1
Method
                  BLASTX
NCBI GI
                  g2738982
BLAST score
                  398
E value
                  1.0e~38
Match length
                  134
% identity
                  55
NCBI Description (AF022157) CYP71A10 [Glycine max]
Seq. No.
                  19863
Contig ID
                  70643 1.R1040
5'-most EST
                  LIB3109-042-Q1-K1-F4
Method
                  BLASTX
NCBI GI
                  g3046815
BLAST score
                  361
E value
                  3.0e-34
Match length
                  84
```



```
NCBI Description (AL021687) cytochrome P450 [Arabidopsis thaliana]
```

Seg. No. 19864

Contig ID 70644 1.R1040

5'-most EST uC-gmflminsoy030e11b1

Method BLASTX
NCBI GI 94539327
BLAST score 872
E value 4.0e-94
Match length 216
% identity 78

NCBI Description (AL035679) putative proton pump [Arabidopsis thaliana]

Seq. No.

19865

Contig ID

70645 1.R1040

5'-most EST

LIB3109-042-Q1-K1-F6

Seq. No.

19866

19867

Contig ID

70647 1.R1040

5'-most EST

LIB3109-042-Q1-K1-F8

Method BLASTX
NCBI GI g4467126
BLAST score 263
E value 1.0e-22
Match length 168
% identity 40

NCBI Description (AL035538) guanine nucleotide-exchange protein-like

[Arabidopsis thaliana]

Seq. No.

Contig ID

70652\_1.R1040

5'-most EST

LIB3109-042-Q1-K1-G2

Seq. No. 19868

Contig ID 70659\_1.R1040 5'-most EST asn701131542.h1

Method BLASTX
NCBI GI g4415931
BLAST score 324
E value 5.0e-30
Match length 146
% identity 49

NCBI Description (AC006418) unknown protein [Arabidopsis thaliana]

>qi 4559393 gb AAD23053.1 AC006526 18 (AC006526) unknown

protein [Arabidopsis thaliana]

Seq. No. 19869

Contig ID 70664\_1.R1040 5'-most EST gsv701044207.h1

Method BLASTX
NCBI GI g3080427
BLAST score 574
E value 3.0e-59
Match length 165
% identity 73

NCBI Description (AL022604) putative protein [Arabidopsis thaliana]



Seq. No. 19870

Contig ID 70664 2.R1040

5'-most EST uC-qmrominsoy198h05b1

Method BLASTX
NCBI GI g3080427
BLAST score 242
E value 3.0e-20
Match length 60
% identity 83

NCBI Description (AL022604) putative protein [Arabidopsis thaliana]

Seq. No. 19871

Contig ID 70664\_3.R1040

5'-most EST LIB3139-010-P1-N1-C2

Seq. No. 19872

Contig ID 70692 1.R1040

5'-most EST LIB3109-044-Q1-K1-A3

Seq. No. 19873

Contig ID 70731 1.R1040

5'-most EST LIB3109-045-Q1-K1-B5

Seq. No. 19874

Contig ID 70735\_1.R1040

5'-most EST jC-gmro02910066a10a1

Seq. No. 19875

Contig ID 70744 1.R1040

5'-most EST LIB3109-045-Q1-K1-C9

Seq. No. 19876

Contig ID 70754 1.R1040

5'-most EST jC-gmf102220103c06a1

Method BLASTX
NCBI GI g4454452
BLAST score 976
E value 1.0e-106
Match length 331
% identity 55

NCBI Description (AC006234) unknown protein [Arabidopsis thaliana]

Seq. No. 19877

Contig ID 70757\_1.R1040 5'-most EST gsv701055109.h1

Seq. No. 19878

Contig ID 70759\_1.R1040

5'-most EST jC-gmf102220079e06a1

Method BLASTX
NCBI GI g2459431
BLAST score 208
E value 4.0e-16
Match length 149
% identity 46

NCBI Description (AC002332) unknown protein [Arabidopsis thaliana]



```
Seq. No. 19879
Contig ID 70760 1.R1040
5'-most EST LIB3109-046-Q1-K1-B6
Seq. No. 19880
Contig ID 70762_1.R1040
5'-most EST jC-gmst02400040a01a1
```

Method BLASTX
NCBI GI g3420054
BLAST score 191
E value 7.0e-23
Match length 324
% identity 30

NCBI Description (AC004680) unknown protein [Arabidopsis thaliana]

 Seq. No.
 19881

 Contig ID
 70779\_1.R1040

 5'-most EST
 uC-gmronoir033b04b1

 Method
 BLASTN

 NCBI GI
 g1372965

 BLAST score
 452

NCBI GI g137296
BLAST score 452
E value 0.0e+00
Match length 750
% identity 90

NCBI Description Vicia faba CREB-like protein mRNA, complete cds

Seq. No. 19882

Contig ID 70782\_1.R1040 5'-most EST bnu700967637.h1

Seq. No. 19883

Contig ID 70806 1.R1040 5'-most EST epx701104816.h1

Method BLASTX
NCBI GI g3355308
BLAST score 150
E value 2.0e-09
Match length 156
% identity 29

NCBI Description (AJ009695) wall-associated kinase 4 [Arabidopsis thaliana]

Seq. No. 19884

Contig ID 70823\_1.R1040

5'-most EST LIB3109-047-Q1-K1-E1

Method BLASTX
NCBI GI g1491712
BLAST score 241
E value 4.0e-23
Match length 118
% identity 53

NCBI Description (X99961) unknown [Homo sapiens]

Seq. No. 19885

Contig ID 70824\_1.R1040

5'-most EST LIB3138-095-Q1-N1-D12

Method BLASTX NCBI GI g2341042



BLAST score 296 E value 1.0e-26 Match length 134 % identity 52

NCBI Description (AC000104) F19P19.26 [Arabidopsis thaliana]

Seq. No. 19886

Contig ID 70825\_1.R1040 5'-most EST uC-gmropic039b07b1

Seq. No. 19887

Contig ID 70828 1.R1040 5'-most EST hrw701063387.h1

Seq. No. 19888

Contig ID 70829\_1.R1040 5'-most EST rlr700895472.h1

Method BLASTX
NCBI GI g1314711
BLAST score 1362
E value 1.0e-151
Match length 338
% identity 80

NCBI Description (U54615) calcium-dependent protein kinase [Arabidopsis

thaliana] >gi\_3068712 (AF049236) calcium dependent protein

kinase [Arabidopsis thaliana]

Seq. No. 19889

Contig ID 70855\_1.R1040

5'-most EST LIB3 $\overline{10}$ 9-048-Q1-K1-E5

Method BLASTX
NCBI GI g3859594
BLAST score 336
E value 1.0e-31
Match length 122
% identity 53

NCBI Description (AF104919) contains similarity to ribosomal protein L7Ae

(Pfam: PF01248, E=0.0017, N=1) [Arabidopsis thaliana]

Seq. No. 19890

Contig ID 70856 1.R1040

5'-most EST LIB3109-048-Q1-K1-E6

Seq. No. 19891

Contig ID 70857\_1.R1040 5'-most EST seb700650564.h1

Seq. No. 19892

Contig ID 70859 1.R1040

5'-most EST LIB3109-048-Q1-K1-F10

Seq. No. 19893

Contig ID 70862\_1.R1040

5'-most EST LIB3109-048-Q1-K1-F2

Method BLASTX NCBI GI g3367534 BLAST score 507



E value 1.0e-51 Match length 134 % identity 72

NCBI Description (AC004392) Strong similarity to coatamer alpha subunit (HEPCOP) homolog gb\_U24105 from Homo sapiens. [Arabidopsis

thaliana]

Seq. No. 19894

Contig ID 70871 1.R1040

5'-most EST uC-gmrominsoy304a03b1

Method BLASTX
NCBI GI g2832605
BLAST score 170
E value 5.0e-12
Match length 111
% identity 39

NCBI Description (AL021633) predicted protein [Arabidopsis thaliana]

Seq. No. 19895

Contig ID 70876 1.R1040

5'-most EST uC-gmrominsoy235f03b1

Method BLASTX
NCBI GI g3548810
BLAST score 170
E value 8.0e-12
Match length 182
% identity 30

NCBI Description (AC005313) putative chloroplast nucleoid DNA binding

protein [Arabidopsis thaliana]

Seq. No. 19896

Contig ID 70890\_1.R1040

5'-most EST LIB3109-050-Q1-K1-H1

Method BLASTX
NCBI GI g2829923
BLAST score 567
E value 4.0e-58
Match length 208
% identity 32

NCBI Description (AC002291) Similar to uridylyl transferases [Arabidopsis

thaliana]

Seq. No.

19897

Contig ID 7

70898\_1.R1040

5'-most EST

LIB3109-050-Q1-K1-G3

Method BLASTX
NCBI GI g2501102
BLAST score 421
E value 2.0e-41
Match length 107
% identity 76

NCBI Description SYNTAXIN-RELATED PROTEIN KNOLLE >gi\_1184165 (U39451)

syntaxin-related [Arabidopsis thaliana] >gi 1184167 (U39452) syntaxin-related [Arabidopsis thaliana]

>gi\_3063443 (AC003981) F22013.4 [Arabidopsis thaliana]
>gi\_1587182\_prf\_\_2206310A syntaxin-related protein

[Arabidopsis thaliana]



Seq. No. 19898

Contig ID 70904 1.R1040

5'-most EST jC-gmst02400025g04a1

Method BLASTX
NCBI GI g1170312
BLAST score 475
E value 1.0e-47
Match length 148
% identity 74

NCBI Description HOMEOBOX PROTEIN SBH1 >gi\_629614\_pir\_\_S42543 hypothetical protein - soybean >gi\_485406 (L13663) SBH1 [Glycine max]

Seq. No. 19899

Contig ID 70910 1.R1040

5'-most EST LIB3139-099-P1-N1-H1

Method BLASTX
NCBI GI g2435519
BLAST score 403
E value 2.0e-39
Match length 116
% identity 67

NCBI Description (AF024504) similar to mouse MEM3 (GB:U47024 and S.

cerevisiae vacuolar sorting protein 35 (SW; P34110)

[Arabidopsis thaliana]

Seq. No. 19900

Contig ID 70912\_1.R1040

5'-most EST LIB3109-052-Q1-K1-A8

Method BLASTX
NCBI GI g2435519
BLAST score 495
E value 1.0e-49
Match length 209
% identity 50

NCBI Description (AF024504) similar to mouse MEM3 (GB:U47024 and S.

cerevisiae vacuolar sorting protein 35 (SW; P34110)

[Arabidopsis thaliana]

Seq. No. 19901

Contig ID 70913 1.R1040

5'-most EST LIB3109-052-Q1-K1-B10

Seq. No. 19902

Contig ID 70920\_1.R1040 5'-most EST bth700846753.h1

Method BLASTX
NCBI GI g3169178
BLAST score 402
E value 4.0e-39
Match length 113
% identity 73

NCBI Description (AC004401) hypothetical protein [Arabidopsis thaliana]

Seq. No. 19903

Contig ID 70942\_1.R1040 5'-most EST eep700864313.h1



Method BLASTX
NCBI GI g2244756
BLAST score 718
E value 1.0e-75
Match length 277
% identity 55

NCBI Description (Z97335) hypothetical protein [Arabidopsis thaliana]

Seq. No. 19904

Contig ID 70949\_1.R1040 5'-most EST uC-gmropic024c04b1

Method BLASTX
NCBI GI g462671
BLAST score 591
E value 2.0e-60
Match length 155
% identity 66

NCBI Description MYB-LIKE PROTEIN >gi 4467385 emb CAB37862 (Z11534) Myb

protein [Dictyostelium discoideum]

Seq. No. 19905

Contig ID 70950\_1.R1040 5'-most EST uC-gmropic102g02b1

Method BLASTX
NCBI GI g3249071
BLAST score 238
E value 6.0e-20
Match length 70
% identity 57

NCBI Description (AC004473) Contains similarity to protein-tyrosine

phosphatase 2 gb\_L15420 from Dictyostelium discoideum. EST

gb\_N38718 comes from this g [Arabidopsis thaliana]

Seq. No. 19906

Contig ID 70953\_1.R1040

5'-most EST LIB3109-053-Q1-K1-E10

Seq. No. 19907

Contig ID 70973\_1.R1040 5'-most EST awf700842734.h1

Seq. No. 19908

Contig ID 70976\_1.R1040 5'-most EST pmv700894357.h1

Seq. No. 19909

Contig ID 70976\_2.R1040 5'-most EST bth700849325.h1

Seq. No. 19910

Contig ID 70979 1.R1040

5'-most EST LIB3109-054-Q1-K1-A4

Method BLASTX
NCBI GI g2911081
BLAST score 152
E value 1.0e-09
Match length 158



% identity 30

NCBI Description (AL021960) putative protein [Arabidopsis thaliana]

Seq. No. 19911

Contig ID 71002\_1.R1040

5'-most EST LIB3109-055-Q1-K1-A11

Method BLASTX
NCBI GI g3219355
BLAST score 699
E value 1.0e-73
Match length 264
% identity 53

NCBI Description (AF062371) ROOT HAIRLESS 1 [Arabidopsis thaliana]

Seq. No. 19912

Contig ID 71005\_1.R1040 5'-most EST pmv700888421.h1

Method BLASTX
NCBI GI g2507426
BLAST score 461
E value 6.0e-88
Match length 251
% identity 68

NCBI Description ALANYL-TRNA SYNTHETASE, MITOCHONDRIAL PRECURSOR

(ALANINE--TRNA LIGASE) (ALARS) >gi\_1673365\_emb\_CAA80380\_(Z22673) mitochondrial tRNA-Ala synthetase [Arabidopsis

thaliana]

Seq. No. 19913

Contig ID 71006 1.R1040

5'-most EST LIB3109-055-Q1-K1-A8

Seq. No. 19914

Contig ID 71008 1.R1040

5'-most EST LIB3109-055-Q1-K1-B1

Seq. No. 19915

Contig ID 71023 1.R1040

5'-most EST jC-gmst02400014h06a1

Method BLASTX
NCBI GI g3695019
BLAST score 617
E value 5.0e-64
Match length 261
% identity 50

NCBI Description (AF055848) subtilisin-like protease [Arabidopsis thaliana]

Seq. No. 19916

Contig ID 71025\_1.R1040

5'-most EST LIB3109-055-Q1-K1-C6

Method BLASTX
NCBI GI g2191168
BLAST score 584
E value 4.0e-60
Match length 213
% identity 52

NCBI Description (AF007270) contains similarity to myosin heavy chain



## [Arabidopsis thaliana]

```
Seq. No.
                  19917
                  71036 1.R1040
Contig ID
5'-most EST
                  LIB3109-055-Q1-K1-D6
Method
                  BLASTX
NCBI GI
                  g4101589
BLAST score
                  161
E value
                  1.0e-10
                  60
Match length
% identity
                  48
NCBI Description (AF005050) aspartyl aminopeptidase [Homo sapiens]
Seq. No.
                  19918
Contig ID
                  71044 1.R1040
5'-most EST
                  sat701007139.h1
Method
                  BLASTX
NCBI GI
                  g107350
BLAST score
                  306
E value
                  9.0e-28
Match length
                  174
% identity
                  40
NCBI Description Pm5 protein - human >gi_1335273_emb_CAA40655_ (X57398) pm5
                  protein [Homo sapiens]
Seq. No.
                  19919
                  71061 1.R1040
Contig ID
5'-most EST
                  LIB3109-056-Q1-K1-G12
                  19920
Seq. No.
                  71077 1.R1040
Contig ID
5'-most EST
                  LIB3109-057-Q1-K1-A1
Method
                  BLASTX
                  g1171577
NCBI GI
BLAST score
                  1195
E value
                  1.0e-131
                  337
Match length
% identity
                  66
NCBI Description (X95343) hypersensitivity-related gene [Nicotiana tabacum]
Seq. No.
                  19921
                  71078 1.R1040
Contig ID
5'-most EST
                  LIB3109-057-Q1-K1-A10
Method
                  BLASTX
NCBI GI
                  g1351678
BLAST score
                  180
                  5.0e-13
E value
Match length
                  125
% identity
                  36
NCBI Description HYPOTHETICAL 41.5 KD PROTEIN C1F5.03C IN CHROMOSOME I
                  >gi 1103730 emb CAA92231 (Z68136) unknown
                  [Schizosaccharomyces pombe]
                  19922
Seq. No.
```

71078 2.R1040 Contig ID 5'-most EST rca701001587.h1

```
Seq. No.
                  19923
                  71079 1.R1040
Contig ID
5'-most EST
                  LIB3109-057-Q1-K1-A11
                  19924
Seq. No.
                  71084 1.R1040
Contig ID
5'-most EST
                  gsv701053043.h1
Seq. No.
                  19925
                  71104 1.R1040
Contig ID
5'-most EST
                  sat701014105.h1
                  19926
Seq. No.
Contig ID
                  71106 1.R1040
5'-most EST
                  LIB3109-035-Q1-K4-E12
                  19927
Seq. No.
                  71126 1.R1040
Contig ID
5'-most EST
                  LIB3109-020-Q1-K1-C3
Method
                  BLASTX
NCBI GI
                  g4512263
BLAST score
                  172
                  3.0e-12
E value
Match length
                  39
                  79
% identity
NCBI Description (AB018526) H+/Ca2+ exchanger 2 [Ipomoea nil]
Seq. No.
                  19928
                  71127 1.R1040
Contig ID
5'-most EST
                  uC-gmropic020d03b1
                  BLASTX
Method
```

NCBI GI g3249105 879 BLAST score 1.0e-94 E value 221 Match length 73 % identity

NCBI Description (AC003114) Contains similarity to protein phosphatase 2C (ABI1) gb X78886 from A. thaliana. [Arabidopsis thaliana]

Seq. No. 19929 Contig ID 71131 1.R1040

5'-most EST jC-gmf102220053b12a1

19930 Seq. No.

71147 1.R1040 Contig ID

5'-most EST LIB3109-014-Q1-K1-G9

Seq. No. 19931

Contig ID 71223 1.R1040

5'-most EST LIB3109-021-Q1-K3-D10

Method BLASTX NCBI GI g282963 BLAST score 245 E value 8.0e-21 Match length 86 % identity 56

NCBI Description transforming protein (myb) homolog (clone myb.Ph2) - garden



x hybrida]

petunia >gi\_20561\_emb\_CAA78387\_ (Z13997) protein 2 [Petunia

19932 Seq. No.

71303 1.R1040 Contig ID

LIB3109-006-Q1-K1-D10 5'-most EST

Seq. No. 19933

71303 2.R1040 Contig ID

5'-most EST jC-gmst02400072c02a1

Seq. No. 19934

71314 1.R1040 Contig ID kl1701208133.h1 5'-most EST

Method BLASTN NCBI GI g1370147 BLAST score 48 6.0e-18 E value 253 Match length 83 % identity

NCBI Description L.japonicus mRNA for small GTP-binding protein, RAB11D

19935 Seq. No.

Contig ID 71323 1.R1040

5'-most EST LIB3109-044-Q1-K1-E7

19936 Seq. No.

Contig ID 71337 1.R1040

5'-most EST LIB3138-001-Q1-N1-E11

Method BLASTX NCBI GI g4455367 BLAST score 483 1.0e-48 E value 168 Match length

% identity

NCBI Description (AL035524) putative protein [Arabidopsis thaliana]

Seq. No. 19937

Contig ID 71345 1.R1040 5'-most EST vwf700678057.h1

19938 Seq. No.

71351 1.R1040 Contig ID 5'-most EST pxt700940983.h1

Method BLASTX g2314166 NCBI GI BLAST score 162 E value 9.0e-11 Match length 70 % identity 49

NCBI Description (AE000610) co-chaperone-curved DNA binding protein A (CbpA)

[Helicobacter pylori 26695]

19939 Seq. No.

Contig ID 71352 1.R1040

5'-most EST LIB3139-051-P1-N1-D12

Method BLASTX



```
g4263710
NCBI GI
BLAST score
                  145
                  5.0e-09
E value
Match length
                  30
                  90
% identity
NCBI Description (AC006223) putative pur-alpha transcriptional activator
                  protein [Arabidopsis thaliana]
                  19940
Seq. No.
                  71359 1.R1040
Contig ID
                  ssr700555465.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g2341043
BLAST score
                  312
E value
                  2.0e-28
Match length
                  119
% identity
                  52
NCBI Description (AC000104) Strong similarity to Arabidopsis REV3C
                   (gb X62461). [Arabidopsis thaliana]
Seq. No.
                  19941
                  71381 1.R1040
Contig ID
                  fde700875770.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g2739002
BLAST score
                  1135
E value
                  1.0e-124
Match length
                  451
% identity
                  50
NCBI Description (AF022460) CYP83D1p [Glycine max]
                  19942
Seq. No.
                  71395 1.R1040
Contig ID
5'-most EST
                  zpv700761178.h1
Method
                  BLASTX
NCBI GI
                  q4490314
BLAST score
                   322
                  2.0e-29
E value
Match length
                  105
% identity
NCBI Description (AL035678) putative protein [Arabidopsis thaliana]
                  19943
Seq. No.
                  71403_1.R1040
Contig ID
                  jC-gmle01810075d01d1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q2129635
BLAST score
                  307
E value
                  8.0e-28
```

Match length 146 47 % identity

NCBI Description light repressible receptor protein kinase - Arabidopsis

thaliana >gi\_1321686\_emb\_CAA66376\_ (X97774) light

repressible receptor protein kinase [Arabidopsis thaliana]

Seq. No. 19944

Contig ID 71411 1.R1040

% identity

NCBI Description



```
5'-most EST
                  rca700997486.h1
Method
                  BLASTN
NCBI GI
                  g18660
                  190
BLAST score
E value
                  1.0e-103
Match length
                  190
                  100
% identity
NCBI Description G.max hsp22 gene for low MW heat shock protein
                  19945
Seq. No.
                  71416 1.R1040
Contig ID
5'-most EST
                  ncj700981993.h1
Method
                  BLASTX
NCBI GI
                  g3025189
BLAST score
                  511
E value
                  2.0e-51
Match length
                  164
% identity
                  59
NCBI Description HYPOTHETICAL 67.1 KD PROTEIN SLL1770
                  >gi 1652753 dbj BAA17672 (D90908) ABC1-like [Synechocystis
                  sp.]
                  19946
Seq. No.
Contig ID
                  71424 1.R1040
5'-most EST
                  LIB3138-045-Q1-N1-B9
Seq. No.
                  19947
Contig ID
                  71446 1.R1040
5'-most EST
                  jC-gmle01810091c03d1
Seq. No.
                  19948
                  71452 1.R1040
Contig ID
5'-most EST
                  LIB3138-019-Q1-N1-C8
                  19949
Seq. No.
Contig ID
                  71468 1.R1040
5'-most EST
                  fC-gmst700888494f3
Method
                  BLASTX
NCBI GI
                  g3582333
BLAST score
                  706
E value
                  8.0e-75
Match length
                  149
% identity
NCBI Description (AC005496) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  19950
Contig ID
                  71483 1.R1040
                  wvk700681425.h2
5'-most EST
Method
                  BLASTN
NCBI GI
                  g4519194
BLAST score
                  40
E value
                  1.0e-12
Match length
                  140
```

MHM17, complete sequence

Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:



```
19951
Seq. No.
Contig ID
                  71486 1.R1040
5'-most EST
                  jsh701068647.h1
Method
                  BLASTX
NCBI GI
                  g4102582
BLAST score
                  274
                  6.0e-24
E value
Match length
                  126
% identity
                  28
NCBI Description (AF013115) CAO [Arabidopsis thaliana]
                  19952
Seq. No.
                  71495 1.R1040
Contig ID
                  fde700876462.hl
5'-most EST
                  BLASTX
Method
NCBI GI
                  g2880049
BLAST score
                  925
                  1.0e-100
E value
                  270
Match length
                  67
% identity
NCBI Description (AC002340) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  19953
                  71502 1.R1040
Contig ID
5'-most EST
                  zhf700953044.h1
Seq. No.
                  19954
                  71508_1.R1040
Contig ID
5'-most EST
                  uC-gmflminsoy080h12b1
Method
                  BLASTX
                  g3298538
NCBI GI
BLAST score
                  217
E value
                   3.0e-17
Match length
                  119
% identity
                   42
NCBI Description (AC004681) hypothetical protein [Arabidopsis thaliana]
                  19955
Seq. No.
                  71511 1.R1040
Contig ID
5'-most EST
                  smc700750001.h1
                  19956
Seq. No.
Contig ID
                  71533 1.R1040
                  LIB3138-035-Q1-N1-F11
5'-most EST
                  BLASTX
Method
NCBI GI
                  q4539006
BLAST score
                   527
                  7.0e-54
E value
Match length
                  143
% identity
                  73
NCBI Description (AL049481) putative protein [Arabidopsis thaliana]
                  19957
```

Contig ID 71554 1.R1040

5'-most EST uC-qmflminsoy024e10b1

Method BLASTN NCBI GI g2995454

NCBI GI

E value

BLAST score



```
BLAST score
                   620
E value
                  0.0e+00
                  1000
Match length
% identity
                  92
NCBI Description L.luteus mRNA for tRNA-glutamine synthetase
Seq. No.
                  19958
Contig ID
                  71554 2.R1040
5'-most EST
                  uC-gmflminsoy070d09b1
Method
                  BLASTN
NCBI GI
                  q2995454
BLAST score
                  211
E value
                  1.0e-115
Match length
                  472
                  88
% identity
NCBI Description L.luteus mRNA for tRNA-glutamine synthetase
Seq. No.
                  19959
Contig ID
                  71554 3.R1040
5'-most EST
                  fC-gmle700683850a1
                  19960
Seq. No.
Contig ID
                  71555 1.R1040
5'-most EST
                  LIB3138-037-Q1-N1-C10
Method
                  BLASTX
NCBI GI
                  g2129798
BLAST score
                  456
E value
                  2.0e-45
Match length
                  143
% identity
                  59
NCBI Description
                  pathogenesis-related protein la homolog precursor - rape
                  >gi 722274 (U21849) PR-la [Brassica napus] >gi 1575758
                   (U70666) pathogenesis-related protein PR1 [Brassica napus]
Seq. No.
                  19961
Contig ID
                  71555 2.R1040
5'-most EST
                  kmv700741379.hl
Method
                  BLASTX
NCBI GI
                  g282959
BLAST score
                  208
                  8.0e-17
E value
Match length
                  68
                  57
% identity
NCBI Description
                  pathogenesis-related protein 1b - common tobacco
                  >gi_19970_emb_CAA47374_ (X66942) prb-1b [Nicotiana tabacum]
Seq. No.
Contig ID
                  71559 1.R1040
                  zhf700954422.h1
5'-most EST
                  19963
Seq. No.
                  71560 1.R1040
Contig ID
5'-most EST
                  epx701110251.hl
Method
                  BLASTX
```

q1894771

2.0e-16

209



Match length 166 % identity 34

NCBI Description (Z92954) product highly similar to metabolite transport proteins [Bacillus subtilis] >gi\_2636109\_emb\_CAB15600.1\_(Z99122) similar to metabolite transport protein [Bacillus

subtilis]

Seq. No. 19964

Contig ID 71593 1.R1040

5'-most EST uC-gmflminsoy058d11b1

Method BLASTX
NCBI GI g1929998
BLAST score 265
E value 1.0e-22
Match length 173
% identity 49

NCBI Description (U77463) NADPH-dependent HC-toxin reductase [Hordeum

vulgare]

Seq. No. 19965

Contig ID 71593 2.R1040

5'-most EST LIB31 $\overline{3}8-038-Q1-N1-G1$ 

Method BLASTX
NCBI GI g2911362
BLAST score 423
E value 2.0e-41
Match length 178
% identity 53

NCBI Description (AF041045) NADPH HC toxin reductase [Zea mays]

Seq. No. 19966

Contig ID 71609\_1.R1040

5'-most EST LIB3138-039-Q1-N1-A3

Seq. No. 19967

Contig ID 71616 1.R1040

5'-most EST jC-gmle01810053e08d1

Seq. No. 19968

Contig ID 71658\_1.R1040

5'-most EST LIB3138-033-Q1-N1-E2

Seq. No. 19969

Contig ID 71695 1.R1040

5'-most EST LIB3138-042-Q1-N1-E7

Seq. No. 19970

Contig ID 71705\_1.R1040 5'-most EST bth700846632.h1

Seq. No. 19971

Contig ID 71711\_1.R1040 5'-most EST fC-gmro700848338a1

Method BLASTX
NCBI GI g2398525
BLAST score 345
E value 4.0e-32



Match length 150 % identity 53

NCBI Description (Y13722) Transcription factor [Arabidopsis thaliana]

Seq. No. 19972

Contig ID 71722\_1.R1040 5'-most EST leu701148221.h1

Method BLASTX
NCBI GI g2982461
BLAST score 176
E value 2.0e-12
Match length 207
% identity 31

NCBI Description (AL022223) putative protein [Arabidopsis thaliana]

Seq. No. 19973

Contig ID 71741 1.R1040

5'-most EST LIB3138-044-Q1-N1-E10

Method BLASTX
NCBI GI g3776557
BLAST score 334
E value 3.0e-31
Match length 128
% identity 52

NCBI Description (AC005388) Contains similarity to gi\_2924495 hypothetical

protein Rv1920 from Mycobacterium tuberculosis genome

gb AL022020. [Arabidopsis thaliana]

Seq. No. 19974

Contig ID 71765\_1.R1040 5'-most EST kmv700740750.h1

Seq. No. 19975

Contig ID 71778 1.R1040

5'-most EST LIB3138-047-Q1-N1-C2

Method BLASTX
NCBI GI g417488
BLAST score 436
E value 4.0e-43
Match length 150
% identity 53

NCBI Description ALPHA-GLUCAN PHOSPHORYLASE, H ISOZYME (STARCH PHOSPHORYLASE

H) >gi\_100452\_pir\_\_A40995 starch phosphorylase (EC 2.4.1.1) H - potato >gi 169473 (M69038) alpha-glucan phosphorylase

type H isozyme [Solanum tuberosum]

Seq. No. 19976

Contig ID 71780\_1.R1040 5'-most EST ssr700553595.h1

Seq. No. 19977

Contig ID 71782\_1.R1040

5'-most EST LIB3138-048-Q1-N1-A5

Seq. No. 19978

Contig ID 71800 1.R1040

5'-most EST LIB3170-071-Q1-J1-H10



55

thaliana]

% identity

```
Method
                  BLASTX
NCBI GI
                  a3395439
BLAST score
                  448
E value
                  8.0e-57
Match length
                  301
                  45
% identity
NCBI Description (AC004683) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  19979
                  71800 2.R1040
Contig ID
                  pcp700995607.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g3395439
BLAST score
                  380
E value
                  1.0e-36
Match length
                  152
% identity
                  51
NCBI Description (AC004683) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  19980
Contig ID
                  71801 1.R1040
                  xpa700796165.h1
5'-most EST
                  19981
Seq. No.
                  71807 1.R1040
Contig ID
5'-most EST
                  crh700854362.h1
Method
                  BLASTX
                  g2827655
NCBI GI
BLAST score
                  196
                  2.0e-14
E value
Match length
                  189
% identity
                  25
NCBI Description (AL021637) hypothetical protein [Arabidopsis thaliana]
                  19982
Seq. No.
                  71818 1.R1040
Contig ID
5'-most EST
                  pcp700992863.h1
                  BLASTX
Method
                  q2829887
NCBI GI
BLAST score
                  273
E value
                  4.0e-24
Match length
                  122
% identity
                  43
NCBI Description (AC002396) Hypothetical protein [Arabidopsis thaliana]
                  19983
Seq. No.
                  71826_1.R1040
Contig ID
5'-most EST
                  zhf700953751.h1
Method
                  BLASTX
NCBI GI
                  q4455276
BLAST score
                  568
E value
                  2.0e-58
Match length
                  212
```

NCBI Description (AL035527) peptide transporter-like protein [Arabidopsis



Contig ID 71832 1.R1040

5'-most EST LIB3138-049-Q1-N1-F7

Seq. No. 19985

Contig ID 71835\_1.R1040 5'-most EST uaw700666219.h1

Method BLASTX
NCBI GI g4467128
BLAST score 449
E value 1.0e-44
Match length 115
% identity 71

NCBI Description (AL035538) putative protein [Arabidopsis thaliana]

Seq. No. 19986

Contig ID 71836\_1.R1040 5'-most EST trc700562277.h1

Method BLASTX
NCBI GI g3004565
BLAST score 221
E value 5.0e-18
Match length 74
% identity 65

NCBI Description (AC003673) putative protein kinase [Arabidopsis thaliana]

Seq. No. 19987

Contig ID 71845\_1.R1040 5'-most EST ssr700555165.h1

Method BLASTX
NCBI GI g3702327
BLAST score 184
E value 1.0e-13
Match length 45
% identity 62

NCBI Description (AC005397) unknown protein [Arabidopsis thaliana]

Seq. No. 19988

Contig ID 71891\_1.R1040 5'-most EST rca700999014.h1

Method BLASTX
NCBI GI g3281846
BLAST score 287
E value 2.0e-25
Match length 71
% identity 72

NCBI Description (AJ006404) late elongated hypocotyl [Arabidopsis thaliana]

Seq. No. 19989

Contig ID 71891\_2.R1040 5'-most EST ssr700555309.h1

Seq. No. 19990

Contig ID 71900 1.R1040

5'-most EST jC-gmst02400074e05a1

Seq. No. 19991



71901 1.R1040 Contig ID

5'-most EST LIB3138-052-Q1-N1-D7

Method BLASTN NCBI GI g3329365 BLAST score 67 E value 3.0e-29Match length 179 % identity 84

NCBI Description Lotus japonicus nodule-specific protein N1j70 mRNA,

complete cds

19992 Seq. No.

Contig ID 71920 1.R1040

5'-most EST uC-gmrominsoy138h04b1

Method BLASTX NCBI GI q2827534 BLAST score 328 E value 2.0e-30 Match length 94 % identity 72

NCBI Description (AL021633) predicted protein [Arabidopsis thaliana]

19993 Seq. No.

71920 2.R1040 Contig ID 5'-most EST ek1700968265.h1

Method BLASTX g2827534 NCBI GI BLAST score 222 E value 5.0e-18 Match length 64

70 % identity

NCBI Description (AL021633) predicted protein [Arabidopsis thaliana]

19994 Seq. No.

71932 1.R1040 Contig ID 5'-most EST epx701104382.h1

19995 Seq. No.

71938 1.R1040 Contig ID

5'-most EST LIB3138-054-Q1-N1-A6

19996 Seq. No.

Contig ID 71946 1.R1040

5'-most EST LIB3138-054-Q1-N1-B5

BLASTX Method NCBI GI q4539423 BLAST score 1674 0.0e+00E value Match length 426 % identity 76

NCBI Description (AL049171) pyrophosphate-dependent phosphofructo-1-kinase

[Arabidopsis thaliana]

Seq. No. 19997

71950 1.R1040 Contig ID 5'-most EST leu701156939.h1

Method BLASTX

Method

NCBI GI

E value

BLAST score

BLASTX

601 2.0e-62

g3805853

```
NCBI GI
                  q2642158
BLAST score
                  290
E value
                  6.0e-26
Match length
                  114
% identity
                  49
NCBI Description (AC003000) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  19998
                  71970 1.R1040
Contig ID
5'-most EST
                  gsv701045037.hl
Method
                  BLASTN
                  g169326
NCBI GI
BLAST score
                  403
                  0.0e + 00
E value
Match length
                  550
% identity
                  95
NCBI Description Bean (P.vulgaris) NADP-dependent malic enzyme mRNA,
                  complete cds
                  19999
Seq. No.
                  71978 1.R1040
Contig ID
5'-most EST
                  pxt700943793.hl
Method
                  BLASTX
NCBI GI
                  g3121867
BLAST score
                  229
                  3.0e-19
E value
Match length
                  72
                  65
% identity
NCBI Description COP1 REGULATORY PROTEIN >gi 1694900 emb CAA70768 (Y09579)
                  Cop1 protein [Pisum sativum]
Seq. No.
                  20000
                  71990 1.R1040
Contig ID
5'-most EST
                  pcp700990306.hl
                  BLASTX
Method
NCBI GI
                  g4539400
BLAST score
                  174
E value
                  5.0e-12
Match length
                  163
% identity
                  39
NCBI Description (AL035526) putative protein [Arabidopsis thaliana]
                  20001
Seq. No.
                  71990 2.R1040
Contig ID
5'-most EST
                  jC-gmf102220053f09d1
Seq. No.
                  20002
                  71990 3.R1040
Contig ID
                  LIB3138-055-Q1-N1-H1
5'-most EST
Seq. No.
                  20003
                  72001 2.R1040
Contig ID
5'-most EST
                  LIB3138-040-Q1-N1-F3
```



Match length 150 % identity 77

NCBI Description (AL031986) putative protein [Arabidopsis thaliana]

Seq. No. 20004

Contig ID 72004\_1.R1040 5'-most EST pcp700991376.h1

Seq. No. 20005

Contig ID 72005 1.R1040

5'-most EST LIB3138-056-Q1-N1-G12

Method BLASTX
NCBI GI g3367516
BLAST score 806
E value 3.0e-86
Match length 260
% identity 58

NCBI Description (AC004392) Similar to beta-glucosidase BGQ60 precursor

gb\_L41869 from Hordeum vulgare. [Arabidopsis thaliana]

Seq. No. 20006

Contig ID 72010 1.R1040

5'-most EST LIB3138-056-Q1-N1-H10

Seq. No. 20007

Contig ID 72016\_1.R1040 5'-most EST pxt700945394.h1

Method BLASTX
NCBI GI g3738208
BLAST score 830
E value 7.0e-89
Match length 327
% identity 52

NCBI Description (AL031853) strong similarity to human Rev interacting

protein Rip-1 [Schizosaccharomyces pombe]

Seq. No. 20008

Contig ID 72022 1.R1040

5'-most EST LIB3170-084-Q1-J1-H12

Seq. No. 20009

Contig ID 72028\_1.R1040 5'-most EST ncj700976118.h1

Method BLASTX
NCBI GI g4538928
BLAST score 182
E value 5.0e-13
Match length 92

% identity 51

NCBI Description (AL049483) putative protein [Arabidopsis thaliana]

Seq. No. 20010

Contig ID 72040\_1.R1040 5'-most EST zzp700833979.h1

Seq. No. 20011

Contig ID 72059 1.R1040



5'-most EST vwf700676268.h1
Method BLASTX
NCBI GI g1172872
BLAST score 370
E value 2.0e-35
Match length 108
% identity 70

NCBI Description CYSTEINE PROTEINASE RD19A PRECURSOR >gi 541856\_pir\_\_JN0718 drought-inducible cysteine proteinase (EC 3.4.22.-) RD19A precursor - Arabidopsis thaliana >gi 435618 dbj BAA02373\_

(D13042) thiol protease [Arabidopsis thaliana]

>gi\_4539328\_emb\_CAB38829.1\_ (AL035679) drought-inducible
cysteine proteinase RD19A precursor [Arabidopsis thaliana]

Seq. No. 20012

Contig ID 72060\_1.R1040 5'-most EST leu701148648.h1

Method BLASTX
NCBI GI g3859534
BLAST score 737
E value 3.0e-78
Match length 148
% identity 91

NCBI Description (AF095452) asparagine synthetase [Arabidopsis thaliana]

Seq. No. 20013

Contig ID 72063\_1.R1040 5'-most EST uC-gmropic025c09b1

Seq. No. 20014

Contig ID 72076\_1.R1040
5'-most EST 94290694
Method BLASTX
NCBI GI 93107905
BLAST score 1334
E value 1.0e-164
Match length 412

Match length 412 % identity 22

NCBI Description (D85101) leaf protein [Ipomoea nil]

Seq. No. 20015

Contig ID 72080 1.R1040 5'-most EST 6HA-02-Q1-B1-G12

Method BLASTX
NCBI GI g4467147
BLAST score 295
E value 2.0e-26
Match length 75
% identity 84

NCBI Description (AL035540) putative protein [Arabidopsis thaliana]

Seq. No. 20016

Contig ID 72082 1.R1040

5'-most EST LIB3138-066-Q1-N1-D4

Method BLASTX
NCBI GI g1669655
BLAST score 354



E value 2.0e-33 Match length 154 % identity 45

NCBI Description (X95962) CER3 [Arabidopsis thaliana]

20017 Seq. No.

72083 1.R1040 Contig ID 5'-most EST 2DC-01-Q1-B1-F8

Method BLASTX g3914665 NCBI GI BLAST score 273 E value 5.0e-24 Match length 101 58 % identity

NCBI Description CHLOROPLAST 50S RIBOSOMAL PROTEIN L4 PRECURSOR

>gi 2792007\_emb\_CAA75149\_ (Y14932) chloroplast ribosomal

protein L4 [Spinacia oleracea]

20018 Seq. No.

Contig ID 72090 1.R1040

5'-most EST LIB3138-066-Q1-N1-E6

20019 Seq. No.

72099 1.R1040 Contig ID 5'-most EST rca700996321.hl

20020 Seq. No.

Contig ID 72100 1.R1040

5'-most EST jC-gmle01810059h12a1

BLASTX Method NCBI GI g1652197 254 BLAST score E value 2.0e-21 225 Match length

34 % identity

NCBI Description (D90903) hypothetical protein [Synechocystis sp.]

Seq. No. 20021

72104 1.R1040 Contig ID

5'-most EST LIB3138-100-Q1-N1-E1

Method BLASTX NCBI GI q2245136 BLAST score 144 8.0e-09 E value Match length 34 82 % identity

NCBI Description (Z97344) trehalose-6-phosphate synthase homolog

[Arabidopsis thaliana]

Seq. No. 20022

72104 2.R1040 Contiq ID 5'-most EST zhf700956127.h1

Seq. No. 20023

72123 1.R1040 Contig ID

5'-most EST LIB3138-003-Q1-N1-G11



```
20024
Seq. No.
                   72125 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy119a10b1
Method
                  BLASTX
                  g542050
NCBI GI
                  633
BLAST score
E value
                  1.0e-103
                  353
Match length
                  54
% identity
NCBI Description catechol O-methyltransferase (EC 2.1.1.6) III - common
                   tobacco >gi_429114_emb_CAA50561 (X71430) catechol
                  O-methyltransferase [Nicotiana tabacum]
                   20025
Seq. No.
Contig ID
                   72136 1.R1040
5'-most EST
                  LIB3138-003-Q1-N1-H8
Method
                  BLASTX
                  g4490325
NCBI GI
                   344
BLAST score
E value
                   3.0e-36
Match length
                  126
% identity
                   61
NCBI Description (AL035656) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   20026
Contig ID
                   72143 1.R1040
5'-most EST
                  jC-gmle01810093b03a1
Seq. No.
                   20027
                   72157 1.R1040
Contig ID
                   sat701004929.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2979554
BLAST score
                  565
E value
                   4.0e-58
                  197
Match length
% identity
                   55
NCBI Description (AC003680) CDC4 like protein [Arabidopsis thaliana]
Seq. No.
                   20028
Contig ID
                   72158 1.R1040
5'-most EST
                   awf700836674.h1
Method
                  BLASTX
NCBI GI
                  q4510377
BLAST score
                   689
                   9.0e-73
E value
Match length
                  164
% identity
                   79
NCBI Description (AC007017) putative RNA helicase A [Arabidopsis thaliana]
Seq. No.
                   20029
Contig ID
                   72160 1.R1040
```

5'-most EST jC-qmro02910074f01d1

Mothed DIACTIV

Method BLASTX
NCBI GI g3341680
BLAST score 159
E value 1.0e-10



127 Match length 39 % identity

NCBI Description (AC003672) unknown protein [Arabidopsis thaliana]

Seq. No.

20030

Contig ID 5'-most EST 72165 1.R1040 wvk700682860.hl

Method NCBI GI BLAST score E value

BLASTX q1076762 165

2.0e-11 123 Match length 16 % identity

NCBI Description AWJL175 protein - wheat >gi\_551210\_emb\_CAA57133\_ (X81368)

AWJL175 [Triticum aestivum]

Seq. No.

20031

Contig ID

72166 1.R1040

5'-most EST jC-gmle01810005g12a1

Seq. No.

20032

Contig ID

72172 1.R1040

5'-most EST

uC-gmflminsoy031h11b1

Seq. No.

20033

Contig ID 5'-most EST

72174 1.R1040 leu701154691.h1

Seq. No.

20034

Contig ID

72185 1.R1040

5'-most EST

LIB3138-006-Q1-N1-A4

Seq. No.

20035

Contig ID

72190 1.R1040

5'-most EST

LIB3138-006-Q1-N1-B2

Seq. No.

20036

Contig ID 5'-most EST 72214 1.R1040 kl1701215334.h1

Method

BLASTX

NCBI GI BLAST score g3377813

E value

193

Match length

1.0e-14 64

% identity

52 NCBI Description (AF076275) No definition line found [Arabidopsis thaliana]

Seq. No.

20037

Contig ID

72216 1.R1040

5'-most EST

LIB3138-006-Q1-N1-F10

Seq. No.

20038

Contig ID 5'-most EST 72227 1.R1040 jex700906971.h1

Method NCBI GI BLASTX

g2739002

BLAST score 643



```
E value
                   4.0e-67
Match length
                  200
% identity
                  59
NCBI Description
                  (AF022460) CYP83D1p [Glycine max]
Seq. No.
                  20039
Contig ID
                  72234 1.R1040
                  uC-gmrominsoy250e07b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3341693
BLAST score
                  160
E value
                  1.0e-10
                  93
Match length
% identity
                  35
```

NCBI Description (AC003672) unknown protein [Arabidopsis thaliana]

Seq. No. 20040 72239 1.R1040 Contig ID 5'-most EST LIB3138-007-Q1-N1-G4 Method BLASTX g2462834 NCBI GI 233 BLAST score

3.0e-19 E value Match length 92 % identity 50

(AF000657) hypothetical protein [Arabidopsis thaliana] NCBI Description

20041 Seq. No.

Contig ID 72255 1.R1040

5'-most EST LIB3138-008-Q1-N1-B12

20042 Seq. No.

72265 1.R1040 Contig ID 5'-most EST ssr700557754.h1

BLASTX Method g1694711 NCBI GI BLAST score 224 6.0e-18 E value Match length 138 36 % identity

NCBI Description (Y09581) FR01 [Arabidopsis thaliana]

Seq. No. 20043

Contig ID 72269 1.R1040

5'-most EST LIB3138-009-Q1-N1-A8

Method BLASTX NCBI GI q3290022 BLAST score 454 5.0e-45E value Match length 106 % identity 82

(AF044173) cysteine synthase; CS-B; O-acetylserine (thiol) NCBI Description

lyase; plastidic isoform [Solanum tuberosum]

Seq. No. 20044

72277 1.R1040 Contig ID ssr700554424.h1 5'-most EST



Method BLASTX
NCBI GI g534982
BLAST score 543
E value 4.0e-63
Match length 170
% identity 71

NCBI Description (X75898) phosphoglucomutase [Spinacia oleracea]

Seq. No. 20045

Contig ID 72288\_1.R1040 5'-most EST fC-gmst700667079f2

Method BLASTX
NCBI GI g4204912
BLAST score 434
E value 4.0e-42
Match length 199
% identity 47

NCBI Description (U58918) MEK kinase [Arabidopsis thaliana]

Seq. No. 20046

Contig ID 72293\_1.R1040 5'-most EST fde700874843.h1

Seq. No. 20047

Contig ID 72304 1.R1040 5'-most EST yz1700967089.h1

Seq. No. 20048

Contig ID 72316\_1.R1040 5'-most EST kl1701204812.h1

Method BLASTX
NCBI GI g3242709
BLAST score 399
E value 2.0e-38
Match length 187
% identity 44

NCBI Description (AC003040) putative guanine nucleotide-binding protein

[Arabidopsis thaliana]

Seq. No. 20049

Contig ID 72321 2.R1040 5'-most EST awf700842535.h1

Seq. No. 20050

Contig ID 72327 1.R1040

5'-most EST LIB3138-010-Q1-N1-G7

Seq. No. 20051

Contig ID 72337\_1.R1040 5'-most EST fde700877290.h1

Seq. No. 20052

Contig ID 72361 1.R1040

5'-most EST jC-gmro02910014d03a1

Method BLASTX NCBI GI g2832652 BLAST score 452

Contig ID



```
3.0e-45
E value
Match length
                   119
                   80
% identity
NCBI Description (AL021710) putative protein [Arabidopsis thaliana]
Seq. No.
                   72375 1.R1040
Contig ID
5'-most EST
                   uC-qmflminsoy031e05b1
Seq. No.
                   20054
                   72381 1.R1040
Contig ID
                   LIB3139-075-P1-N1-D1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3510253
BLAST score
                   397
E value
                   4.0e-38
Match length
                   134
% identity
                   54
NCBI Description (AC005310) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   20055
                   72382 1.R1040
Contig ID
                   uC-gmrominsoy102f11b1
5'-most EST
Method
                   BLASTX
                   g1184075
NCBI GI
BLAST score
                   146
                   3.0e-09
E value
Match length
                   85
% identity
                   39
                   (U42444) Cf-2.1 [Lycopersicon pimpinellifolium] >gi_1587673_prf__2207203A Cf-2 gene [Lycopersicon
NCBI Description
                   esculentum]
                   20056
Seq. No.
                   72402 1.R1040
Contig ID
                   LIB3139-052-P1-N1-E3
5'-most EST
Method
                   BLASTX
                   g2739008
NCBI GI
BLAST score
                   442
                   8.0e-44
E value
Match length
                   127
% identity
                   65
NCBI Description (AF022463) CYP78A3p [Glycine max]
                   20057
Seq. No.
                   72402 2.R1040
Contig ID
                   LIB3139-026-P1-N1-F1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2739008
BLAST score
                   341
E value
                   5.0e - 32
                   123
Match length
% identity
                   55
```

3237

NCBI Description (AF022463) CYP78A3p [Glycine max]

72403 1.R1040

20058



```
5'-most EST
                  fC-qmle7000742351f1
Method
                  BLASTX
NCBI GI
                  a1946368
BLAST score
                  486
E value
                  2.0e-48
Match length
                  268
% identity
                  40
NCBI Description (U93215) unknown protein [Arabidopsis thaliana]
Seq. No.
                  20059
                  72405 1.R1040
Contig ID
5'-most EST
                  jC-gmro02800023b10a1
                  BLASTX
Method
NCBI GI
                  g3941543
BLAST score
                  950
E value
                  1.0e-103
Match length
                  226
% identity
                  81
NCBI Description (AF069497) pelota [Arabidopsis thaliana]
                  >gi 4469016 emb CAB38277 (AL035602) pelota (PEL1)
                  [Arabidopsis thaliana]
                  20060
Seq. No.
Contig ID
                  72417 1.R1040
5'-most EST
                  eep700866429.h1
                  20061
Seq. No.
Contig ID
                  72433 1.R1040
5'-most EST
                  uC-gmrominsoy185h07b1
Seq. No.
                  20062
                  72433 2.R1040
Contig ID
5'-most EST
                  LIB3138-030-Q1-N1-F8
                  20063
Seq. No.
                  72433 3.R1040
Contig ID
5'-most EST
                  zzp700829624.hl
                  20064
Seq. No.
Contig ID
                  72433 4.R1040
5'-most EST
                  pcp700995011.h1
                  20065
Seq. No.
                  72435 1.R1040
Contig ID
5'-most EST
                  LIB3138-030-Q1-N1-G1
Method
                  BLASTX
NCBI GI
                  g4454051
BLAST score
                  697
E value
                  2.0e-73
Match length
                  253
% identity
NCBI Description (AL035394) putative polygalacturonase [Arabidopsis
                  thaliana]
```

Contig ID 72449 1.R1040 5'-most EST crh700852214.h1



Contig ID 72450 1.R1040

5'-most EST jC-gmle01810087g08a1

Method BLASTX
NCBI GI g399866
BLAST score 301
E value 6.0e-27
Match length 125
% identity 29

NCBI Description P59 PROTEIN (HSP BINDING IMMUNOPHILIN) (HBI) (POSSIBLE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE) (PPIASE) (ROTAMASE)

(FKBP52 PROTEIN) (52 KD FK506 BINDING PROTEIN) (P52) (FKBP59) >gi\_422824\_pir\_ A46372 immunophilin FKBP52 - human

>gi\_186390 (M88279) 'FKBP52; 52 kD FK506 binding protein'

[Homo sapiens] >gi\_4503729\_ref\_NP\_002005.1\_pFKBP4\_

FK506-binding protein 4 (59kD)

Seq. No. 20068

Contig ID 72453 1.R1040

5'-most EST LIB3138-031-Q1-N1-A4

Method BLASTN
NCBI GI g4388705
BLAST score 33
E value 8.0e-09
Match length 157
% identity 83

NCBI Description Arabidopsis thaliana chromosome I BAC F20D21 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 20069

Contig ID 72460\_1.R1040

5'-most EST LIB31 $\overline{3}$ 8-031-Q1-N1-G3

Method BLASTX
NCBI GI g123537
BLAST score 163
E value 3.0e-11
Match length 95
% identity 42

NCBI Description 12 KD HEAT SHOCK PROTEIN (GLUCOSE AND LIPID-REGULATED

PROTEIN) >gi\_72231\_pir\_\_ HHBY12 heat shock protein 12 - yeast (Saccharomyces cerevisiae) >gi\_3800\_emb\_CAA39306\_ (X55785) hsp12 [Saccharomyces cerevisiae] >gi\_171607 (M60827) 15 kD glucose and lipid regulated protein [Saccharomyces cerevisiae] >gi\_559934\_emb\_CAA86349\_ (Z46255) hsp12, glp1, len: 109, CAI: 0.65, HS12\_YEAST P22943 12 KD HEAT SHOCK PROTEIN [Saccharomyces cerevisiae] >gi\_836740\_dbj\_BAA09224\_ (D50617) 12KD heat shock protein

[Saccharomyces cerevisiae] >gi\_1100790\_dbj\_BAA08003\_(D44596) 15kD glucose and lipid regulated protein [Saccharomyces cerevisiae] >gi\_1742028\_dbj\_BAA14033\_

(D89864) Sc-Hsp12p [Saccharomyces pastorianus]

Seg. No. 20070

Contig ID 72470\_1.R1040 5'-most EST smc700748404.h1



```
Seq. No.
                   72496 1.R1040
Contig ID
5'-most EST
                   trc700566485.h1
Method
                  BLASTX
NCBI GI
                   g3426038
BLAST score
                   360
                   3.0e-38
E value
Match length
                  126
% identity
                   74
                 (AC005168) unknown protein [Arabidopsis thaliana]
NCBI Description
                   20072
Seq. No.
                  72498 1.R1040
Contig ID
                   jex70\overline{0}906980.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                   q3288823
BLAST score
                   690
E value
                   1.0e-72
Match length
                   185
                   74
% identity
NCBI Description
                  (AF063852) FUS5 [Arabidopsis thaliana]
                   20073
Seq. No.
                   72499 1.R1040
Contig ID
5'-most EST
                   vwf700677474.h1
                  BLASTX
Method
                   g1944132
NCBI GI
BLAST score
                   234
E value
                   2.0e-19
Match length
                   59
                   73
% identity
NCBI Description
                  (AB002560) CUC2 [Arabidopsis thaliana]
                   20074
Seq. No.
                   72509 1.R1040
Contig ID
                   fde700874780.h1
5'-most EST
                   BLASTX
Method
                   g4406757
NCBI GI
                   470
BLAST score
                   4.0e-47
E value
Match length
                   141
% identity
                   64
NCBI Description
                   (AC006836) putative integral membrane protein A3
                   [Arabidopsis thaliana]
                   20075
Seq. No.
Contig ID
                   72526 1.R1040
5'-most EST
                   LIB3138-033-Q1-N1-D10
                   20076
Seq. No.
```

72532\_1.R1040 Contig ID 5'-most EST leu701156286.h1

Seq. No. 20077

72543 1.R1040 Contig ID zhf700958426.h1 5'-most EST



Contig ID 72546\_1.R1040

5'-most EST jC-gmle01810011c03a1

Seq. No. 20079

Contig ID 72554\_1.R1040

5'-most EST LIB3138-034-Q1-N1-E4

Seq. No. 20080

Contig ID 72556\_1.R1040 5'-most EST bth700846645.h1

Seq. No. 20081

Contig ID 72561 1.R1040

5'-most EST LIB3138-034-Q1-N1-F4

Method BLASTX
NCBI GI g2494742
BLAST score 244
E value 8.0e-21
Match length 65

% identity 68

NCBI Description GLUTAMINE SYNTHETASE (GLUTAMATE--AMMONIA LIGASE)

>gi 2104791\_emb\_CAA73235\_ (Y12704) glutamine synthetase

[Agaricus bisporus]

Seq. No. 20082

Contig ID 72568 1.R1040

5'-most EST LIB3138-034-Q1-N1-G5

Seq. No. 20083

Contig ID 72570\_1.R1040

5'-most EST jC-gmle01810028b10a1

Seq. No. 20084

Contig ID 72579 1.R1040 5'-most EST ssr700557021.h1

Method BLASTN
NCBI GI g169295
BLAST score 311
E value 1.0e-174
Match length 687
% identity 86

NCBI Description Pharbitis nil heat shock protein 83 (Hsp83) gene, complete

cd

Seq. No. 20085

Contig ID 72579\_2.R1040 5'-most EST epx701104425.h1

Method BLASTX
NCBI GI g547684
BLAST score 627
E value 2.0e-65
Match length 167
% identity 63

NCBI Description HEAT SHOCK PROTEIN 82 >gi 100336 pir S18865 heat shock

protein 82 - common tobacco (fragment)

>gi 19880 emb CAA44877 (X63195) heat shock protein 82



## [Nicotiana tabacum]

```
Seq. No. 20086
Contig ID 72584_1.R1040
5'-most EST rca701002070.h1
```

Seq. No. 20087

Contig ID 72588 1.R1040

5'-most EST LIB3138-123-Q1-N1-E5

Seq. No. 20088

Contig ID 72614 1.R1040

5'-most EST jC-gmle01810028a10a1

Method BLASTN
NCBI GI g643454
BLAST score 214
E value 1.0e-117
Match length 416
% identity 94

NCBI Description Aureobasidium pullulans translation elongation factor

1-alpha (tef1) gene, complete cds

Seq. No. 20089

Contig ID 72614\_5.R1040 5'-most EST wvk700684818.h1

Method BLASTN
NCBI GI 94521246
BLAST score 115
E value 4.0e-58
Match length 159
% identity 93

NCBI Description Aspergillus oryzae tef gene for translation elongation

factor 1 alpha, complete cds

Seq. No. 20090

Contig ID 72618\_1.R1040
5'-most EST g5752596
Method BLASTX
NCBI GI g3298536
BLAST score 255
E value 9.0e-22
Match length 82
% identity 67

NCBI Description (AC004681) unknown protein [Arabidopsis thaliana]

Seq. No. 20091

Contig ID 72667\_1.R1040 5'-most EST rlr700896142.h1

Method BLASTX
NCBI GI g4106395
BLAST score 1608
E value 1.0e-180
Match length 403
% identity 73

NCBI Description (AF073744) raffinose synthase [Cucumis sativus]

Seq. No. 20092



Contig ID 72688\_1.R1040 5'-most EST LIB3138-044-Q1-N1-G4

Seq. No. 20093

Contig ID 72700\_1.R1040

5'-most EST jC-gmle01810067f05a1

Method BLASTX
NCBI GI g1685005
BLAST score 432
E value 1.0e-42
Match length 164
% identity 54

NCBI Description (U32644) immediate-early salicylate-induced

glucosyltransferase [Nicotiana tabacum]

Seq. No. 20094

Contig ID 72721 1.R1040

5'-most EST LIB3138-019-Q1-N1-B4

Method BLASTX
NCBI GI g1888357
BLAST score 632
E value 4.0e-66
Match length 159
% identity 71

NCBI Description (X98130) alpha-mannosidase [Arabidopsis thaliana]

>gi 1890154 emb CAA72432 (Y11767) alpha-mannosidase

precursor [Arabidopsis thaliana]

Seq. No. 20095

Contig ID 72722\_1.R1040 5'-most EST uC-gmropic062a08b1

Method BLASTX
NCBI GI g2738982
BLAST score 406
E value 2.0e-39
Match length 153
% identity 56

NCBI Description (AF022157) CYP71A10 [Glycine max]

Seq. No. 20096

Contig ID 72723 1.R1040

5'-most EST LIB3138-019-Q1-N1-B6

Seq. No. 20097

Contig ID 72727 1.R1040 5'-most EST g5605964 Method BLASTX NCBI GI g2829887 BLAST score 197 E value 1.0e-14 Match length 175 % identity 32

NCBI Description (AC002396) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 20098

Contig ID 72735\_1.R1040 5'-most EST wvk700686117.h1



```
BLASTX
Method
NCBI GI
                  q2914703
BLAST score
                  662
E value
                  2.0e-69
Match length
                  190
                  71
% identity
NCBI Description (AC003974) unknown protein [Arabidopsis thaliana]
Seq. No.
                  20099
Contig ID
                  72743 1.R1040
                  ssr700560610.hl
5'-most EST
                  BLASTX
Method
NCBI GI
                  q3582333
BLAST score
                  701
                  5.0e-95
E value
                  247
Match length
                  73
% identity
NCBI Description (AC005496) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  20100
                  72743 2.R1040
Contig ID
5'-most EST
                  jC-gmle01810053a09d1
Seq. No.
                  20101
Contig ID
                  72758 1.R1040
5'-most EST
                  LIB3138-023-Q1-N1-B2
Seq. No.
                  20102
                  72761 1.R1040
Contig ID
5'-most EST
                  LIB3138-023-Q1-N1-B5
Seq. No.
                   20103
                  72806 1.R1040
Contiq ID
5'-most EST
                  uC-gmropic101a06b1
Method
                  BLASTX
NCBI GI
                  g3236240
BLAST score
                   348
E value
                  1.0e-32
                  94
Match length
                   69
% identity
NCBI Description (AC004684) unknown protein [Arabidopsis thaliana]
Seq. No.
                   20104
Contig ID
                   72821 1.R1040
5'-most EST
                   leu701155117.h1
Method
                  BLASTN
NCBI GI
                   g3869069
BLAST score
                  33
                  1.0e-08
E value
Match length
                  164
                   88
% identity
```

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MEB5, complete sequence [Arabidopsis thaliana]

Seq. No. 20105

72821 2.R1040 Contig ID jex700905923.hl 5'-most EST

E value

Match length

% identity

0.0e+00

1109

97



```
Seq. No.
                  20106
Contig ID
                  72826 1.R1040
5'-most EST
                  jC-gmle01810059b04a1
                  20107
Seq. No.
                  72840 1.R1040
Contig ID
5'-most EST
                  LIB3138-038-Q1-N1-B4
Method
                  BLASTX
NCBI GI
                  g3822036
BLAST score
                  221
                  5.0e-18
E value
Match length
                  100
% identity
                  53
NCBI Description (AF072326) endo-1,3-1,4-beta-D-glucanase [Zea mays]
                  20108
Seq. No.
                  72845 1.R1040
Contig ID
5'-most EST
                  uC-gmflminsoy076c06b1
                  20109
Seq. No.
                  72853 1.R1040
Contig ID
5'-most EST
                  LIB3138-038-Q1-N1-D12
Seq. No.
                  20110
Contig ID
                  72866 1.R1040
5'-most EST
                  LIB3138-039-Q1-N1-B8
Method
                  BLASTX
                  g2494144
NCBI GI
BLAST score
                  997
E value
                  1.0e-108
Match length
                  279
                  50
% identity
NCBI Description (AC002329) predicted leucine-rich protein [Arabidopsis
                  thaliana]
                  20111
Seq. No.
                  72868 1.R1040
Contig ID
5'-most EST
                  rlr700900578.h1
Method
                  BLASTX
NCBI GI
                  g3980396
BLAST score
                  658
E value
                  6.0e-69
Match length
                  127
% identity
                  92
NCBI Description (AC004561) putative C-4 sterol methyl oxidase [Arabidopsis
                  thaliana]
Seq. No.
                  20112
Contig ID
                  72872 1.R1040
5'-most EST
                  epx701109518.h1
Method
                  BLASTN
NCBI GI
                  g402752
BLAST score
                  669
```



## NCBI Description G.max gene fusA

Seq. No. 20113

Contig ID 72872\_3.R1040 5'-most EST ncj700984131.h1

Method BLASTN
NCBI GI 9402752
BLAST score 92
E value 2.0e-44
Match length 206
% identity 89

NCBI Description G.max gene fusA

Seq. No. 20114

Contig ID 72873 1.R1040 5'-most EST rlr700897079.h1

Method BLASTN
NCBI GI g2827075
BLAST score 269
E value 1.0e-149
Match length 496
% identity 89

NCBI Description Medicago sativa chloroplast malate dehydrogenase precursor

(plmdh) mRNA, nuclear gene encoding chloroplast protein,

complete cds

Seq. No. 20115

Contig ID 72876\_1.R1040 5'-most EST wrg700790049.h2

Seq. No. 20116

Contig ID 72877 1.R1040

5'-most EST LIB3138-039-Q1-N1-D12

Seq. No. 20117

Contig ID 72878\_1.R1040 5'-most EST rca701001844.h1

Method BLASTX
NCBI GI g3877513
BLAST score 216
E value 3.0e-17
Match length 100
% identity 43

NCBI Description (Z66513) similar to DNAJ protein; cDNA EST EMBL:T00067

comes from this gene; cDNA EST EMBL:T02094 comes from this gene; cDNA EST EMBL:T02291 comes from this gene; cDNA EST EMBL:D71936 comes from this gene; cDNA EST EMBL:D74432

dr

Seq. No. 20118

Contig ID 72886\_1.R1040

5'-most EST jC-gmro02910046h03d1

Method BLASTX
NCBI GI g4126473
BLAST score 618
E value 2.0e-64
Match length 181
% identity 69



NCBI Description (AB014884) adenylyl cyclase associated protein [Gossypium hirsutum]

Seq. No. 20119

Contig ID 72905\_1.R1040 5'-most EST leu701157571.h1

Seq. No. 20120

Contig ID 72910\_1.R1040
5'-most EST g5606298
Method BLASTX
NCBI GI g4567251
BLAST score 201
E value 2.0e-15
Match length 51

% identity 67

NCBI Description (AC007070) unknown protein [Arabidopsis thaliana]

Seq. No. 20121

Contig ID 72921\_1.R1040 5'-most EST uC-gmropic061b12b1

Method BLASTX
NCBI GI g3790581
BLAST score 186
E value 6.0e-14
Match length 60
% identity 58

NCBI Description (AF079179) RING-H2 finger protein RHBla [Arabidopsis

thaliana]

Seq. No. 20122

Contig ID 72921\_3.R1040 5'-most EST bth700849096.h1

Method BLASTX
NCBI GI g3790581
BLAST score 182
E value 2.0e-13
Match length 63
% identity 51

NCBI Description (AF079179) RING-H2 finger protein RHB1a [Arabidopsis

thaliana]

Seq. No. 20123

Contig ID 72921\_4.R1040

5'-most EST LIB3138-040-Q1-N1-H8

Method BLASTX
NCBI GI g3790581
BLAST score 201
E value 1.0e-15
Match length 70
% identity 54

NCBI Description (AF079179) RING-H2 finger protein RHBla [Arabidopsis

thaliana]

Seq. No. 20124

Contig ID 72922\_1.R1040

5'-most EST LIB3138-040-Q1-N1-H9



Method BLASTX NCBI GI g1495251 BLAST score 434 E value 7.0e-43 92 Match length 89 % identity

NCBI Description (Z70314) heat-shock protein [Arabidopsis thaliana]

Seq. No. Contig ID 5'-most EST 20125 72924 1.R1040 trc700562221.h1

Seq. No.

20126

Contig ID 5'-most EST 72925 1.R1040 sat701004938.h1

Seq. No.

20127

Contig ID

72935 1.R1040

5'-most EST

LIB3138-050-Q1-N1-F10

Method BLASTX NCBI GI g2492597 BLAST score 227 1.0e-18 E value Match length 102 % identity 46

NCBI Description HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN SLL0182

>gi 1001688 dbj BAA10424 (D64002) ABC transporter

[Synechocystis sp.]

Seq. No.

20128

Contig ID

72937 1.R1040

5'-most EST

LIB3138-041-Q1-N1-G10

Seq. No.

20129

Contig ID 5'-most EST

72940 1.R1040 wvk700685406.hl

Seq. No.

20130

Contig ID 5'-most EST 72940 2.R1040 epx701106989.h1

Seq. No.

20131

Contig ID 5'-most EST 72940 3.R1040 rca700999101.h1

Seq. No.

20132

Contig ID

72941 1.R1040

5'-most EST

LIB3138-041-Q1-N1-H12

Method BLASTX NCBI GI g3122765 BLAST score 656 E value 2.0e-68 Match length 358 % identity 43

NCBI Description DNA-DIRECTED RNA POLYMERASE III LARGEST SUBUNIT (RPC155) >gi 2460208 (AF021351) RNA polymerase III largest subunit

[Homo sapiens]



Seq. No. 20133 72961 1.R1040 Contig ID 5'-most EST LIB3138-043-Q1-N1-B3 20134 Seq. No. Contig ID 72968 1.R1040 5'-most EST jC-gmle01810093g08a1 Seq. No. 20135 Contig ID 72978 1.R1040 uC-gmrominsoy298a09b1 5'-most EST BLASTX Method NCBI GI q3935187 BLAST score 346 E value 2.0e-63

Match length 171 % identity 71

NCBI Description (AC004557) F17L21.30 [Arabidopsis thaliana]

20136 Seq. No. 73004 1.R1040 Contig ID

5'-most EST LIB3138-046-Q1-N1-E3

Seq. No. 20137

Contig ID 73008 1.R1040

5'-most EST LIB3138-043-Q1-N1-A4

Method BLASTN NCBI GI g210811 BLAST score 67 E value 1.0e-29 Match length 151 % identity 86

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 20138

73052 1.R1040 Contig ID

5'-most EST LIB3167-023-P4-K4-G2

20139 Seq. No.

73056 1.R1040 Contig ID

5'-most EST LIB3138-047-Q1-N1-H8

20140 Seq. No.

73082 1.R1040 Contig ID

5'-most EST jC-gmle01810061c05d1

Seq. No. 20141

73086 1.R1040 Contig ID

5'-most EST LIB3138-049-Q1-N1-B8

Method BLASTX g2190540 NCBI GI BLAST score 413 E value 1.0e-40 Match length 101 % identity 72



NCBI Description (AC001229) Similar to Arabidopsis TFL1 (gb\_U77674). [Arabidopsis thaliana]

Seq. No. 20142

Contig ID 73087 1.R1040

5'-most EST LIB3138-049-Q1-N1-B9

Seq. No. 20143

Contig ID 73093\_1.R1040

5'-most EST LIB3139-072-P1-N1-C6

Method BLASTX
NCBI GI g3775999
BLAST score 457
E value 4.0e-45
Match length 101
% identity 85

NCBI Description (AJ010463) RNA helicase [Arabidopsis thaliana]

Seq. No. 20144

Contig ID 73099\_1.R1040 5'-most EST crh700850378.h1

Seq. No. 20145

Contig ID 73108\_1.R1040

5'-most EST jC-gmle01810005e10a1

Seq. No. 20146

Contig ID 73108\_2.R1040

5'-most EST uC-gmflminsoy055g01b1

Seq. No. 20147

Contig ID 73118 1.R1040 5'-most EST ncj700978919.h1

Seq. No. 20148

Contig ID 73130\_1.R1040

5'-most EST LIB3138-050-Q1-N1-F12

Method BLASTX
NCBI GI g3482970
BLAST score 320
E value 1.0e-29
Match length 106
% identity 69

NCBI Description (AL031369) putative protein [Arabidopsis thaliana]

Seq. No. 20149

Contig ID 73159\_1.R1040 5'-most EST pcp700988804.h1

Method BLASTX
NCBI GI g2444180
BLAST score 1229
E value 1.0e-135
Match length 272
% identity 87

NCBI Description (U94785) unconventional myosin [Helianthus annuus]

Seq. No. 20150



73162 1.R1040 Contig ID 5'-most EST LIB3138-051-Q1-N1-H5 Method BLASTX NCBI GI g2529665 BLAST score 305 E value 9.0e-44 147 Match length % identity 64 NCBI Description (AC002535) putative ribosomal protein L7A [Arabidopsis thaliana] Seq. No. 20151 Contig ID 73169 1.R1040 5'-most EST LIB3138-052-Q1-N1-A4 Method BLASTX NCBI GI q3033389 BLAST score 156 5.0e-10 E value Match length 82 % identity 38 NCBI Description (AC004238) Cf-2.1-like protein [Arabidopsis thaliana] 20152 Seq. No. Contig ID 73189 1.R1040 5'-most EST LIB3138-015-Q1-N1-G9 BLASTX Method NCBI GI q4115379 BLAST score 843 2.0e-90 E value Match length 286 59 % identity NCBI Description (AC005967) putative carbonyl reductase [Arabidopsis thaliana] Seq. No. 20153 Contig ID 73206 1.R1040 5'-most EST LIB3138-053-Q1-N1-D7 Seq. No. 20154 Contig ID 73225 1.R1040 5'-most EST uC-gmrominsoy214c06b1 20155 Seq. No. 73238 1.R1040 Contig ID 5'-most EST LIB3138-054-Q1-N1-G3 Seq. No. 20156 Contig ID 73250 1.R1040 5'-most EST seb700649147.h1 Seq. No. 20157

Contig ID 73264\_1.R1040

5'-most EST LIB3138-002-Q1-N1-B7

Seq. No. 20158

Contig ID 73265 1.R1040 5'-most EST vwf700674452.h1



Method BLASTX
NCBI GI g2829887
BLAST score 654
E value 1.0e-68
Match length 170
% identity 74

NCBI Description (AC002396) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 20159

Contig ID 73267\_1.R1040 5'-most EST hrw701060682.h1

Method BLASTX
NCBI GI g1653291
BLAST score 312
E value 3.0e-31
Match length 138
% identity 48

NCBI Description (D90912) hypothetical protein [Synechocystis sp.]

Seq. No. 20160

Contig ID 73281\_1.R1040 5'-most EST kmv700740113.h1

Method BLASTX
NCBI GI g4539422
BLAST score 915
E value 6.0e-99
Match length 270
% identity 64

NCBI Description (AL049171) putative protein [Arabidopsis thaliana]

Seq. No. 20161

Contig ID 73283\_1.R1040 5'-most EST uxk700669688.h1

Method BLASTX
NCBI GI g3510253
BLAST score 411
E value 9.0e-40
Match length 147
% identity 54

NCBI Description (AC005310) hypothetical protein [Arabidopsis thaliana]

Seq. No. 20162

Contig ID 73293\_1.R1040 5'-most EST kmv700738721.h1

Method BLASTX
NCBI GI g1653608
BLAST score 145
E value 1.0e-08
Match length 92
% identity 39

NCBI Description (D90915) hypothetical protein [Synechocystis sp.]

Seq. No. 20163

Contig ID 73329\_1.R1040 5'-most EST smc700748172.h1

Seq. No. 20164



Contig ID 73351 1.R1040 g4397006 5'-most EST Method BLASTX NCBI GI q1361982 BLAST score 233 4.0e-19 E value 144 Match length 35 % identity

NCBI Description 4-coumarate--CoA ligase (EC 6.2.1.12) - Arabidopsis

thaliana >qi 609340 (U18675) 4-coumarate--coenzyme A ligase

[Arabidopsis thaliana]

Seq. No. 20165

Contig ID 73352 1.R1040

5'-most EST LIB3170-013-Q1-J1-F6

Seq. No. 20166

Contig ID 73353 1.R1040

5'-most EST LIB3138-066-Q1-N1-A11

Seq. No. 20167

Contig ID 73354\_1.R1040 5'-most EST zhf700959734.h1

Seq. No. 20168

Contig ID 73355\_1.R1040

5'-most EST LIB3138-066-Q1-N1-A4

Method BLASTX
NCBI GI g3928096
BLAST score 209
E value 2.0e-16
Match length 97

% identity 41

NCBI Description (AC005770) hypothetical protein [Arabidopsis thaliana]

Seq. No. 20169

Contig ID 73362\_1.R1040

5'-most EST LIB3138-066-Q1-N1-B2

Method BLASTX
NCBI GI g2832685
BLAST score 422
E value 1.0e-41
Match length 111
% identity 70

NCBI Description (AL021712) putative protein [Arabidopsis thaliana]

Seq. No. 20170

Contig ID 73363\_1.R1040 5'-most EST trc700562250.h1

Method BLASTX
NCBI GI g3582343
BLAST score 213
E value 5.0e-17
Match length 113
% identity 42

NCBI Description (AC005496) putative flavonol 3-o-glucosyltransferase

[Arabidopsis thaliana]



Contig ID 73381 1.R1040

5'-most EST jC-gmle01810048f10a1

Method BLASTX
NCBI GI g2065436
BLAST score 264
E value 9.0e-23
Match length 202
% identity 10

NCBI Description (Y12709) tealp [Schizosaccharomyces pombe]

>gi 3618212 emb CAA20875 (AL031579) cell polarity protein

[Schizosaccharomyces pombe]

Seq. No. 20172

Contig ID 73388\_1.R1040 5'-most EST ncj700978411.h1

Method BLASTN
NCBI GI g294665
BLAST score 199
E value 1.0e-107
Match length 635
% identity 83

NCBI Description Castor bean chloroplast beta-ketoacyl-ACP synthase mRNA,

complete cds

Seq. No. 20173

Contig ID 73389 1.R1040 5'-most EST zsg701117911.h2

Seq. No. 20174

Contig ID 73393 1.R1040

5'-most EST LIB3138-003-Q1-N1-C8

Method BLASTX
NCBI GI g2160692
BLAST score 777
E value 8.0e-83
Match length 195
% identity 77

NCBI Description (U73527) B' regulatory subunit of PP2A [Arabidopsis

thaliana]

Seq. No. 20175

Contig ID 73399\_1.R1040
5'-most EST g5606917
Method BLASTN
NCBI GI g4138188
BLAST score 34
E value 3.0e-09

Match length 58 % identity 90

NCBI Description M.fuscata microsatellite DNA, MFGT27 region

Seq. No. 20176

Contig ID 73402\_1.R1040 5'-most EST epx701109988.h1

Method BLASTN



```
q4324494
NCBI GI
                  370
BLAST score
                  0.0e + 00
E value
Match length
                  754
% identity
                  97
                  Glycine max glutamyl-tRNA reductase precursor (gtr1) gene,
NCBI Description
                  complete cds
                  20177
Seq. No.
                  73402 2.R1040
Contig ID
                  bth700843591.h1
5'-most EST
                  BLASTN
Method
                  g4324494
NCBI GI
BLAST score
                   142
                   6.0e-74
E value
Match length
                   395
% identity
                   90
                  Glycine max glutamyl-tRNA reductase precursor (gtr1) gene,
NCBI Description
                   complete cds
                   20178
Seq. No.
                   73406 1.R1040
Contig ID
                   LIB3138-003-Q1-N1-E6
5'-most EST
                   BLASTX
Method
                   g4512688
NCBI GI
BLAST score
                   489
                   3.0e-49
E value
                   194
Match length
                   55
% identity
NCBI Description (AC006931) hypothetical protein [Arabidopsis thaliana]
                   20179
Seq. No.
                   73408 1.R1040
Contig ID
                   ejt700606134.h2
5'-most EST
                   BLASTX
Method
                   g4154352
NCBI GI
                   487
BLAST score
                   1.0e-48
E value
                   313
Match length
                   36
 % identity
NCBI Description (AF110333) PrMC3 [Pinus radiata]
                   20180
 Seq. No.
                   73410 1.R1040
 Contig ID
                   LIB3138-004-Q1-N1-B7
 5'-most EST
                   BLASTX
 Method
                   g3451068
 NCBI GI
                   273
 BLAST score
                   5.0e-24
 E value
                   100
 Match length
 % identity
                   56
 NCBI Description (AL031326) putative protein [Arabidopsis thaliana]
```

Contig ID 73413 1.R1040

5'-most EST LIB3138-004-Q1-N1-C1

BLAST score

E value

142

1.0e-08



```
20182
Seq. No.
Contig ID
                  73415 1.R1040
5'-most EST
                  trc700563435.h1
Method
                  BLASTX
NCBI GI
                  g3831443
BLAST score
                  325
E value
                  5.0e-30
Match length
                  90
                  70
% identity
NCBI Description (AC005819) putative auxin-regulated protein [Arabidopsis
                  thaliana]
                  20183
Seq. No.
                  73424 1.R1040
Contig ID
                  pmv700892842.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2342719
BLAST score
                  339
E value
                  1.0e-31
Match length
                  146
% identity
                  46
NCBI Description (AC002341) SF16 protein isolog [Arabidopsis thaliana]
                  20184
Seq. No.
Contig ID
                  73429 1.R1040
                  g5058493
5'-most EST
Method
                  BLASTX
NCBI GI
                  a3649778
BLAST score
                  895
E value
                  2.0e-96
Match length
                  344
                  51
% identity
NCBI Description (AJ011303) pepc2 [Vicia faba]
                  20185
Seq. No.
                  73431 2.R1040
Contig ID
                  leu701145851.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g166341
BLAST score
                  158
E value
                  2.0e-10
Match length
                  71
% identity
NCBI Description (M98267) alliinase [Allium cepa] >gi 1044969 (L48614)
                  allinase [Allium cepa]
                  20186
Seq. No.
                  73431 3.R1040
Contig ID
5'-most EST
                  LIB3138-004-Q1-N1-E1
                  20187
Seq. No.
                  73438 1.R1040
Contig ID
5'-most EST
                  jC-gmle01810071d09a1
Method
                  BLASTX
                  g1001449
NCBI GI
```



Match length 117 % identity 29

NCBI Description (D63999) hypothetical protein [Synechocystis sp.]

Seq. No. 20188

Contig ID 73439\_1.R1040

5'-most EST LIB3138-004-Q1-N1-F2

Method BLASTX
NCBI GI g2623298
BLAST score 260
E value 2.0e-22
Match length 105
% identity 68

NCBI Description (AC002409) putative 4-alpha-glucanotransferase [Arabidopsis

thaliana]

Seq. No. 20189

Contig ID 73442\_1.R1040 5'-most EST trc700562148.h1

Method BLASTN
NCBI GI g2627180
BLAST score 530
E value 0.0e+00
Match length 858
% identity 90

NCBI Description Pisum sativum mRNA for cycloartenol synthase, complete cds

Seq. No. 20190

Contig ID 73452 1.R1040 5'-most EST leu701151993.h1

Method BLASTX
NCBI GI g3176676
BLAST score 335
E value 6.0e-31
Match length 107
% identity 60

NCBI Description (AC003671) Similar to carbonic anhydrase gb L19255 from

Nicotiana tabacum. ESTs gb\_AA597643, gb\_T45390, gb\_T43963 and gb\_AA597734 come from this gene. [Arabidopsis thaliana]

Seq. No. 20191

Contig ID 73470\_1.R1040

5'-most EST LIB3138-005-Q1-N1-G3

Seq. No. 20192

Contig ID 73478\_1.R1040

5'-most EST LIB3138-005-Q1-N1-H3

Seq. No. 20193

Contig ID 73483\_1.R1040

5'-most EST LIB3138-006-Q1-N1-A11

Seq. No. 20194

Contig ID 73484 1.R1040 5'-most EST leu701155458.h1

Seq. No. 20195



73489 1.R1040 Contig ID leu701157821.h1 5'-most EST

Method BLASTN NCBI GI g3236477 BLAST score 94 2.0e-45 E value Match length 194 % identity 87

Gossypium hirsutum 26S protease regulatory subunit (PRA2) NCBI Description

mRNA, partial cds

Seq. No. 20196

73498 1.R1040 Contig ID

5'-most EST jC-gmle01810060f05a1

20197 Seq. No.

73517 1.R1040 Contig ID 5'-most EST zhf700954721.h1

BLASTX Method q3738304 NCBI GI BLAST score 300 E value 6.0e-27 Match length 81 % identity 64

(AC005309) hypothetical protein [Arabidopsis thaliana] NCBI Description

20198 Seq. No.

73518 2.R1040 Contig ID

LIB3138-007-Q1-N1-D3 5'-most EST

Method BLASTX NCBI GI g3510253 339 BLAST score 1.0e-31 E value Match length 116

% identity

NCBI Description (AC005310) hypothetical protein [Arabidopsis thaliana]

20199 Seq. No.

73518 3.R1040 Contig ID

jC-gmle01810055h04a1 5'-most EST

BLASTX Method NCBI GI g3510253 BLAST score 204 E value 1.0e-15 Match length 214 45 % identity

NCBI Description (AC005310) hypothetical protein [Arabidopsis thaliana]

20200 Seq. No.

Contig ID 73518 4.R1040 5'-most EST kmv700743220.h1

Method BLASTX g3510253 NCBI GI BLAST score 358 5.0e-34 E value Match length 118 64 % identity



```
(AC005310) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   20201
Seq. No.
                   73522 1.R1040
Contig ID
5'-most EST
                   kmv700743684.hl
                   20202
Seq. No.
Contig ID
                   73524 1.R1040
                   LIB3138-007-Q1-N1-E2
5'-most EST
Seq. No.
                   20203
                   73529 1.R1040
Contig ID
                   rca70\overline{1}001686.h1
5'-most EST
                   20204
Seq. No.
                   73531 1.R1040
Contig ID
5'-most EST
                   vzy700755309.hl
Method
                   BLASTX
                   g2462839
NCBI GI
BLAST score
                   410
                   3.0e-46
E value
Match length
                   231
                   49
% identity
                  (AF000657) unknown protein [Arabidopsis thaliana]
NCBI Description
                   20205
Seq. No.
                   73536 1.R1040
Contig ID
                   uC-gmropic061b01b1
5'-most EST
Method
                   BLASTX
                   q2944180
NCBI GI
BLAST score
                   148
                   2.0e-09
E value
                   97
Match length
                   43
% identity
                   (AF007779) trehalose-6-phosphate phosphatase [Arabidopsis
NCBI Description
                   thaliana]
                   20206
Seq. No.
                   73560 1.R1040
Contig ID
5'-most EST
                   LIB3138-009-Q1-N1-G5
                   BLASTX
Method
                   g629561
NCBI GI
                   593
BLAST score
                   3.0e-61
E value
                   186
Match length
                   59
```

% identity SRG1 protein - Arabidopsis thaliana NCBI Description

>gi\_479047\_emb\_CAA55654\_ (X79052) SRG1 [Arabidopsis

thaliana]

Seq. No. Contig ID 20207

73565 1.R1040

LIB3138-009-Q1-N1-H12 5'-most EST

Seq. No.

20208

73567 1.R1040 Contig ID V4L-02-Q1-E1-C4 5'-most EST



```
Seq. No.
                  20209
Contig ID
                  73569 1.R1040
5'-most EST
                  LIB3138-010-Q1-N1-A1
Seq. No.
                  20210
Contig ID
                  73575 1.R1040
                  LIB3139-106-P1-N1-B5
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3894166
BLAST score
                  168
E value
                  6.0e-15
Match length
                  114
                  41
% identity
NCBI Description (AC005312) similar to phloem-specific lectin [Arabidopsis
                  thaliana]
Seq. No.
                  20211
Contig ID
                  73575 3.R1040
5'-most EST
                  uC-gmropic050g10b1
Method
                  BLASTX
NCBI GI
                  g3894159
BLAST score
                  240
                  3.0e-20
E value
Match length
                  120
% identity
                  40
NCBI Description (AC005312) hypothetical protein [Arabidopsis thaliana]
                  20212
Seq. No.
Contig ID
                  73614 1.R1040
5'-most EST
                  gsv701050902.h1
Method
                  BLASTX
NCBI GI
                  q4138209
BLAST score
                  301
E value
                  3.0e-27
Match length
                  127
                  42
% identity
NCBI Description
                  (AJ223071) serine/threonine kinase protein MSTK2L,long-form
                  [Mus musculus]
                  20213
Seq. No.
                  73625 1.R1040
Contig ID
                  wvk700685792.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q1651689
BLAST score
                  282
                  8.0e-25
E value
                  138
Match length
% identity
                  47
NCBI Description
                 (D90899) hypothetical protein [Synechocystis sp.]
Seq. No.
                  20214
```

Contig ID 73640\_1.R1040 5'-most EST kmv700740633.h1

Method BLASTX NCBI GI g3063709 BLAST score 147



E value 4.0e-09
Match length 80
% identity 46

NCBI Description (AL022537) putative protein [Arabidopsis thaliana]

Seq. No. 20215

Contig ID 73640\_2.R1040 5'-most EST dpv701099352.h1

Method BLASTX
NCBI GI g3063709
BLAST score 141
E value 1.0e-08
Match length 68
% identity 50

NCBI Description (AL022537) putative protein [Arabidopsis thaliana]

Seq. No. 20216

Contig ID 73653\_1.R1040

5'-most EST LIB3138-028-Q1-N1-G12

Seq. No. 20217

Contig ID 73656\_1.R1040

5'-most EST LIB3138-028-Q1-N1-G7

Seq. No. 20218

Contig ID 73687\_1.R1040 5'-most EST kwa701015552.h1

Method BLASTX
NCBI GI g2253010
BLAST score 657
E value 6.0e-69
Match length 148
% identity 82

NCBI Description (Y14199) MAP3K delta-1 protein kinase [Arabidopsis

thaliana]

Seq. No. 20219

Contig ID 73695\_1.R1040

5'-most EST jC-gmfl02220088f07a1

Seq. No. 20220

Contig ID 73697\_1.R1040

5'-most EST uC-gmrominsoy095d10b1

Seq. No. 20221

Contig ID 73699\_1.R1040

5'-most EST LIB3138-030-Q1-N1-C8

Seq. No. 20222

Contig ID 73705\_1.R1040 5'-most EST trc700565129.h1

Seq. No. 20223

Contig ID 73716\_1.R1040

5'-most EST LIB3138-031-Q1-N1-C11

Method BLASTX NCBI GI g3928543



BLAST score 577 E value 5.0e-59 Match length 443 % identity 36

NCBI Description (AB016819) UDP-glucose glucosyltransferase [Arabidopsis

thaliana]

Seq. No. 20224

Contig ID 73720\_1.R1040 5'-most EST zhf700952490.h1

Seq. No. 20225

Contig ID 73741 1.R1040

5'-most EST LIB3138-031-Q1-N1-F3

Seq. No. 20226

Contig ID 73743 1.R1040

5'-most EST LIB3138-032-Q1-N1-C6

Method BLASTX
NCBI GI 94455304
BLAST score 201
E value 2.0e-33
Match length 153
% identity 53

NCBI Description (AL035528) hypothetical protein [Arabidopsis thaliana]

Seq. No. 20227

Contig ID 73757\_1.R1040 5'-most EST cle700967802.h1

Seq. No. 20228

Contig ID 73768 1.R1040

5'-most EST LIB3138-032-Q1-N1-G11

Method BLASTX
NCBI GI g2765817
BLAST score 432
E value 9.0e-43
Match length 112
% identity 68

NCBI Description (Z95352) AtMlo-hl [Arabidopsis thaliana]

>gi\_3892049\_gb\_AAC78258.1\_AAC78258 (AC002330) AtMlo-hl

[Arabidopsis thaliana]

Seq. No. 20229

Contig ID 73777\_1.R1040

5'-most EST LIB3138-032-Q1-N1-H12

Seq. No. 20230

Contig ID 73784 1.R1040

5'-most EST LIB3138-033-Q1-N1-F10

Method BLASTX
NCBI GI g2832304
BLAST score 507
E value 2.0e-51
Match length 172
% identity 56

NCBI Description (AF044489) receptor-like protein kinase [Oryza sativa]



```
20231
Seq. No.
Contig ID
                  73788 1.R1040
5'-most EST
                  smc700745082.h1
                  20232
Seq. No.
Contig ID
                  73807 1.R1040
5'-most EST
                  pxt700945763.hl
Method
                  BLASTX
                  g3395428
NCBI GI
BLAST score
                  249
                  9.0e-21
E value
                  74
Match length
                  70
% identity
NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]
Seq. No.
                  20233
Contig ID
                  73807 2.R1040
                  LIB3139-092-P1-N1-E5
5'-most EST
                  BLASTX
Method
NCBI GI
                  q3395428
BLAST score
                  178
E value
                  7.0e-13
Match length
                  49
                  78
% identity
NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]
                  20234
Seq. No.
Contig ID
                  73833 1.R1040
                  LIB3138-035-Q1-N1-D4
5'-most EST
Method
                  BLASTX
NCBI GI
                  g4115379
BLAST score
                  568
E value
                  3.0e-58
                  201
Match length
                  57
% identity
NCBI Description (AC005967) putative carbonyl reductase [Arabidopsis
                  thaliana]
Seq. No.
                  20235
Contig ID
                  73845 1.R1040
5'-most EST
                  pxt700946458.h1
Method
                  BLASTX
NCBI GI
                  q2809246
                  186
BLAST score
E value
                  1.0e-13
Match length
                  56
% identity
                  57
NCBI Description (AC002560) F2401.15 [Arabidopsis thaliana]
Seq. No.
                  20236
                  73845 2.R1040
Contig ID
```

rca700999891.hl 5'-most EST

20237 Seq. No.

Contig ID 73854 1.R1040

5'-most EST LIB3138-002-Q1-N1-A1



Contig ID 73856 1.R1040

5'-most EST LIB3138-002-Q1-N1-A12

BLASTX Method g3116132 NCBI GI BLAST score 475 E value 1.0e-47 Match length 142 % identity

NCBI Description (AL023288) ribosomal protein [Schizosaccharomyces pombe]

>gi\_3201578\_dbj\_BAA28752\_ (AB015169) ribosomal protein L19

homolog [Schizosaccharomyces pombe]

20239 Seq. No.

73888 1.R1040 Contig ID 5'-most EST g5677167

Seq. No. 20240

73890 1.R1040 Contig ID

5'-most EST LIB3138-001-Q1-N1-A8

Method BLASTX NCBI GI g4559356 BLAST score 226 E value 1.0e-18 Match length 131

% identity 11

NCBI Description (AC006585) hypothetical protein [Arabidopsis thaliana]

20241 Seq. No.

73901 1.R1040 Contig ID

5'-most EST uC-gmrominsoy230h12b1

Method BLASTX NCBI GI g2190553 BLAST score 288 E value 1.0e-25 Match length 131 % identity 63

(AC001229) Strong similarity to Arabidopsis NCBI Description

zeta-crystallin-like protein (gb\_Z49268). [Arabidopsis

thaliana]

Seq. No. 20242

73905 1.R1040 Contig ID

5'-most EST uC-gmflminsoy043c02b1

Seq. No. 20243

73906 1.R1040 Contig ID

5'-most EST LIB3138-001-Q1-N1-E3

Seq. No. 20244

73917 2.R1040 Contig ID 5'-most EST  $crh70\overline{0}855376.h1$ 

Seq. No. 20245

Contig ID 73917 3.R1040

5'-most EST LIB3138-001-Q1-N1-H8



Contig ID 73924 1.R1040

5'-most EST LIB3138-004-Q1-N1-B5

Seq. No. 20247

Contig ID 73935 1.R1040

5'-most EST uC-gmrominsoy073h05b1

Seq. No. 20248

Contig ID 73984 1.R1040

5'-most EST LIB3138-011-Q1-N1-A12

Seq. No. 20249

Contig ID 73993 1.R1040

5'-most EST LIB3138-011-Q1-N1-B12

Seq. No. 20250

Contig ID 74022 1.R1040

5'-most EST jC-gmst02400011f08a1

Method BLASTX
NCBI GI g3660465
BLAST score 850
E value 3.0e-91
Match length 299
% identity 55

NCBI Description (AJ001753) Inositol 1,3,4-Trisphosphate 5/6 kinase

[Arabidopsis thaliana]

Seq. No. 20251

Contig ID 74031\_1.R1040 5'-most EST zsg701127593.h1

Method BLASTX
NCBI GI 94455367
BLAST score 646
E value 8.0e-68
Match length 139
% identity 51

NCBI Description (AL035524) putative protein [Arabidopsis thaliana]

Seq. No. 20252

Contig ID 74033\_1.R1040

5'-most EST fC-gmle7000741249a1

Method BLASTX
NCBI GI g2499613
BLAST score 410
E value 6.0e-40
Match length 94
% identity 78

NCBI Description MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG MMK2

>gi\_1204129\_emb\_CAA57719\_ (X82268) protein kinase [Medicago

sativa]

Seq. No. 20253

Contig ID 74036\_1.R1040 5'-most EST g4396501 Method BLASTX

```
NCBI GI
                  q2316016
BLAST score
                   582
E value
                   3.0e-60
Match length
                  165
                   33
% identity
NCBI Description
                  (U92650) MRP-like ABC transporter [Arabidopsis thaliana]
Seq. No.
                  20254
                  74056 2.R1040
Contig ID
5'-most EST
                  epx701104601.hl
Method
                  BLASTX
NCBI GI
                  q3643610
BLAST score
                  154
E value
                   4.0e-10
                  33
Match length
                   85
% identity
NCBI Description
                   (AC005395) putative serine/threonine protein kinase
                   [Arabidopsis thaliana]
Seq. No.
                   20255
                   74057 1.R1040
Contig ID
5'-most EST
                  wvk700686167.hl
Method
                  BLASTX
NCBI GI
                  g3096910
BLAST score
                   324
E value
                  7.0e-30
Match length
                  100
% identity
                   59
                   (AJ005813) neoxanthin cleavage enzyme [Arabidopsis
NCBI Description
                  thaliana]
                   20256
Seq. No.
Contig ID
                   74057 2.R1040
5'-most EST
                   rca700998178.h1
Method
                  BLASTX
NCBI GI
                   g3096910
BLAST score
                   397
                   5.0e-42
E value
                  105
Match length
                   83
% identity
                  (AJ005813) neoxanthin cleavage enzyme [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   20257
Contig ID
                   74075 1.R1040
5'-most EST
                  LIB3138-011-Q1-N2-G4
Method
                  BLASTX
NCBI GI
                  g4314378
BLAST score
                   353
                   4.0e-33
E value
Match length
                  172
                   46
% identity
```

NCBI Description

Contig ID 74076\_1.R1040

5'-most EST uC-gmflminsoy071h08b2

(AC006232) putative lipase [Arabidopsis thaliana]

% identity

86



```
BLASTN
Method
                  g2062691
NCBI GI
                  33
BLAST score
                  5.0e-09
E value
                  37
Match length
% identity
                  61
NCBI Description Human sodium phosphate transporter (NPT4) mRNA, complete
                  20259
Seq. No.
Contig ID
                  74100 1.R1040
5'-most EST
                  LIB3138-061-Q1-N1-G5
Method
                  BLASTX
                  g2266947
NCBI GI
BLAST score
                  1994
E value
                  0.0e+00
Match length
                  449
% identity
                  87
NCBI Description (AF008939) phosphoenolpyruvate carboxylase 1 [Gossypium
                  hirsutum]
                  20260
Seq. No.
                  74134 1.R1040
Contig ID
5'-most EST
                  zhf700954523.hl
Method
                  BLASTX
                  g3413706
NCBI GI
BLAST score
                  735
                  1.0e-77
E value
Match length
                  233
                  56
% identity
NCBI Description (AC004747) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  20261
                  74140 1.R1040
Contig ID
5'-most EST
                  zsg701120218.hl
Seq. No.
                  20262
                  74141 1.R1040
Contig ID
5'-most EST
                  jC-gmro02800039f06a1
Method
                  BLASTX
                  g3386618
NCBI GI
BLAST score
                  146
E value
                  3.0e-09
Match length
                  86
% identity
NCBI Description (AC004665) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  20263
Contig ID
                  74154 1.R1040
5'-most EST
                  LIB3138-013-Q1-N1-B3
Method
                  BLASTN
NCBI GI
                  g1022364
BLAST score
                  125
E value
                  7.0e-64
                  364
Match length
```

NCBI Description V.faba mRNA for sucrose phosphate synthase

20264 Seq. No. Contig ID 74167 1.R1040 5'-most EST LIB3138-013-Q1-N1-D1 Method BLASTX NCBI GI g3322278 BLAST score 151 E value 9.0e-10 Match length 123 % identity (AE001187) conserved hypothetical protein [Treponema NCBI Description pallidum] 20265 Seq. No. 74169 1.R1040 Contig ID 5'-most EST zhf700962388.h1 Seq. No. 20266 Contig ID 74185 1.R1040 5'-most EST kmv700737879.h1 Method BLASTN q887572 NCBI GI 250 BLAST score 1.0e-138 E value Match length 621 % identity 85 NCBI Description P.sativum mRNA for starch synthase (2988 bp) Seq. No. 20267 74188 1.R1040 Contig ID 5'-most EST ejt700606271.h1 Seq. No. 20268 Contig ID 74189 1.R1040 5'-most EST LIB3170-043-Q1-J1-F4 20269 Seq. No. Contig ID 74191 2.R1040 5'-most EST LIB3138-013-Q1-N1-F9 20270 Seq. No. 74199 1.R1040 Contig ID 5'-most EST LIB3138-104-Q1-N1-C7 20271 Seq. No. 74201 1.R1040 Contig ID 5'-most EST uC-gmrominsoy236f08b1 20272 Seq. No.

Contig ID 74202 1.R1040

5'-most EST uC-gmflminsoy011b11b1

Method BLASTX NCBI GI g3152608

BLAST score 303 E value 2.0e-43 Match length 121 % identity 79

```
NCBI Description
                  (AC004482) putative BEL1-like homeotic protein [Arabidopsis
                   thaliana]
Seq. No.
                  20273
                  74203 1.R1040
Contig ID
                  zsg701129351.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                   q4510389
BLAST score
                   232
E value
                   3.0e-19
Match length
                  115
% identity
                   48
NCBI Description
                  (AC007017) putative solute carrier protein [Arabidopsis
                  thaliana]
Seq. No.
                  20274
Contig ID
                  74220 1.R1040
5'-most EST
                   jC-qmle01810024f01a1
Method
                  BLASTX
NCBI GI
                  q2252830
BLAST score
                  189
                   4.0e-14
E value
Match length
                   47
                  74
% identity
NCBI Description
                  (AF013293) weak similarity to receptor protein kinase
                   [Arabidopsis thaliana]
Seq. No.
                   20275
                  74220 2.R1040
Contig ID
5'-most EST
                   fC-gmle700873248a1
                  BLASTX
Method
NCBI GI
                  g3355465
BLAST score
                  282
                   6.0e-25
E value
Match length
                  140
% identity
                   46
NCBI Description
                  (AC004218) putative Ser/Thr protein kinase [Arabidopsis
                  thaliana]
Seq. No.
                  20276
                  74242 1.R1040
Contig ID
5'-most EST
                  gsv701052695.h1
Method
                  BLASTX
                  g3242705
NCBI GI
BLAST score
                  663
E value
                  2.0e-69
Match length
                  160
% identity
                   79
```

NCBI Description

(AC003040) putative nicotinate phosphoribosyltransferase

[Arabidopsis thaliana]

Seq. No. 20277 Contig ID 74256 1.R1040 5'-most EST

jC-gmro02910056g03a1

Method BLASTX NCBI GI g2225877 BLAST score 474

E value 1.0e-47 Match length 120 % identity 76

(AB002406) TIP49 [Rattus norvegicus] >gi 4106528 (AF100694) NCBI Description

Pontin52 [Mus musculus] >gi\_4521276\_dbj\_BAA76313.1\_

(AB001581) DNA helicase p50 [Rattus norvegicus]

20278 Seq. No.

Contig ID 74263 1.R1040

5'-most EST LIB3138-014-Q1-N1-H1

Method BLASTX NCBI GI g2500981 BLAST score 721 E value 2.0e-76 Match length 168 % identity 81

NCBI Description GLUTAMYL-TRNA SYNTHETASE (GLUTAMATE--TRNA LIGASE) (GLURS)

>gi\_1084418\_pir\_\_S51685 glutamate--tRNA ligase (EC 6.1.1.17) - common tobacco >gi\_603867\_emb\_CAA58506 (X83524) glutamate--tRNA ligase [Nicotiana tabacum]

20279 Seq. No.

74278 1.R1040 Contig ID 5'-most EST seb700653526.h1

20280 Seq. No.

Contig ID 74278 2.R1040

5'-most EST jC-qmf102220084f02a1

Seq. No. 20281

74302 1.R1040 Contig ID 5'-most EST awf700843291.h1

20282 Seq. No.

Contig ID 74306 1.R1040 5'-most EST pcp700995542.h1

BLASTX Method NCBI GI q2088648 BLAST score 603 E value 2.0e-62 Match length 312 % identity 46

NCBI Description (AF002109) hypothetical protein [Arabidopsis thaliana]

Seq. No. 20283

Contig ID 74306 2.R1040

5'-most EST jC-qmle01810020d03a1

Method BLASTX NCBI GI g2088648 BLAST score 247 E value 6.0e-21 Match length 161 % identity

NCBI Description (AF002109) hypothetical protein [Arabidopsis thaliana]

Seq. No. 20284

74312\_1.R1040 Contig ID



5'-most EST LIB3138-014-Q1-N2-G10

Seq. No. 20285

Contig ID 74330 1.R1040

5'-most EST LIB3138-015-Q1-N1-A12

Seq. No. 20286

Contig ID 74351\_1.R1040 5'-most EST uC-gmropic050a09b1

Method BLASTX
NCBI GI g3281846
BLAST score 172
E value 5.0e-12
Match length 60
% identity 58

NCBI Description (AJ006404) late elongated hypocotyl [Arabidopsis thaliana]

Seq. No. 20287

Contig ID 74369\_1.R1040 5'-most EST jex700904202.h1

Method BLASTX
NCBI GI g4512667
BLAST score 2028
E value 0.0e+00
Match length 603
% identity 68

NCBI Description (AC006931) putative MAP kinase [Arabidopsis thaliana]

Seq. No. 20288

Contig ID 74377\_1.R1040 5'-most EST smc700748641.h1

Method BLASTX
NCBI GI g1708461
BLAST score 246
E value 4.0e-21
Match length 90
% identity 56

NCBI Description IAA-AMINO ACID HYDROLASE HOMOLOG 1 PRECURSOR >gi 902789 (U23795) ILL1 [Arabidopsis thaliana] >gi 2921829 (AF047031)

IAA-amino acid hydrolase [Arabidopsis thaliana]

Seq. No. 20289

Contig ID 74390 1.R1040

5'-most EST uC-gmflminsoy081c01b1

Method BLASTX
NCBI GI g2655098
BLAST score 342
E value 5.0e-32
Match length 170
% identity 44

NCBI Description (AF023472) peptide transporter [Hordeum vulgare]

Seq. No. 20290

Contig ID 74404\_1.R1040 5'-most EST g5606646

Seq. No. 20291



```
74407 1.R1040
Contig ID
                  jC-gm\overline{l}e01810077g01d1
5'-most EST
                  BLASTX
Method
                  g1653791
NCBI GI
                  203
BLAST score
                  8.0e-16
E value
Match length
                  100
                  40
% identity
                  (D90916) hypothetical protein [Synechocystis sp.]
NCBI Description
                  20292
Seq. No.
                  74408 1.R1040
Contig ID
                  zzp700835772.h1
5'-most EST
                  BLASTN
Method
                  g3785968
NCBI GI
                   36
BLAST score
                   1.0e-10
E value
                   144
Match length
                   87
% identity
                  Arabidopsis thaliana chromosome II BAC F2I9 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   20293
Seq. No.
                   74418 1.R1040
Contig ID
                   LIB3138-015-Q1-N2-F1
5'-most EST
                   BLASTX
Method
                   g3355467
NCBI GI
                   238
BLAST score
                   2.0e-25
E value
                   116
Match length
% identity
                  (AC004218) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   20294
Seq. No.
                   74421 1.R1040
Contig ID
                   LIB3138-015-Q1-N2-F4
5'-most EST
                   20295
Seq. No.
                   74438 1.R1040
Contig ID
                   wrg700789441.h2
5'-most EST
Method
                   BLASTX
                   q2239089
NCBI GI
                   905
BLAST score
                   2.0e-97
E value
                   437
Match length
                   45
% identity
                   (Z84386) anthranilate N-hydroxycinnamoyl/benzoyltransferase
NCBI Description
                    [Dianthus caryophyllus] >gi_3288180_emb_CAB11466_ (Z98758)
                   anthranilate N-hydroxycinnamoyl/benzoyltransferase
                    [Dianthus caryophyllus]
                   20296
Seq. No.
```

Contig ID 74438\_2.R1040

5'-most EST jC-gmst02400048b07a1

Method BLASTX
NCBI GI g2239083
BLAST score 240



E value 3.0e-20 \* Match length 113

Match length 113 % identity 48

NCBI Description (Z84383) anthranilate N-hydroxycinnamoyl/benzoyltransferase

[Dianthus caryophyllus] >gi\_2239087\_emb\_CAB06429\_(Z84385)

anthranilate N-hydroxycinnamoyl/benzoyltransferase

[Dianthus caryophyllus]

Seq. No. 20297

Contig ID 74438\_3.R1040 5'-most EST trc700562081.h1

Method BLASTX
NCBI GI g2239083
BLAST score 343
E value 3.0e-32
Match length 160
% identity 44

NCBI Description (Z84383) anthranilate N-hydroxycinnamoyl/benzoyltransferase

[Dianthus caryophyllus] >gi\_2239087\_emb\_CAB06429\_ (Z84385)

anthranilate N-hydroxycinnamoyl/benzoyltransferase

[Dianthus caryophyllus]

Seq. No. 20298

Contig ID 74446\_1.R1040

5'-most EST LIB3138-016-Q1-N1-A4

Method BLASTX
NCBI GI g3540208
BLAST score 674
E value 4.0e-71
Match length 148
% identity 80

NCBI Description (AC004260) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 20299

Contig ID 74453\_1.R1040

5'-most EST jC-gmst02400049g09a1

Method BLASTX
NCBI GI g3687652
BLAST score 538
E value 7.0e-55
Match length 181
% identity 56

NCBI Description (AF047352) rubisco activase precursor [Datisca glomerata]

Seq. No. 20300

Contig ID 74456 1.R1040

5'-most EST jC-gmro02910024b10a1

Method BLASTX
NCBI GI g3776581
BLAST score 565
E value 4.0e-58
Match length 177
% identity 58

NCBI Description (AC005388) Similar to Beta integral membrane protein

homolog gb\_U43629 from A. thaliana. [Arabidopsis thaliana]

Seq. No. 20301



Contig ID 74460\_1.R1040

5'-most EST LIB3138-016-Q1-N1-C5

Method BLASTX
NCBI GI g2244971
BLAST score 566
E value 2.0e-58
Match length 162
% identity 72

NCBI Description (Z97340) hypothetical protein [Arabidopsis thaliana]

Seq. No. 20302

Contig ID 74461\_1.R1040

5'-most EST jC-gmle01810006a02d1

Seq. No. 20303

Contig ID 74466\_1.R1040

5'-most EST LIB3138-016-Q1-N1-D2

Seq. No. 20304

Contig ID 74472\_1.R1040 5'-most EST zsg701119282.h1

Method BLASTX
NCBI GI 94567260
BLAST score 715
E value 1.0e-75
Match length 152
% identity 88

NCBI Description (AC006841) putative NADPH dependent mannose 6-phosphate

reductase [Arabidopsis thaliana]

Seq. No. 20305

Contig ID 74484 1.R1040

5'-most EST uC-gmflminsoy016h10b1

Method BLASTX
NCBI GI g2781345
BLAST score 433
E value 2.0e-42
Match length 276
% identity 34

NCBI Description (AC003113) F2401.2 [Arabidopsis thaliana]

Seq. No. 20306

Contig ID 74491 1.R1040

5'-most EST jC-gmle01810093g06a1

Seq. No. 20307

Contig ID 74491\_2.R1040 5'-most EST kmv700741877.h1

Seq. No. 20308

Contig ID 74522\_1.R1040 5'-most EST kmv700742508.h1

Seq. No. 20309

Contig ID 74525\_1.R1040 5'-most EST g5126278



Contig ID 74525 2.R1040

5'-most EST jC-gmf102220113h03a1

Seq. No. 20311

Contig ID 74535\_1.R1040

5'-most EST LIB3138-017-Q1-N1-F8

Method BLASTX
NCBI GI g2623295
BLAST score 675
E value 5.0e-71
Match length 182
% identity 73

NCBI Description (AC002409) hypothetical protein [Arabidopsis thaliana]

Seq. No. 20312

Contig ID 74548\_1.R1040 5'-most EST gsv701048987.h1

Method BLASTX
NCBI GI g421960
BLAST score 569
E value 1.0e-58
Match length 69

NCBI Description small nuclear ribonucleoprotein U2B'' - potato >gi 169589

(M72892) spliceosomal protein [Solanum tuberosum]

Seq. No. 20313

Contig ID 74566 1.R1040

5'-most EST LIB3138-018-Q1-N1-C6

Seq. No. 20314

Contig ID 74570\_1.R1040 5'-most EST epx701104555.h1

Seq. No. 20315

Contig ID 74588\_1.R1040

5'-most EST LIB3138-018-Q1-N1-F10

Seq. No. 20316

Contig ID 74592\_1.R1040 5'-most EST wrg700790506.h2

Seq. No. 20317

Contig ID 74595 1.R1040

5'-most EST LIB3138-018-Q1-N1-F8

Seq. No. 20318

Contig ID 74608 1.R1040

5'-most EST LIB3138-018-Q1-N1-H8

Seq. No. 20319

Contig ID 74611 1.R1040 5'-most EST gsv701055362.h1

Method BLASTX NCBI GI g2911053

BLAST score 311



E value 1.0e-28 Match length 77 % identity 77

NCBI Description (AL021961) hypothetical protein [Arabidopsis thaliana]

Seq. No. 20320

Contig ID 74612 1.R1040

5'-most EST LIB3138-019-Q1-N1-H2

Seq. No. 20321

Contig ID 74618 1.R1040

5'-most EST jC-gmle01810070c11a1

Method BLASTX
NCBI GI g3426051
BLAST score 236
E value 2.0e-19
Match length 117
% identity 38

NCBI Description (AC005168) hypothetical protein [Arabidopsis thaliana]

Seq. No. 20322

Contig ID 74632 1.R1040

5'-most EST LIB3138-021-Q1-N1-D6

Method BLASTX
NCBI GI g2244904
BLAST score 142
E value 1.0e-08
Match length 144
% identity 9

NCBI Description (Z97339) similar to hypothetical protein C02F5.7 - Caenorha

[Arabidopsis thaliana]

Seq. No. 20323

Contig ID 74635 1.R1040

5'-most EST LIB3138-021-Q1-N1-F2

Seq. No. 20324

Contig ID 74646 1.R1040

5'-most EST LIB3138-022-Q1-N1-C1

Method BLASTN
NCBI GI g4105179
BLAST score 152
E value 8.0e-80
Match length 476
% identity 83

NCBI Description Pisum sativum plastoglobule associated protein PG1

precursor, mRNA, nuclear gene encoding chloroplast protein,

. - 45-

complete cds

Seq. No. 20325

Contig ID 74664\_1.R1040 5'-most EST pmv700893519.h1

Seq. No. 20326

Contig ID 74667 1.R1040

5'-most EST LIB3138-023-Q1-N1-B12

Method BLASTX



NCBI GI g3063693 BLAST score 553 E value 7.0e-57 Match length 132 % identity 75

NCBI Description (AL022537) putative protein [Arabidopsis thaliana]

Seq. No. 20327

Contig ID 74697 1.R1040

5'-most EST LIB3138-025-Q1-N1-A9

Seq. No. 20328

Contig ID 74718 1.R1040

5'-most EST LIB3170-078-Q1-K1-D6

Seq. No. 20329

Contig ID 74726 1.R1040

5'-most EST jC-gmfl02220086c01a1

Seq. No. 20330

Contig ID 74736\_1.R1040 5'-most EST uC-gmropic105e03b1

Method BLASTX
NCBI GI g4559333
BLAST score 574
E value 5.0e-59
Match length 276
% identity 35

NCBI Description (AC007087) unknown protein [Arabidopsis thaliana]

Seq. No. 20331

Contig ID 74736\_2.R1040 5'-most EST uC-gmropic043a12b1

Seq. No. 20332

Contig ID 74757\_1.R1040 5'-most EST gsv701044314.h1

Method BLASTX
NCBI GI g2109293
BLAST score 538
E value 6.0e-55
Match length 138
% identity 78

NCBI Description (U97568) serine/threonine protein kinase [Arabidopsis

thaliana]

Seq. No. 20333

Contig ID 74757\_2.R1040

5'-most EST uC-gmrominsoy275h07b1

Method BLASTX
NCBI GI g2109293
BLAST score 310
E value 2.0e-28
Match length 88
% identity 73

NCBI Description (U97568) serine/threonine protein kinase [Arabidopsis

thaliana]



74763 1.R1040 Contig ID

LIB3138-027-Q1-N1-H1 5'-most EST

BLASTX Method NCBI GI q4432841 446 BLAST score E value 2.0e-44 131 Match length 69 % identity

(AC006283) hypothetical protein [Arabidopsis thaliana] NCBI Description

Seq. No.

20335

74769 1.R1040 Contig ID

LIB3138-029-Q1-N1-B2 5'-most EST

Method BLASTX NCBI GI g1524316 BLAST score 336 1.0e-31 E value 89 Match length

% identity 72

(Y07721) glutathione S-transferase [Petunia x hybrida] NCBI Description

20336 Seq. No.

Contig ID 74814 1.R1040 5'-most EST dpv701098983.h1

Method BLASTX NCBI GI g3878119 BLAST score 273 4.0e-24 E value 131 Match length % identity 45

(Z49068) similar to GTP-binding protein; cDNA EST NCBI Description

EMBL:M89111 comes from this gene; cDNA EST EMBL:D27709 comes from this gene; cDNA EST EMBL:D27708 comes from this gene; cDNA EST EMBL:D73788 comes from this gene; cDNA EST

yk353

20337 Seq. No.

74816 1.R1040 Contig ID

LIB3138-037-Q1-N1-G5 5'-most EST

BLASTX Method g4529972 NCBI GI BLAST score 207 E value 2.0e-16 105 Match length 47 % identity

(AC002330) putative chloroplast outer envelope 86-like NCBI Description

protein [Arabidopsis thaliana]

Seq. No. 20338

74854 1.R1040 Contig ID

jC-gmle01810060g03d1 5'-most EST

20339 Seq. No.

74863 1.R1040 Contig ID uxk700668692.h1 5'-most EST



```
20340
Seq. No.
                  74868 1.R1040
Contig ID
                  LIB3138-041-Q1-N1-H2
5'-most EST
                  BLASTX
Method
NCBI GI
                  q2344871
                  232
BLAST score
                   2.0e-19
E value
                  76
Match length
                   59
% identity
                  (AJ001270) purple acid phosphatase precursor [Phaseolus
NCBI Description
                   vulgaris]
                   20341
Seq. No.
                   74903 1.R1040
Contig ID
                   jC-gmle01810012e03d1
5'-most EST
                   20342
Seq. No.
                   74909 1.R1040
Contig ID
                   jC-gmle01810035d04a2
5'-most EST
                   20343
Seq. No.
                   74914 1.R1040
Contig ID
                   LIB3138-046-Q1-N1-H12
5'-most EST
                   BLASTX
Method
                   q4432844
NCBI GI
BLAST score
                   393
                   6.0e-38
E value
                   116
Match length
                   65
% identity
                  (AC006283) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   20344
                   74938 1.R1040
Contig ID
                   rca700996925.hl
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3928543
                   435
BLAST score
                   5.0e-43
E value
                   123
Match length
% identity
                   (AB016819) UDP-glucose glucosyltransferase [Arabidopsis
NCBI Description
                   thaliana]
                   20345
Seq. No.
                   74940 1.R1040
Contig ID
                   LIB3138-050-Q1-N1-C11
5'-most EST
                   BLASTN
Method
                   g2924257
NCBI GI
                   171
BLAST score
                   3.0e-91
E value
Match length
                   489
                   83
% identity
```

Contig ID 74942\_1.R1040

NCBI Description Tobacco chloroplast genome DNA



```
5'-most EST
                  ncj700979419.hl
                  BLASTX
Method
                  g3342913
NCBI GI
                  731
BLAST score
                 '3.0e-77
E value
                  215
Match length
% identity
                  63
NCBI Description (AF078916) oligopeptidase B [Trypanosoma brucei brucei]
                  20347
Seq. No.
                  74946 1.R1040
Contig ID
                  LIB3138-051-Q1-N1-G1
5'-most EST
                  BLASTN
Method
                  g3892698
NCBI GI
                  37
BLAST score
                  2.0e-11
E value
Match length
                  53
                   92
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F7K2
NCBI Description
                   (ESSAII project)
                   20348
Seq. No.
                   74953 1.R1040
Contig ID
                  LIB3138-054-Q1-N1-C3
5'-most EST
                  BLASTX
Method
                   q121613
NCBI GI
BLAST score
                   142
                   6.0e-09
E value
                   66
Match length
% identity
                   47
                  GLUCOSE-REPRESSIBLE GENE PROTEIN >gi_3014_emb_CAA32907_
NCBI Description
                   (X14801) grg1 [Neurospora crassa]
                   20349
Seq. No.
                   74959_1.R1040
Contig ID
                   uC-gmrominsoy122b04b1
5'-most EST
                   BLASTX
Method
                   g2736155
NCBI GI
BLAST score
                   427
                   3.0e-42
E value
                   124
Match length
                   69
% identity
                   (AF022082) sulfolipid biosynthesis protein [Arabidopsis
NCBI Description
                   thaliana] >gi_3688184_emb_CAA21212_ (AL031804) sulfolipid
                   biosynthesis protein SQD1 [Arabidopsis thaliana]
                   20350
Seq. No.
                   74962 1.R1040
Contig ID
5'-most EST
                   ssr700554826.h1
Seq. No.
                   20351
                   74974 1.R1040
Contig ID
5'-most EST
                   LIB3138-057-Q1-N1-D6
```

Contig ID 74984 1.R1040

5'-most EST LIB3138-059-Q1-N1-A12



Method BLASTX
NCBI GI g4056480
BLAST score 269
E value 1.0e-28
Match length 83
% identity 78

NCBI Description (AC005896) putative adenylate kinase [Arabidopsis thaliana]

Seq. No. 20353

Contig ID 74999\_1.R1040

5'-most EST jC-gmf102220142e10a1

Method BLASTX
NCBI GI g4510401
BLAST score 426
E value 7.0e-42
Match length 92
% identity 80

NCBI Description (AC006587) putative general negative regulator of

transcription [Arabidopsis thaliana]

Seq. No. 20354

Contig ID 75008\_1.R1040 5'-most EST sat701009033.h1

Method BLASTX
NCBI GI g2459412
BLAST score 321
E value 8.0e-30
Match length 79
% identity 75

NCBI Description (AC002332) putative G9a protein [Arabidopsis thaliana]

Seq. No. 20355

Contig ID 75014\_2.R1040 5'-most EST zsg701120210.h1

Seq. No. 20356

Contig ID 75021\_1.R1040 5'-most EST vwf700677268.h1

Seq. No. 20357

Contig ID 75033 1.R1040 5'-most EST zsg701127101.h1

Method BLASTN
NCBI GI g510545
BLAST score 341
E value 0.0e+00
Match length 549
% identity 91

NCBI Description P.sativum mRNA for starch branching enzyme I

Seq. No. 20358

Contig ID 75043\_1.R1040

5'-most EST LIB3138-060-Q1-N1-B11

Seq. No. 20359

Contig ID 75057\_1.R1040 5'-most EST pxt700945650.h1



Contig ID 75073\_1.R1040

5'-most EST jC-gmle01810043f10a1

Seq. No. 20361

Contig ID 75073\_2.R1040 5'-most EST vzy700750556.h1

Seq. No. 20362

Contig ID 75098\_1.R1040 5'-most EST rca700997490.h1

Method BLASTX
NCBI GI g2584787
BLAST score 512
E value 5.0e-52
Match length 150
% identity 63

NCBI Description (X95762) Aminopeptidase P-like [Homo sapiens]

Seq. No. 20363

Contig ID 75106\_1.R1040 5'-most EST zhf700960273.h1

Method BLASTX
NCBI GI g1175016
BLAST score 132
E value 2.0e-15
Match length 180
% identity 36

NCBI Description WHITE PROTEIN HOMOLOG >gi\_1160186\_emb\_CAA62631\_ (X91249)

white [Homo sapiens]

Seq. No. 20364

Contig ID 75110\_1.R1040 5'-most EST zhf700957080.h1

Seq. No. 20365

Contig ID 75119 1.R1040

5'-most EST uC-gmflminsoy098b08b1

Method BLASTX
NCBI GI g3176690
BLAST score 267
E value 4.0e-23
Match length 201
% identity 36

NCBI Description (AC003671) Similar to ubiquitin ligase gb\_D63905 from S.

cerevisiae. EST gb\_R65295 comes from this gene.

[Arabidopsis thaliana]

Seq. No. 20366

Contig ID 75138\_1.R1040

5'-most EST LIB3138-061-Q1-N1-H10

Seq. No. 20367

Contig ID 75145\_1.R1040 5'-most EST rca700996271.h1

Method BLASTX



NCBI GI g4415924 BLAST score 244 E value 5.0e-21 Match length 72 % identity 67

NCBI Description (AC006282) putative glucosyl transferase [Arabidopsis

thaliana]

Seq. No. 20368

Contig ID 75146 1.R1040

5'-most EST LIB3138-061-Q1-N1-H7

Method BLASTX
NCBI GI g3738302
BLAST score 281
E value 4.0e-25
Match length 90
% identity 56

NCBI Description (AC005309) tubby-like protein [Arabidopsis thaliana]

>qi 4249398 (AC006072) putative tubby protein [Arabidopsis

thaliana]

Seq. No. 20369

Contig ID 75161\_1.R1040 5'-most EST kl1701214423.h1

Seq. No. 20370

Contig ID 75169 1.R1040

5'-most EST uC-gmrominsoy126a04b1

Method BLASTX
NCBI GI g3063706
BLAST score 520
E value 1.0e-52
Match length 263
% identity 44

NCBI Description (AL022537) putative protein [Arabidopsis thaliana]

Seq. No. 20371

Contig ID 75180\_1.R1040

5'-most EST jC-qmle01810011e08a1

Seq. No. 20372

Contig ID 75191\_1.R1040 5'-most EST hyd700725680.h1

Seq. No. 20373

Contig ID 75197\_1.R1040

5'-most EST LIB3138-062-Q1-N1-G12

Seq. No. 20374

Contig ID 75207\_1.R1040 5'-most EST seb700653583.h1

Seq. No. 20375

Contig ID 75222 1.R1040

5'-most EST jC-gmle01810006f04d1

Seq. No. 20376



Contig ID 75227\_1.R1040 5'-most EST hyd700725231.h1

Seq. No. 20377

Contig ID 75246 1.R1040 5'-most EST vzy700752157.h1

Method BLASTX
NCBI GI 94539389
BLAST score 192
E value 2.0e-14
Match length 80
% identity 49

NCBI Description (AL035526) putative protein kinase [Arabidopsis thaliana]

Seq. No. 20378

Contig ID 75246\_2.R1040 5'-most EST kmv700739446.h1

Seq. No. 20379

Contig ID 75260 1.R1040

5'-most EST LIB3138-064-Q1-N1-D9

Method BLASTX
NCBI GI g3688186
BLAST score 176
E value 1.0e-12
Match length 130
% identity 36

NCBI Description (AL031804) putative protein [Arabidopsis thaliana]

Seq. No. 20380

Contig ID 75274\_1.R1040 5'-most EST hyd700729267.h1

Seq. No. 20381

Contig ID 75298 1.R1040

5'-most EST jC-gmf102220126h01a1

Method BLASTX
NCBI GI g3372677
BLAST score 238
E value 7.0e-20
Match length 68
% identity 69

NCBI Description (AF061749) tumorous imaginal discs protein Tid56 homolog

[Homo sapiens]

Seq. No. 20382

Contig ID 75298 2.R1040

5'-most EST jC-gmf102220131h01a1

Seq. No. 20383

Contig ID 75308\_1.R1040 5'-most EST pmv700894680.h1

Method BLASTX
NCBI GI g2739368
BLAST score 297
E value 3.0e-27
Match length 86



% identity NCBI Description (AC002505) cyclin-like protein [Arabidopsis thaliana]

20384 Seq. No.

75318 1.R1040 Contig ID

LIB3138-070-P1-N1-A10 5'-most EST

BLASTX Method g2984004 NCBI GI 1274 BLAST score 1.0e-140 E value 434 Match length 53 % identity

NCBI Description (AE000750) threonyl-tRNA synthetase [Aquifex aeolicus]

20385 Seq. No.

75336 1.R1040 Contig ID

jC-gmro02800040a01d1 5'-most EST

BLASTX Method q1619321 NCBI GI 162 BLAST score 4.0e-11 E value 71 Match length 44 % identity

(Y07563) hin1 [Nicotiana tabacum] NCBI Description

20386 Seq. No.

75361 1.R1040 Contig ID

LIB3138-070-P1-N1-F6 5'-most EST

BLASTX Method g2811029 NCBI GI 474 BLAST score 1.0e-47 E value 134 Match length 67

% identity

ACETYLORNITHINE AMINOTRANSFERASE PRECURSOR (ACOAT) NCBI Description

(ACETYLORNITHINE TRANSAMINASE) (AOTA)

>gi 1944511 emb\_CAA69936\_ (Y08680) acetylornithine

aminotransferase [Alnus glutinosa]

20387 Seq. No.

75364 1.R1040 Contig ID

LIB3138-070-P1-N1-G2 5'-most EST

BLASTX Method NCBI GI q2642438 276 BLAST score 2.0e-24 E value 120 Match length 47 % identity

(AC002391) putative indole-3-acetate NCBI Description

beta-glucosyltransferase [Arabidopsis thaliana]

Seq. No. 20388

75391 1.R1040 Contig ID 5'-most EST ary700764454.hl

BLASTX Method g2911075 NCBI GI 678 BLAST score



E value 4.0e-71 Match length 228 % identity 63

NCBI Description (AL021960) putative protein [Arabidopsis thaliana]

Seq. No. 20389

Contig ID 75396\_1.R1040 5'-most EST xpa700794969.h1

Seq. No. 20390

Contig ID 75406\_1.R1040 5'-most EST uC-gmropic047f08b1

Method BLASTX
NCBI GI g4519199
BLAST score 330
E value 1.0e-30
Match length 187
% identity 39

NCBI Description (AB024050) MYC-RP [Perilla frutescens]

Seq. No. 20391

Contig ID 75408\_1.R1040 5'-most EST wvk700684108.h1

Method BLASTX
NCBI GI g3287695
BLAST score 628
E value 2.0e-65
Match length 199
% identity 59

NCBI Description (AC003979) Similar to hypothetical protein C34B7.2

gb 1729503 from C. elegans cosmid gb Z83220. [Arabidopsis

thaliana]

Seq. No. 20392

Contig ID 75423\_1.R1040 5'-most EST uaw700667085.h1

Method BLASTX
NCBI GI g3289002
BLAST score 677
E value 3.0e-71
Match length 185
% identity 11

NCBI Description (AF073522) CRP1 [Zea mays]

Seq. No. 20393

Contig ID 75427\_1.R1040

5'-most EST LIB3138-071-P1-N1-G7

Seq. No. 20394

Contig ID 75445 1.R1040

5'-most EST LIB3170-081-Q1-J1-F11

Method BLASTN
NCBI GI g1816649
BLAST score 86
E value 2.0e-40
Match length 90
% identity 99



NCBI Description Lupinus luteus NADH plastiquinone oxidoreductase subunit J (ndhJ) gene, chloroplast gene encoding chloroplast protein,

complete cds

Seq. No. 20395

Contig ID 75454 1.R1040

5'-most EST LIB3138-072-P1-N1-D6

Seq. No. 20396

Contig ID 75458 1.R1040

5'-most EST LIB3138-072-P1-N1-E12

Method BLASTX
NCBI GI g3738302
BLAST score 560
E value 9.0e-58
Match length 134
% identity 81

NCBI Description (AC005309) tubby-like protein [Arabidopsis thaliana]

>gi 4249398 (AC006072) putative tubby protein [Arabidopsis

thalianal

Seq. No. 20397

Contig ID 75467 1.R1040

5'-most EST LIB3138-072-P1-N1-F10

Method BLASTX
NCBI GI g3289002
BLAST score 164
E value 2.0e-11
Match length 134
% identity 8

NCBI Description (AF073522) CRP1 [Zea mays]

Seq. No. 20398

Contig ID 75476 1.R1040

5'-most EST LIB31 $\overline{3}$ 8-072-P1-N1-G3

Method BLASTX
NCBI GI g4335752
BLAST score 230
E value 3.0e-19
Match length 91
% identity 49

NCBI Description (AC006284) putative myb transcription factor-like protein

[Arabidopsis thaliana]

Seq. No. 20399

Contig ID 75483 1.R1040

5'-most EST LIB3139-074-P1-N1-B2

Seq. No. 20400

Contig ID 75484\_1.R1040 5'-most EST hyd700728979.h1

Method BLASTX
NCBI GI g4544462
BLAST score 367
E value 3.0e-35
Match length 84
% identity 74



## NCBI Description (AC006580) putative NAM protein [Arabidopsis thaliana]

Seq. No. 20401

Contig ID 75491 1.R1040

Method BLASTX
NCBI GI g1495251
BLAST score 314
E value 9.0e-29
Match length 157
% identity 41

NCBI Description (Z70314) heat-shock protein [Arabidopsis thaliana]

Seq. No. 20402

Contig ID 75496\_1.R1040 5'-most EST kl1701212688.h1

Method BLASTX
NCBI GI g1706130
BLAST score 783
E value 1.0e-135
Match length 278
% identity 86

NCBI Description CDPK-RELATED PROTEIN KINASE (PK421) >qi 2129917 pir S60052

calcium-dependent protein kinase homolog - carrot

>gi\_1103386\_emb\_CAA58750\_ (X83869) CDPK-related protein

kinase [Daucus carota]

Seq. No. 20403

Contig ID 75501\_1.R1040 5'-most EST kmv700739384.h1

Method BLASTX
NCBI GI g4049353
BLAST score 637
E value 2.0e-73
Match length 253
% identity 52

NCBI Description (AL034567) putative protein [Arabidopsis thaliana]

Seq. No. 20404

Contig ID 75514\_1.R1040 5'-most EST pcp700991054.h1

Method BLASTX
NCBI GI g2505876
BLAST score 456
E value 2.0e-45
Match length 121
% identity 76

NCBI Description (Y12776) MYB-related protein [Arabidopsis thaliana]

Seq. No. 20405

Contig ID 75518\_1.R1040 5'-most EST rlr700895395.h1

Method BLASTX
NCBI GI g2104949
BLAST score 828
E value 1.0e-88
Match length 194



% identity NCBI Description (U96716) MAP kinase-like protein [Selaginella lepidophylla] 20406 Seq. No. 75531 1.R1040 Contig ID LIB3138-073-P1-N1-H8 5'-most EST BLASTX Method NCBI GI g4160292 324 BLAST score 3.0e - 30E value 114 Match length 59 % identity NCBI Description (Y18209) alpha-N-acetylglucosaminidase [Nicotiana tabacum] 20407 Seq. No. 75539 1.R1040 Contig ID LIB3138-074-P1-N1-A7 5'-most EST 20408 Seq. No. 75548 1.R1040 Contig ID awf700840551.hl 5'-most EST BLASTX Method g3269295 NCBI GI 783 BLAST score 3.0e-83 E value 282 Match length 69 % identity (AL030978) putative protein [Arabidopsis thaliana] NCBI Description 20409 Seq. No. 75558 1.R1040 Contig ID LIB3138-074-P1-N1-E12 5'-most EST BLASTX Method q4455350 NCBI GI BLAST score 424 2.0e-41 E value 136 Match length 68 % identity (AL035524) putative protein [Arabidopsis thaliana] NCBI Description 20410 Seq. No. 75560 1.R1040 Contig ID pmv700889437.hl 5'-most EST Method BLASTX q2829916 NCBI GI 865 BLAST score 6.0e-93 E value 219 Match length % identity (AC002291) Unknown protein [Arabidopsis thaliana] NCBI Description Seq. No. 20411 75570 1.R1040 Contig ID

LIB3138-074-P1-N1-F8 5'-most EST

20412 Seq. No.

75574 2.R1040 Contig ID



5'-most EST zzp700832826.h1

Seq. No. 20413

Contig ID 75577\_1.R1040 5'-most EST zhf700965211.h1

Seq. No. 20414

Contig ID 75577 2.R1040 5'-most EST ssr700559836.h1

Seq. No. 20415

Contig ID 75599\_1.R1040 5'-most EST pcp700992572.h1

Method BLASTX
NCBI GI g1171577
BLAST score 1056
E value 1.0e-115
Match length 257
% identity 75

NCBI Description (X95343) hypersensitivity-related gene [Nicotiana tabacum]

Seq. No. 20416

Contig ID 75599 2.R1040

5'-most EST jC-gmro02910002b02d1

Method BLASTX
NCBI GI g1171577
BLAST score 355
E value 1.0e-33
Match length 90
% identity 74

NCBI Description (X95343) hypersensitivity-related gene [Nicotiana tabacum]

Seq. No. 20417

Contig ID 75599\_3.R1040 5'-most EST kmv700742482.h1

Method BLASTX
NCBI GI g1171577
BLAST score 173
E value 2.0e-12
Match length 53
% identity 66

NCBI Description (X95343) hypersensitivity-related gene [Nicotiana tabacum]

Seq. No. 20418

Contig ID 75600 1.R1040

5'-most EST LIB3138-075-P1-N1-C8

Method BLASTX
NCBI GI g2864618
BLAST score 362
E value 2.0e-34
Match length 152
% identity 43

NCBI Description (AL021811) putative protein [Arabidopsis thaliana]

Seq. No. 20419

Contig ID 75608 1.R1040 5'-most EST kl1701204661.h1



```
Method
                  BLASTX
NCBI GI
                  g1076685
BLAST score
                  365
E value
                  8.0e-35
Match length
                  148
% identity
                  45
NCBI Description SPF1 protein - sweet potato >gi_484261_dbj_BAA06278
                  (D30038) SPF1 protein [Ipomoea batatas]
Seq. No.
                  20420
                  75611 1.R1040
Contig ID
5'-most EST
                  LIB3138-075-P1-N1-F10
Seq. No.
                  20421
```

Contig ID 75617 1.R1040 5'-most EST g4292786 Method BLASTX NCBI GI g3482933 BLAST score 1061 E value 1.0e-116 301 Match length

% identity 67

Seq. No.

NCBI Description (AC003970) Similar to cdc2 protein kinases [Arabidopsis

thaliana]

20422

Contig ID 75638 1.R1040 5'-most EST LIB3138-079-P1-N1-B5 Method BLASTX NCBI GI g4432846 BLAST score 341 E value 6.0e-32

Match length 100 % identity 65

NCBI Description (AC006283) unknown protein [Arabidopsis thaliana]

Seq. No. 20423

Contig ID 75651 1.R1040

5'-most EST uC-gmflminsoy079h10b1

Method BLASTX NCBI GI g4105798 BLAST score 285 E value 2.0e-25 Match length 75 % identity 63

NCBI Description (AF049930) PGP237-11 [Petunia x hybrida]

Seq. No. 20424

Contig ID 75652 1.R1040 5'-most EST  $epx70\overline{1}108475.h1$ 

Seq. No. 20425

Contig ID 75655 1.R1040 5'-most EST pxt700944393.h1

Seq. No. 20426

Contig ID 75661 2.R1040

% identity

75



```
5'-most EST
                  jC-gmro02910037b06d1
                  20427
Seq. No.
Contig ID
                  75692 1.R1040
                  kl1701203301.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4544454
BLAST score
                  922
E value
                  1.0e-99
Match length
                  244
                  73
% identity
NCBI Description (AC006592) putative DNAJ protein [Arabidopsis thaliana]
Seq. No.
                  20428
                  75692 2.R1040
Contig ID
5'-most EST
                  kmv700742967.h1
                  20429
Seq. No.
Contig ID
                  75716 1.R1040
                  bth700848788.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q3287679
BLAST score
                  974
E value
                  1.0e-106
Match length
                  351
% identity
                  61
NCBI Description (AC003979) T22J18.6 [Arabidopsis thaliana]
                  20430
Seq. No.
                  75716 2.R1040
Contig ID
5'-most EST
                  rca700995939.h1
                  BLASTX
Method
NCBI GI
                  q3287679
BLAST score
                  521
E value
                  7.0e-53
Match length
                  190
                  59
% identity
NCBI Description (AC003979) T22J18.6 [Arabidopsis thaliana]
Seq. No.
                  20431
Contig ID
                  75719 1.R1040
                  LIB3170-062-Q1-J1-D3
5'-most EST
Seq. No.
                  20432
Contig ID
                  75724 1.R1040
5'-most EST
                  LIB3170-071-Q1-J1-F7
Seq. No.
                  20433
Contig ID
                  75741 1.R1040
                  jC-gmst02400040f02a1
5'-most EST
Method
                  BLASTX
                  g4115384
NCBI GI
BLAST score
                  1086
E value
                  1.0e-119
Match length
                  262
```

NCBI Description (AC005967) unknown protein [Arabidopsis thaliana]



Contig ID 75743\_1.R1040

5'-most EST LIB3138-080-P1-N1-H6

Method BLASTX
NCBI GI g3377821
BLAST score 229
E value 9.0e-19
Match length 172
% identity 37

NCBI Description (AF076275) No definition line found [Arabidopsis thaliana]

Seq. No. 20435

Contig ID 75753 1.R1040

5'-most EST jC-gmro02910051d10a1

Method BLASTX
NCBI GI g1723449
BLAST score 159
E value 3.0e-10
Match length 194
% identity 26

NCBI Description HYPOTHETICAL 30.9 KD PROTEIN C13G7.03 IN CHROMOSOME I

>gi\_2130225\_pir\_\_S67432 hypothetical protein - fission

yeast (Schizosaccharomyces pombe)

>gi 1204170 emb\_CAA93591.1\_ (Z69729) hypothetical protein

[Schizosaccharomyces pombe]

Seq. No. 20436

Contig ID 75753\_2.R1040

5'-most EST LIB3138-081-P1-N1-B10

Seq. No. 20437

Contig ID 75775\_1.R1040 5'-most EST zhf700964370.h1

Method BLASTX
NCBI GI g115597
BLAST score 313
E value 7.0e-29
Match length 101
% identity 55

NCBI Description F-ACTIN CAPPING PROTEIN BETA SUBUNIT ISOFORMS 1 AND 2 (CAPZ

36/32) (CAPZ B1 AND B2) (BETA-ACTININ SUBUNIT II)

>gi\_104522\_pir\_\_A34335 Z line actin-capping protein beta
chain, form 1 - chicken >gi\_212902 (J04959) actin-capping

protein Z beta subunit [Gallus gallus]

Seq. No. 20438

Contig ID 75777 1.R1040 5'-most EST leu701146235.h1

Seq. No. 20439

Contig ID 75783\_1.R1040 5'-most EST kmv700738987.h1

Method BLASTX
NCBI GI g4006910
BLAST score 918
E value 1.0e-110



Match length 291 % identity 70

NCBI Description (Z99708) putative protein [Arabidopsis thaliana]

Seq. No. 20440

Contig ID 75789\_1.R1040

5'-most EST jC-gmro02910036h04d1

Seq. No. 20441

Contig ID 75804 1.R1040

5'-most EST LIB3138-082-P1-N1-A6

Seq. No. 20442

Contig ID 75826 1.R1040

5'-most EST LIB3138-082-P1-N1-D7

Method BLASTX
NCBI GI g4056427
BLAST score 547
E value 5.0e-56
Match length 194
% identity 59

NCBI Description (AC005322) Contains similarity to gb\_AJ006354 zinc finger

protein (ZAC) from Homo sapiens. [Arabidopsis thaliana]

Seq. No. 20443

Contig ID 75827\_1.R1040 5'-most EST zhf700954040.h1

Method BLASTX
NCBI GI g4415931
BLAST score 805
E value 5.0e-86
Match length 304
% identity 55

NCBI Description (AC006418) unknown protein [Arabidopsis thaliana]

>gi 4559393 gb AAD23053.1\_AC006526\_18 (AC006526) unknown

protein [Arabidopsis thaliana]

Seq. No. 20444

Contig ID 75835\_1.R1040

5'-most EST LIB3138-082-P1-N1-F1

Seq. No. 20445

Contig ID 75839 1.R1040

5'-most EST LIB3138-093-Q1-N1-H2

Method BLASTX
NCBI GI g2129613
BLAST score 273
E value 4.0e-24
Match length 125
% identity 52

NCBI Description homeotic protein BEL1 - Arabidopsis thaliana >gi\_1122533

(U39944) BELL1 [Arabidopsis thaliana]

Seq. No. 20446

Contig ID 75842 1.R1040

5'-most EST LIB3138-082-P1-N1-F7



Contig ID 75843\_1.R1040

5'-most EST jC-gmle01810094a01a1

Seq. No. 20448

Contig ID 75868\_1.R1040

5'-most EST LIB3138-083-P1-N1-B6

Method BLASTX
NCBI GI g3953601
BLAST score 228
E value 5.0e-23
Match length 81
% identity 75

NCBI Description (AB008489) response regulator 6 [Arabidopsis thaliana]

Seq. No. 20449

Contig ID 75873\_1.R1040

5'-most EST LIB3138-083-P1-N1-C12

Method BLASTX
NCBI GI g535454
BLAST score 211
E value 3.0e-28
Match length 123
% identity 53

NCBI Description (U13940) cysteine proteinase [Alnus glutinosa]

Seq. No. 20450

Contig ID 75874 1.R1040

5'-most EST LIB3138-083-P1-N1-C4

Method BLASTX
NCBI GI g544437
BLAST score 425
E value 5.0e-42
Match length 116
% identity 70

NCBI Description GLUTATHIONE PEROXIDASE HOMOLOG (SALT-ASSOCIATED PROTEIN) >gi 296358 emb CAA47018 (X66377) CIT-SAP [Citrus sinensis]

Seq. No. 20451

Contig ID 75882\_1.R1040 5'-most EST zsg701125946.h1

Method BLASTX
NCBI GI g4539242
BLAST score 269
E value 3.0e-23
Match length 119
% identity 49

NCBI Description (AL049489) conserved hypothetical protein

[Schizosaccharomyces pombe]

Seq. No. 20452

Contig ID 75883 1.R1040

5'-most EST uC-gmflminsoy075d05b1

Seq. No. 20453

Contig ID 75905 1.R1040 5'-most EST kl1701211478.h1

3295



Method BLASTX
NCBI GI g3763916
BLAST score 685
E value 4.0e-72
Match length 234
% identity 54

NCBI Description (AC004450) unknown protein [Arabidopsis thaliana]

>gi 4531439 gb AAD22124.1 AC006224 6 (AC006224) unknown

protein [Arabidopsis thaliana]

Seq. No. 20454

Contig ID 75907\_1.R1040 5'-most EST xpa700794032.h1

Method BLASTX
NCBI GI g2827715
BLAST score 527
E value 3.0e-53
Match length 386
% identity 13

NCBI Description (AL021684) receptor protein kinase - like protein

[Arabidopsis thaliana]

Seq. No. 20455

Contig ID 75911\_1.R1040

5'-most EST jC-gmst02400033c09a1

Method BLASTX
NCBI GI g4567273
BLAST score 748
E value 3.0e-79
Match length 213
% identity 70

NCBI Description (AC006841) putative vacuolar proton ATPase subunit

[Arabidopsis thaliana]

Seq. No. 20456

Contig ID 75917\_1.R1040 5'-most EST kl1701204427.h2

Seq. No. 20457

Contig ID 75917 2.R1040

5'-most EST jC-gmle01810050g07a1

Seq. No. 20458

Contig ID 75951\_1.R1040

5'-most EST g5509198
Method BLASTX
NCBI GI g3818624
BLAST score 1134
E value 1.0e-124
Match length 233
% identity 90

NCBI Description (AF095912) actin related protein 2; ARP2 [Arabidopsis

thaliana]

Seq. No. 20459

Contig ID 75965\_1.R1040

5'-most EST jC-gmro02910014b12a1



```
Method
                  BLASTN
NCBI GI
                  g3046849
BLAST score
                  45
                  4.0e-16
E value
                  97
Match length
                  87
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K18L3, complete sequence [Arabidopsis thaliana]
                  20460
Seq. No.
                  75965 2.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy310b02b1
Method
                  BLASTX
                  g2443753
NCBI GI
BLAST score
                  250
                   2.0e-21
E value
Match length
                  74
% identity
                   64
NCBI Description (AF020346) pyridoxal kinase [Rattus norvegicus]
Seq. No.
                   20461
                  75972 1.R1040
Contig ID
5'-most EST
                  uC-gmflminsoy119g07b1
Method
                  BLASTX
                   g3402713
NCBI GI
BLAST score
                   347
                   1.0e-32
E value
Match length
                   106
% identity
                   66
NCBI Description
                  (AC004261) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   20462
Contig ID
                   75974 1.R1040
5'-most EST
                   ssr700557436.h1
                   20463
Seq. No.
Contig ID
                   75974 2.R1040
5'-most EST
                   jC-gmle01810086e11d1
Seq. No.
                   20464
Contig ID
                   75978 1.R1040
                   jC-qmle01810047c08d1
5'-most EST
Method
                   BLASTN
                   g2564045
NCBI GI
BLAST score
                   48
                   1.0e-17
E value
                   160
Match length
% identity
                   86
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K8K14, complete sequence [Arabidopsis thaliana]
```

Contig ID 75978\_2.R1040 5'-most EST sat701011138.h1

Method BLASTX
NCBI GI g1723339
BLAST score 198



E value 1.0e-15 Match length 59

% identity

NCBI Description HYPOTHETICAL 19.2 KD PROTEIN YCF36 (ORF165)

>gi\_2147559\_pir\_\_S73194 hypothetical protein 36 - Porphyra
purpurea chloroplast >gi 1276739 (U38804) hypothetical

chloroplast ORF 36. [Porphyra purpurea]

Seq. No. 20466

Contig ID 76009\_1.R1040

5'-most EST LIB3138-085-P1-N1-G6

Seq. No. 20467

Contig ID 76011 1.R1040

5'-most EST jC-gmst02400057b04d1

Seq. No. 20468

Contig ID 76042 1.R1040

5'-most EST LIB3138-086-P1-N1-C6

Method BLASTX
NCBI GI g3600033
BLAST score 336
E value 2.0e-31
Match length 83

% identity 71

NCBI Description (AF080119) contains similarity to the N terminal domain of

the El protein (Pfam: El\_N.hmm, score: 12.36) [Arabidopsis

thaliana]

Seq. No. 20469

Contig ID 76044\_1.R1040

5'-most EST jC-gmst02400027b09a1

Seq. No. 20470

Contig ID 76049\_1.R1040

5'-most EST LIB3138-086-P1-N1-D3

Seq. No. 20471

Contig ID 76096\_1.R1040

5'-most EST LIB3138-087-P1-N1-C1

Seq. No. 20472

Contig ID 76096\_2.R1040

 5'-most EST
 g4313306

 Method
 BLASTX

 NCBI GI
 g2833311

 BLAST score
 221

E value 8.0e-18
Match length 75
% identity 56

NCBI Description HYPOTHETICAL 18.9 KD PROTEIN R07E5.13 IN CHROMOSOME III

>gi\_630728\_pir\_\_S43605 R07E5.13 protein (clone R07E5) Caenorhabditis elegans >gi\_3878946\_emb\_CAA83622\_ (Z32683)

R07E5.13 [Caenorhabditis elegans]

Seq. No. 20473

Contig ID 76112\_1.R1040



```
rca700998589.hl
5'-most EST
                  20474
Seq. No.
Contig ID
                  76128 1.R1040
5'-most EST
                  fde700871792.hl
                  20475
Seq. No.
Contig ID
                  76154 1.R1040
5'-most EST
                  leu701156478.hl
                  BLASTX
Method
NCBI GI
                  g3025189
BLAST score
                  429
                  2.0e-42
E value
                  135
Match length
% identity
                  64
NCBI Description
                  HYPOTHETICAL 67.1 KD PROTEIN SLL1770
                  >gi 1652753 dbj BAA17672 (D90908) ABC1-like [Synechocystis
                  sp.]
                  20476
Seq. No.
                  76155 1.R1040
Contig ID
5'-most EST
                  rlr700900416.hl
                  BLASTX
Method
                  q4510395
NCBI GI
                  443
BLAST score
                  5.0e-44
E value
Match length
                  137
% identity
                  66
                  (AC006587) putative beta-galactosidase precursor
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  20477
                  76180 1.R1040
Contig ID
                  bth700846166.h1
5'-most EST
                  20478
Seq. No.
Contig ID
                  76195 1.R1040
                  LIB3138-090-P1-N1-B5
5'-most EST
                  BLASTX
Method
                  g2088647
NCBI GI
BLAST score
                   478
                  7.0e-48
E value
Match length
                  127
                   75
% identity
                   (AF002109) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   >gi 3158394 (AF036340) LRR-containing F-box protein
                   [Arabidopsis thaliana]
                   20479
Seq. No.
Contig ID
                   76198 1.R1040
                   smc700749888.hl
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3377822
                  154
BLAST score
```

3299

4.0e-10

114 37

E value Match length

% identity



NCBI Description (AF076275) contains similarity to Caenorhabditis elegans MEL-26 (GB:U67737) [Arabidopsis thaliana]

 Seq. No.
 20480

 Contig ID
 76198\_2.R1040

 5'-most EST
 yz1700967040.h1

Seq. No. 20481

Contig ID 76205\_1.R1040 5'-most EST leu701156773.h1

Method BLASTX
NCBI GI 94240207
BLAST score 177
E value 3.0e-12
Match length 188
% identity 23

NCBI Description (AB020666) KIAA0859 protein [Homo sapiens]

Seq. No. 20482

Contig ID 76205\_2.R1040

5'-most EST LIB3170-025-Q1-J1-E11

Seq. No. 20483

Contig ID 76244\_1.R1040

5'-most EST LIB3138-090-P1-N1-H4

Method BLASTX
NCBI GI g4490297
BLAST score 261
E value 1.0e-22
Match length 111
% identity 49

NCBI Description (AL035678) putative protein [Arabidopsis thaliana]

Seq. No. 20484

Contig ID 76255\_1.R1040 5'-most EST wvk700686073.h1

Method BLASTX
NCBI GI g1507699
BLAST score 150
E value 1.0e-09
Match length 85
% identity 25

NCBI Description (L81119) COL2 [Arabidopsis thaliana] >gi\_1507701 (L81120)

COL2 [Arabidopsis thaliana]

Seq. No. 20485

Contig ID 76258\_1.R1040

5'-most EST LIB3138-091-Q1-N1-C4

Method BLASTX
NCBI GI g818849
BLAST score 463
E value 5.0e-46
Match length 118
% identity 73

NCBI Description (U25430) nucleotide pyrophosphatase precursor [Oryza

sativa]



```
Seq. No.
                  76266 1.R1040
Contig ID
                  LIB3138-091-Q1-N1-D9
5'-most EST
                  20487
Seq. No.
Contig ID
                  76274 1.R1040
                  LIB3138-091-Q1-N1-F10
5'-most EST
                  20488
Seq. No.
                  76276 1.R1040
Contig ID
5'-most EST
                  ssr700559391.hl
                  BLASTX
Method
NCBI GI
                  g2130082
                  183
BLAST score
                  2.0e-13
E value
                  93
Match length
% identity
                  protein kinase Xa21 (EC 2.7.1.-) - rice >gi_1122443
NCBI Description
                   (U37133) receptor kinase-like protein [Oryza sativa]
                  >gi 2586085 (U72723) receptor kinase-like protein [Oryza
                  longistaminata] >gi_1586408_prf__2203451A receptor
                  kinase-like protein [Oryza sativa]
                  20489
Seq. No.
                  76281 1.R1040
Contig ID
                   zhf700959996.h1
5'-most EST
                  BLASTX
Method
                   q2832698
NCBI GI
                   866
BLAST score
                   2.0e-93
E value
                   196
Match length
                   83
% identity
                  (ALO21713) starch synthase-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   20490
Seq. No.
                   76296 1.R1040
Contig ID
                   LIB3138-091-Q1-N1-H7
5'-most EST
                   BLASTX
Method
                   q1001227
NCBI GI
BLAST score
                   156
                   2.0e-10
E value
Match length
                   45
% identity
                   53
NCBI Description (D64003) hypothetical protein [Synechocystis sp.]
Seq. No.
                   20491
                   76296 2.R1040
Contig ID
                   jC-gmle01810048e10a1
5'-most EST
```

Method BLASTX
NCBI GI g1001227
BLAST score 159
E value 9.0e-11
Match length 45
% identity 56

NCBI Description (D64003) hypothetical protein [Synechocystis sp.]



Contig ID 76308\_1.R1040 5'-most EST uC-gmropic107f03b1

Method BLASTN
NCBI GI g438248
BLAST score 235
E value 1.0e-129
Match length 659
% identity 84

NCBI Description S.tuberosum mRNA for precursor of the mitochondrial NAD+-dependent malic enzyme (malate dehydrogenase)

Seq. No. 20493

Contig ID 76310 1.R1040

5'-most EST uC-gmrominsoy069d03b1

Method BLASTX
NCBI GI g2462749
BLAST score 224
E value 8.0e-30
Match length 290
% identity 33

NCBI Description (AC002292) Putative Serine/Threonine protein kinase

[Arabidopsis thaliana]

Seq. No. 20494

Contig ID 76313 1.R1040

5'-most EST LIB3138-092-Q1-N1-C10

Seq. No. 20495

Contig ID 76313\_2.R1040 5'-most EST g5752652

Seq. No. 20496

Contig ID 76351\_1.R1040 5'-most EST zhf700964083.h1

Method BLASTX
NCBI GI g4220514
BLAST score 572
E value 5.0e-59
Match length 180
% identity 66

NCBI Description (AL035356) putative protein [Arabidopsis thaliana]

Seq. No. 20497

Contig ID 76354\_1.R1040 5'-most EST crh700850065.h1

Method BLASTX
NCBI GI g2129496
BLAST score 653
E value 1.0e-68
Match length 135
% identity 90

NCBI Description acetolactate synthase (EC 4.1.3.18) precursor (clone A19) -

upland cotton

Seq. No. 20498

Contig ID 76358 1.R1040



```
fC-gmst700888547f4
5'-most EST
                  BLASTX
Method
                  g3386604
NCBI GI
                  633
BLAST score
                  1.0e-65
E value
                  255
Match length
                  51
% identity
NCBI Description (AC004665) putative protein kinase [Arabidopsis thaliana]
                  20499
Seq. No.
                  76383 1.R1040
Contig ID
                  pxt700943892.h1
5'-most EST
                  20500
Seq. No.
                  76399 1.R1040
Contig ID
                  jC-gmle01810080g05a1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g2501568
BLAST score
                  293
                   3.0e-26
E value
                  89
Match length
                   60
% identity
                  HYPOTHETICAL 28.8 KD PROTEIN SLL0506
NCBI Description
                   >gi_1001342_dbj_BAA10829_ (D64006) hypothetical protein
                   [Synechocystis sp.]
                   20501
Seq. No.
                   76418 1.R1040
Contig ID
                   kl1701211766.h1
5'-most EST
                   20502
Seq. No.
                   76418 2.R1040
Contig ID
5'-most EST
                   kmv700742624.h1
                   20503
Seq. No.
                   76418 4.R1040
Contig ID
5'-most EST
                   wvk700683028.hl
                   20504
Seq. No.
Contig ID
                   76434 1.R1040
5'-most EST
                   wrq700788412.hl
Method
                   BLASTX
NCBI GI
                   g3024871
BLAST score
                   478
E value
                   6.0e-48
                   171
Match length
% identity
                   54
                   HYPOTHETICAL 77.3 KD PROTEIN SLL0005
NCBI Description
                   >gi 1001579 dbj BAA10206_ (D64000) ABC1-like [Synechocystis
                   sp.]
```

76477 1.R1040 Contig ID  $uxk70\overline{0}672780.h1$ 5'-most EST

20506 Seq. No.

76496 1.R1040 Contig ID



```
pxt700943829.hl
5'-most EST
                  20507
Seq. No.
Contig ID
                  76507 1.R1040
5'-most EST
                  LIB3138-095-Q1-N1-E2
Method
                  BLASTX
                  q3236247
NCBI GI
                  594
BLAST score
                  2.0e-61
E value
                  191
Match length
% identity
                  (AC004684) SCARECROW-like protein [Arabidopsis thaliana]
NCBI Description
                  20508
Seq. No.
                  76513 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy066d11b1
Method
                  BLASTX
NCBI GI
                  q4580513
                  903
BLAST score
E value
                   1.0e-102
                   250
Match length
% identity
                   74
NCBI Description (AF036300) scarecrow-like 1 [Arabidopsis thaliana]
                   20509
Seq. No.
                   76515 1.R1040
Contig ID
5'-most EST
                   LIB3170-057-Q1-J1-F11
                   BLASTX
Method
                   q3024425
NCBI GI
BLAST score
                   298
                   8.0e-27
E value
Match length
                   62
% identity
                   89
                  PYRUVATE, PHOSPHATE DIKINASE PRECURSOR
NCBI Description
                   (PYRUVATE, ORTHOPHOSPHATE DIKINASE) >gi_1076700_pir__S53297
                   pyruvate, orthophosphate dikinase (EC 2.7.9.1) - Flaveria
                   pringlei >gi 577776 emb CAA53223 (X75516)
                   pyruvate, orthophosphate dikinase [Flaveria pringlei]
                   20510
Seq. No.
                   76540 1.R1040
Contig ID
                   eep70\overline{0}867970.h1
5'-most EST
                   BLASTX
Method
                   g2961357
NCBI GI
                   157
BLAST score
                   2.0e-10
E value
Match length
                   66
                   58
% identity
NCBI Description (AL022140) putative protein [Arabidopsis thaliana]
Seq. No.
                   20511
                   76549 1.R1040
Contig ID
                   LIB3138-096-Q1-N1-B5
 5'-most EST
Method
```

BLASTX

q3080425 NCBI GI BLAST score 956 1.0e-104 E value



Match length 205 88 % identity

(AL022604) putative protein [Arabidopsis thaliana] NCBI Description

20512 Seq. No.

76573 1.R1040 Contig ID pcp700990220.hl 5'-most EST

BLASTX Method q2708743 NCBI GI BLAST score 161 6.0e-11 E value 112 Match length 33 % identity

(AC003952) putative Tal-1-like reverse transcriptase NCBI Description

[Arabidopsis thaliana]

20513 Seq. No.

76611 1.R1040 Contig ID  $jsh70\overline{1}068696.h1$ 5'-most EST

BLASTX Method q2618703 NCBI GI BLAST score 301 E value 3.0e-27 65 Match length 85 % identity

(AC002510) putative heat shock transcription factor NCBI Description

[Arabidopsis thaliana]

20514 Seq. No.

Contig ID 76618 1.R1040

5'-most EST LIB3138-097-Q1-N1-D2

BLASTN Method NCBI GI q1143510 BLAST score 199 E value 1.0e-108 Match length 379

% identity 88

M.domestica Borkh mRNA for serine/threonine protein NCBI Description

phosphatase (PPX)

Seq. No. 20515

76622 1.R1040 Contig ID

LIB3138-097-Q1-N1-D7 5'-most EST

20516 Seq. No.

76638 1.R1040 Contig ID fde700876792.h1 5'-most EST

BLASTN Method g2827698 NCBI GI 158 BLAST score 3.0e-83E value Match length 434 84 % identity

NCBI Description Arabidopsis thaliana DNA chromosome 5, BAC clone F6H11

(ESSAII project)

20517 Seq. No.



Contig ID 76640\_1.R1040 5'-most EST kl1701207504.h1

Method BLASTX
NCBI GI 9730302
BLAST score 173
E value 6.0e-12
Match length 173
% identity 28

NCBI Description PUTATIVE MITOCHONDRIAL CARRIER PROTEIN PET8

>gi\_630175\_pir\_\_S45458 PET8 protein - yeast (Saccharomyces cerevisiae) >gi\_495307 (U02536) Pet8p [Saccharomyces cerevisiae] >gi\_496713\_emb\_CAA54377\_ (X77114) ORF N2012

[Saccharomyces cerevisiae] >gi\_1301816\_emb\_CAA95862\_(Z71279) ORF YNL003c [Saccharomyces cerevisiae]

Seq. No. 20518

Contig ID 76659\_1.R1040

5'-most EST LIB3138-098-P1-N1-A11

Method BLASTN
NCBI GI g56079
BLAST score 398
E value 0.0e+00
Match length 446
% identity 97

NCBI Description R.norvegicus mRNA for elongation factor 1 alpha

Seq. No. 20519

Contig ID 76689 1.R1040

5'-most EST LIB3138-099-Q1-N1-D1

Method BLASTN
NCBI GI g190231
BLAST score 390
E value 0.0e+00
Match length 390
% identity 100

NCBI Description Human acidic ribosomal phosphoprotein PO mRNA, complete

cds. >gi\_4506666\_ref\_NM\_001002.1\_RPLP0\_ Homo sapiens

ribosomal protein, large, PO (RPLPO) mRNA

Seq. No. 20520

Contig ID 76705 1.R1040

5'-most EST LIB3138-099-Q1-N1-G3

Method BLASTN
NCBI GI 93077821
BLAST score 274
E value 1.0e-152
Match length 322
% identity 97

NCBI Description Human phosphotyrosine independent ligand p62 for the Lck

SH2 domain mRNA, complete cds

>gi\_4505570\_ref\_NM\_003900.1\_P62\_ Homo sapiens

UBIQUITIN-BINDING PROTEIN P62; phosphotyrosine independent

ligand for the Lck SH2 domain p62 (P62) mRNA

Seq. No. 20521

Contig ID 76711 1.R1040

5'-most EST LIB3138-099-Q1-N1-H3



```
20522
Seq. No.
                   76730 1.R1040
Contig ID
                  LIB3138-106-Q1-N1-B9
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2894606
BLAST score
                   1070
                   1.0e-117
E value
                   354
Match length
% identity
                   61
                  (AL021889) putative protein [Arabidopsis thaliana]
NCBI Description
                   20523
Seq. No.
                   76730 2.R1040
Contig ID
                   fde700874728.h1
5'-most EST
Seq. No.
                   20524
Contig ID
                   76736 1.R1040
5'-most EST
                   hrw701058781.hl
                   20525
Seq. No.
Contig ID
                   76736 2.R1040
                   jC-gmle01810042b07a1
5'-most EST
                   20526
Seq. No.
                   76739 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy053c01b1
                   BLASTX
Method
                   q4006900
NCBI GI
BLAST score
                   1024
                   1.0e-111
E value
Match length
                   360
% identity
                  (Z99708) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   20527
Seq. No.
Contig ID
                   76766 1.R1040
                   leu70\overline{1}150329.h1
5'-most EST
                   BLASTX
Method
                   g3169171
NCBI GI
                   246
BLAST score
                   6.0e-21
E value
                   70
Match length
                   61
% identity
                   (AC004401) putative serine carboxypeptidase I [Arabidopsis
NCBI Description
                   thaliana] >gi 3445213 (AC004786) putative serine
                   carboxypeptidase I [Arabidopsis thaliana]
                   20528
Seq. No.
                   76772 1.R1040
Contig ID
5'-most EST
                   LIB3138-101-Q1-N1-C11
```

BLASTN Method g508550 NCBI GI BLAST score 202

1.0e-109 E value 446 Match length % identity 86



```
NCBI Description Pisum sativum ribulose-1,5 bisphosphate carboxylase large
                  subunit N-methyltransferase (rbcMT) mRNA, complete cds
                  20529
Seq. No.
                  76782 1.R1040
Contig ID
                  jC-gmf102220072h06a1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g3451075
BLAST score
                   347
E value
                  1.0e-59
                  139
Match length
                   77
% identity
                   (AL031326) putative protein [Arabidopsis thaliana]
NCBI Description
                   20530
Seq. No.
                   76786 1.R1040
Contig ID
                   uC-gmflminsoy089c08b1
5'-most EST
                   20531
Seq. No.
Contig ID
                   76794 1.R1040
                   zzp700833433.hl
5'-most EST
                   BLASTX
Method
                   q4490323
NCBI GI
                   501
BLAST score
E value
                   1.0e-50
                   143
Match length
% identity
                   69
                  (AJ131464) nitrate transporter [Arabidopsis thaliana]
NCBI Description
                   20532
Seq. No.
                   76807 1.R1040
Contig ID
                   xpa700792619.h1
5'-most EST
                   BLASTX
Method
                   q2494111
NCBI GI
                   224
BLAST score
                   7.0e-18
E value
                   91
Match length
 % identity
                   (AC002376) Contains similarity to Glycine protein kinase 6
NCBI Description
                    (gb M67449). [Arabidopsis thaliana]
                   20533
 Seq. No.
                    76823 1.R1040
 Contig ID
 5'-most EST
                   jC-gmle01810078c10a1
                    20534
 Seq. No.
                    76823 2.R1040
 Contig ID
                   LIB3138-102-Q1-N1-C7
 5'-most EST
 Method
                   BLASTX
                    g2493895
 NCBI GI
                    492
 BLAST score
                    1.0e-49
 E value
                    128
 Match length
 % identity
                    73
                   CYSTEINE SYNTHASE (O-ACETYLSERINE SULFHYDRYLASE)
 NCBI Description
```

>gi\_1071911\_pir\_\_S46438 cysteine synthase (EC 4.2.99.8) -

(O-ACETYLSERINE (THIOL)-LYASE) (CSASE)



watermelon >gi\_540497\_dbj\_BAA05965\_ (D28777) cysteine synthase [Citrullus lanatus]

20535 Seq. No.

76841 1.R1040 Contig ID

LIB3138-102-Q1-N1-F10 5'-most EST

BLASTX Method NCBI GI g4544451 BLAST score 223 E value 7.0e-18 111 Match length 48 % identity

(AC006592) unknown protein [Arabidopsis thaliana] NCBI Description

Seq. No. 20536

76875 1.R1040 Contig ID g4260129 5'-most EST

BLASTN Method NCBI GI g3241917 33 BLAST score 1.0e-08 E value Match length 237 % identity 88

Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: NCBI Description

K19B1, complete sequence [Arabidopsis thaliana]

20537 Seq. No.

76880 1.R1040 Contig ID rca700998121.hl 5'-most EST

BLASTX Method g4220614 NCBI GI 982 BLAST score 1.0e-106 E value 312 Match length 62

% identity

NCBI Description (AB021935) nicotianamine synathase [Arabidopsis thaliana]

20538 Seq. No.

76895 1.R1040 Contig ID dpv701098290.h1 5'-most EST

20539 Seq. No.

76903 1.R1040 Contig ID 5'-most EST g5687902

20540 Seq. No.

76910 1.R1040 Contig ID

5'-most EST LIB3138-103-Q1-N1-H7

20541 Seq. No.

76911 1.R1040 Contig ID 5'-most EST pcp700994604.h1

BLASTX Method NCBI GI q3859597 BLAST score 206 7.0e-16 E value 153 Match length

3309



```
% identity
                  (AF104919) No definition line found [Arabidopsis thaliana]
NCBI Description
                  20542
Seq. No.
                  76931 1.R1040
Contig ID
5'-most EST
                  uC-gmropic011c12b1
Method
                  BLASTX
                  g3954807
NCBI GI
                  792
BLAST score
                  1.0e-84
E value
                  215
Match length
                   72
% identity
                  (AJ011862) flavonoid 3',5'-hydroxylase [Catharanthus
NCBI Description
                  roseus]
                   20543
Seq. No.
                   76934 1.R1040
Contig ID
                  LIB3138-104-Q1-N1-D12
5'-most EST
                   BLASTX
Method
                   g913141
NCBI GI
                   438
BLAST score
                   3.0e-43
E value
                   177
Match length
                   41
% identity
                  ARK3 product/receptor-like serine/threonine protein kinase
NCBI Description
                   ARK3 [Arabidopsis thaliana, Columbia, Peptide, 851 aa]
                   20544
Seq. No.
                   76949 1.R1040
Contig ID
                   LIB3138-104-Q1-N1-F6
5'-most EST
                   BLASTX
Method
                   q2224911
NCBI GI
BLAST score
                   443
                   3.0e-44
E value
                   107
Match length
                   77
% identity
                   (U93048) somatic embryogenesis receptor-like kinase [Daucus
NCBI Description
                   carota]
                   20545
Seq. No.
                   76974 1.R1040
Contig ID
                   zhf700963330.h1
 5'-most EST
Method
                   BLASTX
                   q2749939
NCBI GI
BLAST score
                   352
                   2.0e-33
 E value
                   132
Match length
                   53
 % identity
                   (U70999) CCS1 [Chlamydomonas reinhardtii] >gi 2749941
 NCBI Description
                    (U71000) CCS1 [Chlamydomonas reinhardtii]
```

76980 1.R1040 Contig ID pxt700943371.hl 5'-most EST

BLASTX Method g4455199 NCBI GI 282 BLAST score



```
9.0e-36
E value
                  110
Match length
                  68
% identity
                  (AL035440) putative protein [Arabidopsis thaliana]
NCBI Description
                  20547
Seq. No.
                  76991 1.R1040
Contig ID
                  LIB3138-105-Q1-N1-D7
5'-most EST
                  20548
Seq. No.
                  76996 1.R1040
Contig ID
                  LIB3138-105-Q1-N1-E2
5'-most EST
                   20549
Seq. No.
                   77012 1.R1040
Contig ID
                  LIB3138-105-Q1-N1-H3
5'-most EST
                   20550
Seq. No.
                   77012 2.R1040
Contig ID
                   sat701004504.h1
5'-most EST
                   BLASTX
Method
                   q4539383
NCBI GI
                   290
BLAST score
                   9.0e-26
E value
                   174
Match length
                   37
% identity
                  (AL035526) putative protein (fragment) [Arabidopsis
NCBI Description
                   thaliana]
                   20551
Seq. No.
                   77027 1.R1040
Contig ID
                   LIB3138-106-Q1-N1-B10
5'-most EST
                   BLASTX
Method
                   q3831441
NCBI GI
                   183
BLAST score
                   3.0e-13
E value
                   49
Match length
% identity
                   84
NCBI Description (AC005819) hypothetical protein [Arabidopsis thaliana]
                   20552
Seq. No.
                   77036 1.R1040
Contig ID
                   LIB3138-106-Q1-N1-C11
5'-most EST
Method
                   BLASTX
                   g2655098
NCBI GI
                   425
BLAST score
                   1.0e-41
E value
                   117
Match length
 % identity
NCBI Description (AF023472) peptide transporter [Hordeum vulgare]
```

Contig ID 77043\_1.R1040

5'-most EST LIB3138-106-Q1-N1-C8

Method BLASTX
NCBI GI g2245120
BLAST score 250



E value 109 Match length % identity NCBI Description

(Z97343) hypothetical protein [Arabidopsis thaliana]

Seq. No. 20554

Contig ID 5'-most EST

77043 2.R1040 uC-qmrominsoy243g11b1

BLASTX Method g2245120 NCBI GI 662 BLAST score 1.0e-69 E value 174 Match length 71 % identity

(Z97343) hypothetical protein [Arabidopsis thaliana] NCBI Description

20555 Seq. No.

77049 1.R1040 Contig ID q5677116 5'-most EST BLASTX Method q3482974 NCBI GI 535 BLAST score 1.0e-54 E value 153 Match length

71 % identity

(AL031369) ATP-dependent Clp proteinase-like protein NCBI Description

[Arabidopsis thaliana]

20556 Seq. No.

Contig ID 77057 1.R1040

LIB3138-106-Q1-N1-E7 5'-most EST

BLASTX Method NCBI GI q730648 BLAST score 392 5.0e-38 E value Match length 105 74 % identity

40S RIBOSOMAL PROTEIN S24E (RP50) >gi\_626902\_pir\_\_S48410 NCBI Description ribosomal protein S24.e - yeast (Saccharomyces cerevisiae)

>gi\_557800\_emb\_CAA86154\_ (Z38060) spliced ribosomal
protein, len: 135, CAI: 0.76, similar to RS24\_HUMAN P16632 40S RIBOSOMAL PROTEIN S24 (S19) [Saccharomyces cerevisiae] >gi 603311 (U18814) Rps24eap: 40S ribosomal protein S24E

(RP50) [Saccharomyces cerevisiae]

20557 Seq. No.

77066\_1.R1040 Contig ID uaw700664218.h1 5'-most EST

BLASTX Method g2244898 NCBI GI 673 BLAST score 6.0e-71 E value 154 Match length 82 % identity

(Z97338) strong similarity to protein phosphatase 2A NCBI Description

regulatory chain, 74K [Arabidopsis thaliana]



20558 Seq. No. 77081 1.R1040 Contig ID g5606634 5'-most EST BLASTX Method g2244910 NCBI GI BLAST score 347 2.0e-32 E value Match length 178 % identity 48 (Z97339) unnamed protein product [Arabidopsis thaliana] NCBI Description 20559 Seq. No. 77103 1.R1040 Contig ID LIB3138-119-Q1-N1-E4 5'-most EST 20560 Seq. No. 77141 1.R1040 Contig ID uC-gmflminsoy067f05b1 5'-most EST Method BLASTX g2245092 NCBI GI 340 BLAST score 9.0e-32 E value 158 Match length 53 % identity (Z97343) unnamed protein product [Arabidopsis thaliana] NCBI Description 20561 Seq. No. 77160 1.R1040 Contig ID uC-gmrominsoy310c12b1 5'-most EST BLASTX Method q1680686 NCBI GI BLAST score 818 2.0e-87 E value Match length 282 56 % identity (U51330) rust resistance kinase Lr10 [Triticum aestivum] NCBI Description 20562 Seq. No. 77163 1.R1040 Contig ID jC-gmle01810075h01d1 5'-most EST BLASTX Method NCBI GI q2281085 BLAST score 760 E value 5.0e-81 194 Match length 73 % identity (AC002333) CTR1 protein kinase isolog [Arabidopsis NCBI Description thaliana] 20563 Seq. No. 77165 1.R1040 Contig ID LIB3138-120-Q1-N1-E11 5'-most EST

Method BLASTX
NCBI GI g3080420
BLAST score 564
E value 1.0e-57
Match length 304

% identity



```
% identity
                     (AL022604) putative sugar transporter protein [Arabidopsis
  NCBI Description
                     thaliana]
                     20564
  Seq. No.
                     77176 1.R1040
  Contig ID
  5'-most EST
                     wvk700685820.h1
                     20565
  Seq. No.
                     77182 1.R1040
  Contig ID
  5'-most EST
                     pcp700995177.h1
                     20566
  Seq. No.
                     77201 1.R1040
  Contig ID
                     uC-gmflminsoy045b02b1
  5'-most EST
                     BLASTX
  Method
                     g3287679
  NCBI GI
  BLAST score
                     1998
                     0.0e + 00
  E value
                     477
  Match length
                     82
  % identity
                     (AC003979) T22J18.6 [Arabidopsis thaliana]
  NCBI Description
                     20567
  Seq. No.
                     77205 1.R1040
  Contig ID
                     wrg70\overline{0}787554.h1
  5'-most EST
                     BLASTX
  Method
                      g4455155
  NCBI GI
                      208
  BLAST score
                      1.0e-16
  E value
  Match length
                      95
                      40
   % identity
                     (AL022023) EF-1 alpha - like protein (fragment)
   NCBI Description
                      [Arabidopsis thaliana]
                      20568
Seq. No.
                      77209 1.R1040
   Contig ID
   5'-most EST
                      uC-gmrominsoy048e06b1
                      BLASTX
   Method
                      q2130096
   NCBI GI
   BLAST score
                      914
                      7.0e-99
   E value
   Match length
                      276
   % identity
                      61
                      cytochrome P450tyr - sorghum >gi_984543 (U32624) cytochrome
   NCBI Description
                      P-450 [Sorghum bicolor]
                      20569
   Seq. No.
                      77236 1.R1040
   Contig ID
                      LIB3138-121-Q1-N1-G11
   5'-most EST
   Method
                      BLASTX
                      g2555159
   NCBI GI
   BLAST score
                      500
   E value
                      1.0e-50
                      136
   Match length
                      68
```

NCBI Description (AF025302) putative aldolase [Arabidopsis thaliana]



Contig ID 77255\_1.R1040 5'-most EST rca700995978.h1

Method BLASTX
NCBI GI g3426048
BLAST score 1102
E value 1.0e-121
Match length 309
% identity 70

NCBI Description (AC005168) putative hydroxymethylglutaryl-CoA lyase

precursor [Arabidopsis thaliana]

Seq. No. 20571

Contig ID 77255 2.R1040

5'-most EST jC-gmle01810092e06a1

Method BLASTX
NCBI GI g3426048
BLAST score 174
E value 2.0e-12
Match length 132
% identity 48

NCBI Description (AC005168) putative hydroxymethylglutaryl-CoA lyase

precursor [Arabidopsis thaliana]

Seq. No. 20572

Contig ID 77269\_1.R1040 5'-most EST pcp700991109.h1

Seq. No. 20573

Contig ID 77276\_1.R1040

5'-most EST LIB3138-122-Q1-N1-D8

Method BLASTX
NCBI GI g584741
BLAST score 102
E value 1.0e-10
Match length 79
% identity 48

NCBI Description ANKYRIN REPEAT PROTEIN (AKRP) >gi\_322461\_pir\_\_JQ1729 ankyrin-repeat protein - Arabidopsis thaliana >gi\_166744

(M82883) ankyrin repeat-containing protein [Arabidopsis

thaliana]

Seq. No. 20574

Contig ID 77319\_1.R1040 5'-most EST xpa700793002.h1

Seq. No. 20575

Contig ID 77326 1.R1040

5'-most EST LIB3138-123-Q1-N1-B12

Seq. No. 20576

Contig ID 77339 1.R1040

5'-most EST jC-gmTe01810060f03a1

Method BLASTX
NCBI GI g3860250
BLAST score 305



E value 2.0e-27
Match length 95
% identity 61
NCBI Description (AC00582)
[Arabido

ICBI Description (AC005824) putative chloroplast prephenate dehydratase

[Arabidopsis thaliana]

Seq. No. 20577

Contig ID 77359\_1.R1040

5'-most EST jC-gmle01810034c11a2

Method BLASTX
NCBI GI g4185141
BLAST score 247
E value 9.0e-21
Match length 182
% identity 39

NCBI Description (AC005724) putative calmodulin-binding protein [Arabidopsis

thaliana]

Seq. No. 20578

Contig ID 77359\_2.R1040

5'-most EST uC-gmrominsoy307h03b1

Method BLASTX
NCBI GI g4539298
BLAST score 290
E value 4.0e-26
Match length 117
% identity 51

NCBI Description (AL049480) putative calmodulin-binding protein [Arabidopsis

thaliana]

Seq. No. 20579

Contig ID 77368\_1.R1040

5'-most EST fC-gmle7000763807f1

Method BLASTX
NCBI GI g2253010
BLAST score 638
E value 8.0e-68
Match length 181
% identity 70

NCBI Description (Y14199) MAP3K delta-1 protein kinase [Arabidopsis

thaliana]

Seq. No. 20580

Contig ID 77377 1.R1040

5'-most EST uC-gmflminsoy008g03b1

Method BLASTX
NCBI GI g4376383
BLAST score 147
E value 4.0e-09
Match length 68
% identity 44

NCBI Description (AE001598) GMP Kinase [Chlamydia pneumoniae]

Seq. No. 20581

Contig ID 77379\_1.R1040 5'-most EST pmv700890819.h1

Method BLASTX

```
g4468813
NCBI GI
                  522
BLAST score
                  9.0e-53
E value
                  254
Match length
                  39
% identity
NCBI Description (AL035601) putative protein [Arabidopsis thaliana]
Seq. No.
                  20582
                  77383 1.R1040
Contig ID
                  LIB3138-124-Q1-N1-B5
5'-most EST
                  BLASTX
Method
                  g4191774
NCBI GI
BLAST score
                  265
                  5.0e-23
E value
                  103
Match length
                  50
% identity
                  (AC005917) putative beta-1,3-endoglucanase [Arabidopsis
NCBI Description
                  thaliana]
                  20583
Seq. No.
                  77385 1.R1040
Contig ID
                  LIB3138-124-Q1-N1-B7
5'-most EST
                  BLASTX
Method
                  g2673918
NCBI GI
                  403
BLAST score
                   6.0e-39
E value
                  140
Match length
                   58
% identity
NCBI Description (AC002561) unknwon protein [Arabidopsis thaliana]
                   20584
Seq. No.
                   77391 1.R1040
Contig ID
5'-most EST
                  LIB3138-124-Q1-N1-C6
                   20585
Seq. No.
                   77392 1.R1040
Contig ID
                   q5677561
5'-most EST
Method
                   BLASTX
                   q4138855
NCBI GI
BLAST score
                   428
                   3.0e-42
E value
Match length
                   104
% identity
                   79
                  (AF098072) IMMUTANS [Arabidopsis thaliana]
NCBI Description
                   20586
Seq. No.
                   77395 1.R1040
Contig ID
                   LIB3138-124-Q1-N1-D10
5'-most EST
                   BLASTX
Method
                   g2739002
NCBI GI
                   380
BLAST score
                   2.0e-36
E value
Match length
                   181
                   41
% identity
                  (AF022460) CYP83D1p [Glycine max]
NCBI Description
```



Contig ID 77395\_2.R1040 5'-most EST rca701001091.h1

Method BLASTX
NCBI GI g2739002
BLAST score 211
E value 7.0e-17
Match length 81
% identity 44

NCBI Description (AF022460) CYP83D1p [Glycine max]

Seq. No. 20588

Contig ID 77401\_1.R1040

5'-most EST LIB3138-124-Q1-N1-E12

Seq. No. 20589

Contig ID 77415\_1.R1040

5'-most EST LIB3138-124-Q1-N1-G1

Seq. No. 20590

Contig ID 77420\_1.R1040

5'-most EST LIB3138-124-Q1-N1-G5

Seq. No. 20591

Contig ID 77429 1.R1040

5'-most EST LIB3138-125-Q1-N1-A10

Method BLASTX
NCBI GI g4006859
BLAST score 346
E value 1.0e-32
Match length 113
% identity 62

NCBI Description (Z99707) putative protein [Arabidopsis thaliana]

Seq. No. 20592

Contig ID 77430 1.R1040

5'-most EST uC-gmrominsoy192e01b1

Seq. No. 20593

Contig ID 77436 1.R1040

5'-most EST LIB3138-125-Q1-N1-A7

Method BLASTX
NCBI GI g2827546
BLAST score 187
E value 6.0e-14
Match length 66
% identity 59

NCBI Description (AL021635) cytochrome P450 like protein [Arabidopsis

thaliana]

Seq. No. 20594

Contig ID 77442\_1.R1040

5'-most EST jC-gmst02400002f03a1

Method BLASTX
NCBI GI g4572675
BLAST score 181
E value 6.0e-13
Match length 60

3318



% identity 63
NCBI Description (AC006954) unknown protein [Arabidopsis thaliana]

Seq. No. 20595

Contig ID 77446 1.R1040

5'-most EST LIB3138-125-Q1-N1-B8

Seq. No. 20596

Contig ID 77447\_1.R1040 5'-most EST vzy700755566.h1

Method BLASTX
NCBI GI g4006917
BLAST score 213
E value 1.0e-16
Match length 88
% identity 51

NCBI Description (299708) putative protein [Arabidopsis thaliana]

Seq. No. 20597

Contig ID 77453\_1.R1040

5'-most EST fC-gmro7000747805a1

Method BLASTX
NCBI GI g4249391
BLAST score 209
E value 2.0e-16
Match length 89
% identity 64

NCBI Description (AC005966) Similar to gi\_3249076 T13D8.16 beta glucosidase

from Arabidopsis thaliana BAC gb AC004473. [Arabidopsis

thaliana]

Seq. No. 20598

Contig ID 77453 2.R1040

5'-most EST jC-gmro02910059b12a1

Method BLASTX
NCBI GI g4249391
BLAST score 718
E value 6.0e-76
Match length 205
% identity 63

NCBI Description (AC005966) Similar to gi\_3249076 T13D8.16 beta glucosidase

from Arabidopsis thaliana BAC gb\_AC004473. [Arabidopsis

thaliana]

Seq. No. 20599

Contig ID 77454\_1.R1040 5'-most EST 6HC-01-Q1-B1-F2

Seq. No. 20600

Contig ID 77472 1.R1040

5'-most EST jC-gmst02400016d06a1

Seq. No. 20601

Contig ID 77473 1.R1040

5'-most EST LIB3138-125-Q1-N1-G4

Method BLASTX NCBI GI g4335731



```
BLAST score
                   3.0e-29
E value
                   108
Match length
                   52
% identity
                  (AC006248) putative polyprotein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   20602
                   77474 1.R1040
Contig ID
                   LIB3138-125-Q1-N1-G6
5'-most EST
                   20603
Seq. No.
                   77480 1.R1040
Contig ID
                   LIB3138-125-Q1-N1-H4
5'-most EST
                   BLASTX
Method
                   g2781351
NCBI GI
                   155
BLAST score
                   5.0e-10
E value
                   145
Match length
                   30
% identity
                   (AC003113) F2401.7 [Arabidopsis thaliana]
NCBI Description
                   20604
Seq. No.
                   77487 1.R1040
Contig ID
                   fC-gmse700678982b1
5'-most EST
                   BLASTX
Method
                   g2826844
NCBI GI
BLAST score
                   403
                   2.0e-39
E value
                   107
Match length
                   71
% identity
                  (AJ002237) loxc homologue [Lycopersicon esculentum]
NCBI Description
                   20605
Seq. No.
                   77505 1.R1040
Contig ID
                   fde700875921.h1
5'-most EST
                   BLASTX
Method
                   q4091806
NCBI GI
BLAST score
                   300
                   9.0e-27
E value
                   169
Match length
% identity
                   (AF052585) CONSTANS-like protein 2 [Malus domestica]
NCBI Description
Seq. No.
                   20606
                   77505 2.R1040
Contig ID
5'-most EST
                   g4295569
Method
                   BLASTX
                   g4091804
NCBI GI
                   332
BLAST score
                   2.0e-30
E value
```

200 Match length 42 % identity

(AF052584) CONSTANS-like protein 1 [Malus domestica] NCBI Description

20607 Seq. No.

77517 1.R1040 Contig ID  $k1170\overline{1}211710.h1$ 5'-most EST



BLASTX Method g1717850 NCBI GI 391 BLAST score 5.0e-43E value 139 Match length 60 % identity

UBIQUITIN-CONJUGATING ENZYME E2-23 KD (UBIQUITIN-PROTEIN NCBI Description

LIGASE) (UBIQUITIN CARRIER PROTEIN)

>gi\_1072386\_emb\_CAA63352\_ (X92664) ubiquitin-conjugating

enzyme UbcM2 [Mus musculus]

20608 Seq. No.

77529 1.R1040 Contig ID

LIB3138-126-Q1-N1-G7 5'-most EST

BLASTX Method g3242702 NCBI GI BLAST score 533 1.0e-54 E value 122 Match length 80 % identity

(AC003040) hypothetical protein [Arabidopsis thaliana] NCBI Description

Seq. No.

20609 77538 1.R1040 Contig ID seb700652904.h1 5'-most EST

BLASTN Method g3702734 NCBI GI BLAST score 34 1.0e-09 E value

Match length 50 92 % identity

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MNB8, complete sequence [Arabidopsis thaliana]

20610 Seq. No.

77540 1.R1040 Contig ID 5'-most EST sat701014005.hl

Seq. No.

20611

77540 2.R1040 Contig ID 5'-most EST epx701104724.h1

Seq. No.

20612

Contig ID 77549 1.R1040

LIB3138-127-Q1-N1-A7 5'-most EST

Seq. No.

20613

Contig ID 77553 1.R1040

LIB3138-127-Q1-N1-B5 5'-most EST

Method BLASTX g1313926 NCBI GI BLAST score 159 E value 1.0e-10 92 Match length 38 % identity

(X97677) non intermediate filament IFA binding protein NCBI Description

[Brassica oleracea]



20614 Seq. No. Contig ID 77558 1.R1040 5'-most EST  $rca70\overline{1}001307.h1$ Method BLASTX NCBI GI g2464905 BLAST score 459 E value 1.0e-45 Match length 152

NCBI Description (Z99708) minor allergen [Arabidopsis thaliana]

Seq. No. 20615

% identity

Contig ID 77561\_1.R1040 5'-most EST dpv701103087.h1

55

Seq. No. 20616

Contig ID 77577\_3.R1040 5'-most EST awf700839282.h1

Seq. No. 20617

Contig ID 77595\_1.R1040 5'-most EST epx701105707.h1

Seq. No. 20618

Contig ID 77600\_1.R1040 5'-most EST rlr700901307.h1

Seq. No. 20619

Contig ID 77623\_1.R1040 5'-most EST zsg701130349.h1

Method BLASTX
NCBI GI g1418331
BLAST score 505
E value 4.0e-51
Match length 176
% identity 57

NCBI Description (X95909) receptor like protein kinase [Arabidopsis

thaliana]

Seq. No. 20620

Contig ID 77624\_1.R1040 5'-most EST fde700875887.h1

Method BLASTX
NCBI GI g4415920
BLAST score 353
E value 2.0e-33
Match length 122
% identity 54

NCBI Description (AC006282) putative glucosyl transferase [Arabidopsis

thaliana]

Seq. No. 20621

Contig ID 77625\_1.R1040

5'-most EST jC-gmro02910064g09a1

Method BLASTX NCBI GI g1743354

3322



BLAST score 6.0e-89 E value 340 Match length 48

% identity NCBI Description (Y09876) aldehyde dehydrogenase (NAD+) [Nicotiana tabacum]

Seq. No.

20622 77659 1.R1040 Contig ID

jC-gmle01810091h06a1 5'-most EST

BLASTN Method g2764523 NCBI GI 320 BLAST score 1.0e-180 E value 592 Match length 89 % identity

NCBI Description Pisum sativum mRNA for Rieske iron-sulfur protein Tic55

20623 Seq. No.

77674 1.R1040 Contig ID

LIB3138-129-Q1-N1-A5 5'-most EST

20624 Seq. No.

77678 1.R1040 Contig ID

jC-gmf102220053f06d1 5'-most EST

20625 Seq. No.

77678 2.R1040 Contig ID

jC-gmle01810060c10d1 5'-most EST

20626 Seq. No.

77680 1.R1040 Contig ID kmv700738652.h1 5'-most EST

BLASTX Method q3550485 NCBI GI 372 BLAST score 6.0e-55 E value 193 Match length 33 % identity

(AJ224325) cp33Hv [Hordeum vulgare] NCBI Description

20627 Seq. No.

Contig ID 77687 1.R1040

5'-most EST LIB3138-129-Q1-N1-C12

Method BLASTX q3402755 NCBI GI BLAST score 431 1.0e-42 E value 132 Match length % identity

(AL031187) putative transposable element [Arabidopsis NCBI Description

thaliana]

Seq. No. 20628

77689\_1.R1040 Contig ID

uC-gmrominsoy172h01b1 5'-most EST

BLASTX Method g3522948 NCBI GI



BLAST score 777 E value 6.0e-83 Match length 199 % identity 68

NCBI Description (AC004411) hypothetical protein [Arabidopsis thaliana]

Seq. No. 20629

Contig ID 77712\_1.R1040 5'-most EST zhf700955067.h1

Seq. No. 20630

Contig ID 77714\_1.R1040

5'-most EST LIB3138-129-Q1-N1-F4

Method BLASTX
NCBI GI g3355474
BLAST score 351
E value 2.0e-33
Match length 88
% identity 70

NCBI Description (AC004218) unknown protein [Arabidopsis thaliana]

Seq. No. 20631

Contig ID 77715\_1.R1040

5'-most EST uC-gmronoir041e07b1

Seq. No. 20632

Contig ID 77776\_1.R1040 5'-most EST bth700849645.h1

Seq. No. 20633

Contig ID 77788\_1.R1040 5'-most EST rca700999749.h1

Seq. No. 20634

Contig ID 77791\_1.R1040

5'-most EST LIB3138-130-Q1-N1-H12

Method BLASTX
NCBI GI g282881
BLAST score 547
E value 8.0e-56
Match length 271
% identity 48

NCBI Description receptor-like protein kinase precursor - Arabidopsis

thaliana >gi\_166846 (M84658) receptor-like protein kinase

[Arabidopsis thaliana]

Seq. No. 20635

Contig ID 77793\_1.R1040 5'-most EST zhf700958268.h1

Method BLASTX
NCBI GI g4455226
BLAST score 328
E value 3.0e-30
Match length 114
% identity 54

NCBI Description (AL035440) putative protein [Arabidopsis thaliana]



```
20636
Seq. No.
                   77793 2.R1040
Contig ID
                   LIB3138-130-Q1-N1-H3
5'-most EST
                   BLASTX
Method
                   g4455226
NCBI GI
                   147
BLAST score
                   3.0e-09
E value
Match length
                   64
% identity
                  (AL035440) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   20637
                   77806 1.R1040
Contig ID
                   LIB3139-078-P1-N1-B3
5'-most EST
                   20638
Seq. No.
                   77810 1.R1040
Contig ID
                   ssr70\overline{0}555274.h1
5'-most EST
                   20639
Seq. No.
                   77812 1.R1040
Contig ID
                   smc70\overline{0}744429.h1
5'-most EST
                   20640
Seq. No.
                   77816 1.R1040
Contig ID
                   bth700843655.h1
5'-most EST
                   BLASTX
Method
                   q2459429
NCBI GI
                   170
BLAST score
                    6.0e-12
E value
                    90
Match length
                    39
% identity
                   (AC002332) unknown protein [Arabidopsis thaliana]
NCBI Description
                    20641
Seq. No.
                    77817 1.R1040
Contig ID
                    zzp700830794.hl
5'-most EST
                    20642
Seq. No.
                    77817 2.R1040
 Contig ID
                    leu70\overline{1}146626.h1
 5'-most EST
                    20643
 Seq. No.
 Contig ID
                    77829 1.R1040
                    uC-gmrominsoy168c05b1
 5'-most EST
                    BLASTX
 Method
                    a2739385
 NCBI GI
 BLAST score
                    373
 E value
                    1.0e-35
```

89 Match length % identity

(AC002505) putative beta-1,3-glucanase [Arabidopsis NCBI Description

thaliana]

Seq. No. 20644

77829 2.R1040 Contig ID

LIB3139-084-P1-N1-E5 5'-most EST



```
20645
Seq. No.
                   77830 1.R1040
Contig ID
                   jC-gmf102220062d02a1
5'-most EST
                   20646
Seq. No.
                   77859 1.R1040
Contig ID
                   vwf700677833.h1
5'-most EST
Method
                   BLASTX
                   g1001135
NCBI GI
BLAST score
                   447
                   4.0e-44
E value
                   154
Match length
                   60
% identity
                   (D64001) acetolactate synthase [Synechocystis sp.]
NCBI Description
                   20647
Seq. No.
                   77872 1.R1040
Contig ID
5'-most EST
                   LIB3139-001-Q1-N1-A3
                   20648
Seq. No.
                   77874 1.R1040
Contig ID
                   jC-gmf102220084g04a1
5'-most EST
                   BLASTX
Method
                   q4220489
NCBI GI
BLAST score
                   223
                   6.0e-18
E value
                   78
Match length
                   56
% identity
                   (AC006069) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   20649
Seq. No.
                   77877 1.R1040
Contig ID
                   uC-gmrominsoy182c10b1
5'-most EST
Method
                   BLASTX
                   q3402686
NCBI GI
                   320
BLAST score
                   3.0e-29
E value
                   169
Match length
                    44
 % identity
                    (AC004697) putative serine/threonine protein kinase
NCBI Description
                    [Arabidopsis thaliana]
                    20650
 Seq. No.
                    77877 2.R1040
 Contig ID
                    LIB3139-001-Q1-N1-F7
 5'-most EST
                    BLASTX
 Method
                    q3402686
 NCBI GI
                    231
 BLAST score
                    3.0e-19
 E value
                    98
 Match length
                    50
 % identity
                    (AC004697) putative serine/threonine protein kinase
 NCBI Description
                    [Arabidopsis thaliana]
```

20651

77880 1.R1040

Seq. No. Contig ID



```
uC-gmrominsoy165e08b1
5'-most EST...
                  BLASTX
Method
                  g3980415
NCBI GI
                  558
BLAST score
                  2.0e-57
E value
                  166
Match length
% identity
                  62
                  (AC004561) putative tropinone reductase [Arabidopsis
NCBI Description
                  thaliana]
                   20652
Seq. No.
                   77922 1.R1040
Contig ID
                  LIB3139-085-P4-N4-G5
5'-most EST
                   20653
Seq. No.
                   77923 1.R1040
Contig ID
                  LIB3139-085-P1-N1-G6
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3335359
                   388
BLAST score
                   1.0e-37
E value
                   130
Match length
                   59
% identity
                  (AC003028) unknown protein [Arabidopsis thaliana]
NCBI Description
                   20654
Seq. No.
                   77924 1.R1040
Contig ID
                   LIB3139-085-P1-N1-G7
5'-most EST
                   BLASTX
Method
                   g2961357
NCBI GI
                   638
BLAST score
                   8.0e-67
E value
                   157
Match length
                   78
% identity
                  (AL022140) putative protein [Arabidopsis thaliana]
NCBI Description
                   20655
Seq. No.
                   77929 1.R1040
Contig ID
                   LIB3139-085-P4-N4-H2
5'-most EST
Method
                   BLASTX
                   q4467135
NCBI GI
BLAST score
                   115
E value
                   1.0e-11
Match length
                   72
% identity
                  (AL035540) putative protein [Arabidopsis thaliana]
NCBI Description
                   20656
Seq. No.
                   77933 1.R1040
Contig ID
                   zsg701126543.hl
5'-most EST
                   20657
Seq. No.
                   77981_1.R1040
 Contig ID
                   sat701013485.h1
 5'-most EST
```

BLASTX

289

q3395431

Method

NCBI GI

BLAST score



E value 1.0e-25
Match length 190
% identity 37

NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]

Seq. No. 20658

Contig ID 77981\_2.R1040 5'-most EST ujr700646687.h1

Seq. No. 20659

Contig ID 77981 4.R1040 5'-most EST ncj700979794.h2

Seq. No. 20660

Contig ID 77992\_1.R1040

5'-most EST LIB3139-002-Q1-N1-H8

Seq. No. 20661

Contig ID 77999\_1.R1040 5'-most EST sat701015339.h1

Method BLASTX
NCBI GI g3064039
BLAST score 247
E value 6.0e-21
Match length 120
% identity 39

NCBI Description (AF054445) major latex protein homolog [Mesembryanthemum

crystallinum]

Seq. No. 20662

Contig ID 78003\_1.R1040 5'-most EST zhf700964084.h1

Seq. No. 20663

Contig ID 78011\_1.R1040

5'-most EST jC-gmro02910040e09a1

Method BLASTX
NCBI GI g3913008
BLAST score 370
E value 1.0e-35
Match length 86
% identity 87

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME

>gi\_3021338\_emb\_CAA06308\_ (AJ005041) cytosolic

fructose-1,6-bisphosphate aldolase [Cicer arietinum]

Seq. No. 20664

Contig ID 78026\_1.R1040

5'-most EST LIB3139-003-P1-N1-C3

Method BLASTX
NCBI GI g3080434
BLAST score 289
E value 1.0e-25
Match length 157
% identity 42

NCBI Description (AL022605) putative gamma-glutamyltransferase [Arabidopsis

thaliana]



Contig ID 78036 1.R1040

LIB3139-003-P1-N1-D6 5'-most EST

Method BLASTX NCBI GI q3695388 BLAST score 267 4.0e-23 E value 91 Match length 53 % identity

NCBI Description (AF096371) No definition line found [Arabidopsis thaliana]

Seq. No.

20666 78052 1.R1040 Contig ID 5'-most EST trc700562064.h1

Seq. No.

20667

Contig ID 5'-most EST 78052 2.R1040 taw700657314.h1

Method BLASTX NCBI GI g3880602 BLAST score 228 E value 2.0e-18 Match length 286 25 % identity

NCBI Description (Z82080) cDNA EST EMBL:D66071 comes from this gene; cDNA

EST yk274a10.3 comes from this gene; cDNA EST yk289f12.3 comes from this gene; cDNA EST yk289f12.5 comes from this gene; cDNA EST yk274a10.5 comes from this gene; cDNA ES

Seq. No. 20668

78059 1.R1040 Contig ID

LIB3139-046-P1-N1-G8 5'-most EST

Seq. No. 20669

Contig ID 78062 1.R1040

5'-most EST jC-gmro02910066a07a1

Seq. No. 20670

78064 1.R1040 Contig ID 5'-most EST ncj700983229.h1

Seq. No. 20671

78074 1.R1040 Contig ID

5'-most EST LIB3139-003-P1-N1-H7

Seq. No. 20672

Contig ID 78076 1.R1040 5'-most EST uC-gmropic020a08b1

Seq. No. 20673

Contig ID 78079\_1.R1040 5'-most EST djj700606047.h2

20674 Seq. No.

78087 1.R1040 Contig ID

5'-most EST LIB3139-004-P1-N1-B2



Contig ID 78115 1.R1040

5'-most EST LIB3139-004-P1-N1-E12

Method BLASTX
NCBI GI g3947854
BLAST score 144
E value 6.0e-09
Match length 96
% identity 35

NCBI Description (AL034381) conserved hypothetical PFAM UPF0031 containing

protein [Schizosaccharomyces pombe]

Seq. No. 20676

Contig ID 78115 2.R1040

5'-most EST jC-gmro02910008e12a1

Seq. No. 20677

Contig ID 78116 1.R1040

5'-most EST LIB3139-004-P1-N1-E2

Seq. No. 20678

Contig ID 78122\_1.R1040 5'-most EST gsv70\overline{1}049168.h1

Seq. No. 20679

Contig ID 78129\_1.R1040 5'-most EST ncj700985447.h1

Method BLASTX
NCBI GI g3402751
BLAST score 264
E value 4.0e-23
Match length 121
% identity 22

NCBI Description (AL031187) putative protein [Arabidopsis thaliana]

Seq. No. 20680

Contig ID 78130\_1.R1040 5'-most EST zhf700960673.h1

Seq. No. 20681

Contig ID 78132\_1.R1040 5'-most EST hrw70\overline{1}060982.h1

Method BLASTN
NCBI GI g3449325
BLAST score 43
E value 1.0e-14
Match length 235
% identity 80

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K16H17, complete sequence [Arabidopsis thaliana]

Seq. No. 20682

Contig ID 78141\_1.R1040

5'-most EST LIB3139-004-P1-N1-H5

Seq. No. 20683



```
78157 1.R1040
Contig ID
                  dpv701097667.h1
5'-most EST
Method
                  BLASTX
                  g4102839
NCBI GI
BLAST score
                  314
                  1.0e-28
E value
Match length
                  157
% identity
NCBI Description (AF016713) LeOPT1 [Lycopersicon esculentum]
Seq. No.
                  20684
                  78163 1.R1040
Contig ID
5'-most EST
                  jC-qmf102220137c10a1
Method
                  BLASTX
                  g3395553
NCBI GI
BLAST score
                  237
E value
                  5.0e-27
Match length
                  155
                  50
% identity
NCBI Description (AL031180) probable cation-transporting atpase
                  [Schizosaccharomyces pombe]
Seq. No.
                  20685
Contig ID
                  78164 1.R1040
5'-most EST
                  jC-gmf102220085g04a1
Seq. No.
                  20686
Contig ID
                  78172 1.R1040
5'-most EST
                  eep700865433.h1
Method
                  BLASTN
NCBI GI
                  q4097879
BLAST score
                  226
                  1.0e-124
E value
                  590
Match length
% identity
                  85
NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein
                  gene, complete cds
                  20687
Seq. No.
Contig ID
                  78172 3.R1040
5'-most EST
                  zpv700759366.h1
                  BLASTN
Method
NCBI GI
                  g256428
BLAST score
                  97
E value
                  4.0e-47
Match length
                  111
% identity
                  97
NCBI Description KTi3 (KTi3+)=Kunitz trypsin inhibitor [soybeans, Dare and
                  Forrest, mRNA, 1259 nt]
                  20688
Seq. No.
```

78177 1.R1040 Contig ID 5'-most EST zzp700831096.h1

Seq. No. 20689

Contig ID 78181 1.R1040 5'-most EST vzy700755388.h1



```
BLASTX
Method
                  q4406780
NCBI GI
                  745
BLAST score
                  3.0e-79
E value
                  178
Match length
                  78
% identity
                   (AC006532) putative multispanning membrane protein
NCBI Description
                   [Arabidopsis thaliana]
                   20690
Seq. No.
                  78190 1.R1040
Contig ID
                   uaw700666772.h1
5'-most EST
                   BLASTX
Method
                   q2501459
NCBI GI
BLAST score
                   484
                   1.0e-48
E value
                   232
Match length
% identity
                   UBIQUITIN CARBOXYL-TERMINAL HYDROLASE T-3 (UBIQUITIN
NCBI Description
                   THIOLESTERASE T-3) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE
                   T-3) (DEUBIQUITINATING ENZYME T-3) (ISOPEPTIDASE T-3)
                   (ISOT-3) >gi_1658463 (U75362) isopeptidase T-3 [Homo
                   sapiens] >gi_4507849_ref_NP_003931.1_pUSP13_ UNKNOWN
                   20691
Seq. No.
                   78198 1.R1040
Contig ID
                   LIB3139-005-P1-N1-H6
5'-most EST
                   20692
Seq. No.
                   78216 1.R1040
Contig ID
                   fua701039263.hl
5'-most EST
                   BLASTX
Method
                   g3935187
NCBI GI
BLAST score
                   449
E value
                   1.0e-47
Match length
                   263
% identity
                   48
                   (AC004557) F17L21.30 [Arabidopsis thaliana]
NCBI Description
                   20693
 Seq. No.
                   78247 1.R1040
 Contig ID
                   eep700865870.hl
 5'-most EST
                   20694
 Seq. No.
                   78247 2.R1040
 Contig ID
 5'-most EST
                   uC-gmropic087a04b1
                   20695
 Seq. No.
                   78250 1.R1040
 Contig ID
                   uxk700672002.h1
 5'-most EST
                   BLASTX
```

Method NCBI GI q3046695 247 BLAST score E value 3.0e-20 Match length 82

% identity NCBI Description (AL022224) putative protein [Arabidopsis thaliana]



```
Seq. No.
                   20696
                   78250 2.R1040
Contig ID
                   kl1701207585.hl
5'-most EST
                   20697
Seq. No.
                   78250 5.R1040
Contig ID
                   leu701155368.h1
5'-most EST
                   20698
Seq. No.
                   78251 1.R1040
Contig ID
                   LIB3139-043-P1-N1-C2
5'-most EST
```

BLASTX Method q1706958 NCBI GI 1153 BLAST score 1.0e-127 E value 273 Match length

76 % identity

(U58284) cellulose synthase [Gossypium hirsutum] NCBI Description

20699 Seq. No. 78251 2.R1040 Contig ID pmv700888770.hl 5'-most EST BLASTX Method g2827143 NCBI GI

726 BLAST score 5.0e-77 ( E value 179 Match length 73 % identity

(AF027174) cellulose synthase catalytic subunit NCBI Description

[Arabidopsis thaliana]

20700 Seq. No.

78266 1.R1040 Contig ID 5'-most EST  $jsh70\overline{1}069496.h1$ 

20701 Seq. No.

Contig ID 78268 1.R1040 uaw700665686.hl 5'-most EST

BLASTX Method q4006873 NCBI GI BLAST score 145 E value 7.0e-09 Match length 110 % identity

(Z99707) hypothetical protein [Arabidopsis thaliana] NCBI Description

20702 Seq. No.

78270\_1.R1040 Contig ID asn701142550.hl 5'-most EST

20703 Seq. No.

Contig ID 78281 1.R1040 tku700646336.hl 5'-most EST

20704 Seq. No.

78294 1.R1040 Contig ID



```
5'-most EST LIB3139-007-P1-N1-B2
```

Contig ID 78299\_1.R1040 5'-most EST zsg701125705.h1

Method BLASTX
NCBI GI g4530126
BLAST score 478
E value 3.0e-48
Match length 116
% identity 76

NCBI Description (AF078082) receptor-like protein kinase homolog RK20-1

[Phaseolus vulgaris]

Seq. No. 20706

Contig ID 78303\_1.R1040 5'-most EST zlv700807665.h1

Seq. No. 20707

Contig ID 78312 1.R1040

5'-most EST jC-gmle01810056g03a1

Method BLASTX
NCBI GI g2760321
BLAST score 498
E value 2.0e-60
Match length 158
% identity 78

NCBI Description (AC002130) F1N21.6 [Arabidopsis thaliana]

Seq. No. 20708

Contig ID 78312\_2.R1040 5'-most EST tku700646413.h1

Method BLASTX
NCBI GI g2760321
BLAST score 567
E value 2.0e-58
Match length 145
% identity 79

NCBI Description (AC002130) F1N21.6 [Arabidopsis thaliana]

Seq. No. 20709

Contig ID 78313\_1.R1040

5'-most EST LIB31 $\overline{3}$ 9-083-P1-N1-G5

Method BLASTX
NCBI GI g4454012
BLAST score 499
E value 3.0e-50
Match length 174
% identity 54

NCBI Description (AL035396) Pollen-specific protein precursor like

[Arabidopsis thaliana]

Seq. No. 20710

Contig ID 78314\_1.R1040 5'-most EST ncj700978005.h1

Seq. No. 20711



```
78318 1.R1040
Contig ID
5'-most EST
                   g5678048
                   BLASTX
Method
                   g4204259
NCBI GI
                   366
BLAST score
                   7.0e-35
E value
                   155
Match length
                   49
% identity
NCBI Description (AC005223) 18074 [Arabidopsis thaliana]
                   20712
Seq. No.
                   78327 1.R1040
Contig ID
                   q5753687
5'-most EST
                   BLASTX
Method
                   g2244818
NCBI GI
                   492
BLAST score
                   2.0e-49
E value
                   216
Match length
                   51
% identity
                   (Z97336) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   20713
Seq. No.
                   78336 1.R1040
Contig ID
                   fC-gmse7000753222f1
5'-most EST
                   BLASTX
Method
                   q4008006
NCBI GI
                   642
BLAST score
                   7.0e-67
E value
                   261
Match length
                   53
% identity
                   (AF084034) receptor-like protein kinase [Arabidopsis
NCBI Description
                   thaliana]
                   20714
Seq. No.
                   78336 2.R1040
Contig ID
                   lus701015817.hl
5'-most EST
                   BLASTX
Method
                   g4008006
NCBI GI
                   145
BLAST score
                    2.0e-09
E value
                    42
Match length
 % identity
                    (AF084034) receptor-like protein kinase [Arabidopsis
NCBI Description
                    thaliana]
                    20715
 Seq. No.
                    78338 1.R1040
 Contig ID
                    uC-gmrominsoy185h10b1
 5'-most EST
                    20716
 Seq. No.
                    78343 1.R1040
 Contig ID
                    jC-gmf102220070g03a1
 5'-most EST
                    BLASTX
 Method
 NCBI GI
                    g2435517
 BLAST score
                    891
```

3335

5.0e-96

284

E value

Match length



% identity

NCBI Description (AF024504) contains similarity to peptidase family A1

[Arabidopsis thaliana]

Seq. No. 20717

Contig ID 78345\_1.R1040 5'-most EST xpa700796891.h1

Seq. No. 20718

Contig ID 78347\_1.R1040

5'-most EST jC-gmro02910072a03a1

Seq. No. 20719

Contig ID 78351 1.R1040

5'-most EST LIB3139-007-P1-N1-H8

Seq. No. 20720

Contig ID 78352\_1.R1040

5!-most EST LIB3139-008-P1-N1-A1

Method BLASTN
NCBI GI g3695058
BLAST score 228
E value 1.0e-125
Match length 332

Match length 332 % identity 92

NCBI Description Lotus japonicus rac GTPase activating protein 1 mRNA,

complete cds

Seq. No. 20721

Contig ID 78356\_1.R1040 5'-most EST fua701038842.h1

Seq. No. 20722

Contig ID 78368\_1.R1040 5'-most EST fC-gmse700654584a5

Method BLASTX
NCBI GI g3420054
BLAST score 507
E value 1.0e-50
Match length 466
% identity 33

NCBI Description (AC004680) unknown protein [Arabidopsis thaliana]

Seq. No. 20723

Contig ID 78371\_1.R1040

5'-most EST LIB3139-008-P1-N1-C6

Seq. No. 20724

Contig ID 78383\_1.R1040 5'-most EST uC-gmropic100d12b1

Seq. No. 20725

Contig ID 78385\_1.R1040 5'-most EST uC-gmropic097g02b1

Method BLASTX
NCBI GI g1311386
BLAST score 1862



E value 0.0e+00 Match length 477 % identity 69

NCBI Description Cyanogenic Beta-Glucosidase Mol\_id: 1; Molecule: Cyanogenic

Beta-Glucosidase; Chain: Null; Ec: 3.2.1.21

Seq. No. 20726

Contig ID 78385 2.R1040 5'-most EST xpa700796938.h1

Method BLASTX
NCBI GI g1311386
BLAST score 373
E value 2.0e-35
Match length 127
% identity 70

NCBI Description Cyanogenic Beta-Glucosidase Mol\_id: 1; Molecule: Cyanogenic

Beta-Glucosidase; Chain: Null;  $\overline{E}c: 3.2.1.21$ 

Seq. No. 20727

Contig ID 78395 1.R1040 5'-most EST sat701005049.h1

Method BLASTX
NCBI GI g2129831
BLAST score 302
E value 4.0e-27
Match length 195
% identity 43

NCBI Description heat shock transcription factor 34 - soybean

>gi\_662930\_emb\_CAA87077\_ (Z46953) heat shock transcription

factor 34 [Glycine max]

Seq. No. 20728

Contig ID 78408\_1.R1040 5'-most EST uC-gmropic059b10b1

Method BLASTX
NCBI GI g3080395
BLAST score 246
E value 2.0e-20
Match length 171
% identity 42

NCBI Description (AL022603) hypothetical protein [Arabidopsis thaliana]

Seq. No. 20729

Contig ID 78408\_2.R1040

5'-most EST jC-gmro02800039c12a1

Method BLASTX
NCBI GI g3080395
BLAST score 180
E value 4.0e-13
Match length 100
% identity 45

NCBI Description (AL022603) hypothetical protein [Arabidopsis thaliana]

Seq. No. 20730

Contig ID 78410\_1.R1040 5'-most EST kl1701208822.h1

Method BLASTN



```
g1142620
NCBI GI
                  107
BLAST score
                  5.0e-53
E value
Match length
                  360
                  87
% identity
                  Phaseolus vulgaris phaseolin G-box binding protein PG2
NCBI Description
                   (PG2) mRNA, partial cds
                  20731
Seq. No.
                  78412 1.R1040
Contig ID
                  dpv701098005.hl
5'-most EST
Method
                  BLASTX
                  q4539386
NCBI GI
                   278
BLAST score
                   9.0e-25
E value
                   72
Match length
                   69
% identity
                   (AL035526) extensin-like protein [Arabidopsis thaliana]
NCBI Description
                   20732
Seq. No.
                   78415 1.R1040
Contig ID
                   LIB3139-009-P1-N1-A10
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3805964
                   481
BLAST score
                   2.0e-48
E value
                   132
Match length
% identity
                  (Y13773) laccase [Populus balsamifera subsp. trichocarpa]
NCBI Description
                   20733
Seq. No.
                   78422 1.R1040
Contig ID
                   LIB3139-111-P1-N1-G7
5'-most EST
                   20734
Seq. No.
                   78424 1.R1040
Contig ID
                   qsv701056182.hl
5'-most EST
                   BLASTX
Method
                   g2330649
NCBI GI
                   243
BLAST score
                   2.0e-20
E value
                   151
Match length
                   44
 % identity
                   (Y14558) topoisomerase I [Pisum sativum]
NCBI Description
 Seq. No.
                   20735
                   78429 1.R1040
Contig ID
                   LIB3139-009-P1-N1-B2
 5'-most EST
                   BLASTX
Method
                   g2104422
 NCBI GI
                   214
 BLAST score
                   6.0e-17
 E value
                   166
 Match length
 % identity
                   (Z95395) putative membrane transport protein
 NCBI Description
```

[Schizosaccharomyces pombe]



Contig ID 78430 1.R1040

5'-most EST jC-qmf102220141b09a1

Seq. No. 20737

Contig ID 78442 1.R1040

5'-most EST jC-gmst02400052d01a1

Seq. No. 20738

Contig ID 78465\_1.R1040 5'-most EST sat701009344.h1

Method BLASTX
NCBI GI g3935181
BLAST score 1047
E value 1.0e-114
Match length 218
% identity 85

NCBI Description (AC004557) F17L21.24 [Arabidopsis thaliana]

Seq. No. 20739

Contig ID 78465\_2.R1040 5'-most EST ssr700554983.h1

Method BLASTN
NCBI GI g2760165
BLAST score 46
E value 7.0e-17
Match length 78
% identity 90

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MAC9, complete sequence [Arabidopsis thaliana]

Seq. No. 20740

Contig ID 78478\_1.R1040

5'-most EST LIB31 $\overline{3}$ 9-009-P1-N1-G8

Method BLASTX
NCBI GI g4432855
BLAST score 382
E value 7.0e-37
Match length 136
% identity 58

NCBI Description (AC006300) unknown protein [Arabidopsis thaliana]

Seq. No. 20741

Contig ID 78483\_1.R1040 5'-most EST gsv701053113.h1

Method BLASTX
NCBI GI g555655
BLAST score 145
E value 1.0e-08
Match length 69
% identity 46

NCBI Description (U06712) DNA-binding protein [Nicotiana tabacum]

Seq. No. 20742

Contig ID 78483 2.R1040

5'-most EST LIB3139-009-P1-N1-H5



```
20743
Seq. No.
Contig ID
                   78500 1.R1040
5'-most EST
                   zzp700835459.hl
Method
                  BLASTX
NCBI GI
                  q3451065
BLAST score
                   421
E value
                   3.0e-41
Match length
                  82
% identity
                  (AL031326) water channel - like protein [Arabidopsis
NCBI Description
                   thaliana]
                   20744
Seq. No.
                   78501 1.R1040
Contig ID
                  LIB3139-010-P1-N1-B8
5'-most EST
Method
                  BLASTX
NCBI GI
                   g4544409
BLAST score
                  193
                  1.0e-14
E value
Match length
                  84
% identity
                 (AC006955) putative transcription factor [Arabidopsis
NCBI Description
                  thaliana]
                   20745
Seq. No.
                   78504 1.R1040
Contig ID
5'-most EST
                  hrw701057994.h1
Method
                  BLASTX
NCBI GI
                  q3668083
BLAST score
                  212
                  1.0e-16
E value
Match length
                  160
% identity
                   41
NCBI Description (AC004667) hypothetical protein [Arabidopsis thaliana]
                   20746
Seq. No.
Contig ID
                   78506 1.R1040
                   trc700562222.hl
5'-most EST
Seq. No.
                   20747
Contia ID
                   78521 1.R1040
5'-most EST
                  bth700844901.h1
Seq. No.
                   20748
                   78521 2.R1040
Contig ID
5'-most EST
                   jC-qmst02400050d01d1
Seq. No.
                   20749
                   78527 1.R1040
Contig ID
5'-most EST
                   6HC - 0\overline{1} - Q1 - E1 - C10
                  BLASTX
Method
NCBI GI
                   g4263771
BLAST score
                   161
```

% identity 31
NCBI Description (AC006218) putative nonspecific lipid-transfer protein

1.0e-10

104

E value Match length



# precursor [Arabidopsis thaliana]

 Seq. No.
 20750

 Contig ID
 78529 1.R1040

 5'-most EST
 LIB3139-010-P1-N1-F1

Seq. No. 20751

Contig ID 78542\_1.R1040 5'-most EST fua701037763.h1

Seq. No. 20752

Contig ID 78555 1.R1040 5'-most EST g5057901

Seq. No. 20753

Contig ID 78559\_1.R1040

5'-most EST LIB3139-011-P1-N1-A12

Seq. No. 20754

Contig ID 78561\_1.R1040 5'-most EST jex700906441.h1

Method BLASTX
NCBI GI g3414809
BLAST score 140
E value 1.0e-08
Match length 58
% identity 4

NCBI Description (AF061529) rjs [Mus musculus]

Seq. No. 20755

Contig ID 78562\_1.R1040

5'-most EST g5606168
Method BLASTX
NCBI GI g3287857
BLAST score 410
E value 7.0e-40
Match length 182
% identity 46

NCBI Description 3-HYDROXYBUTYRYL-COA DEHYDROGENASE (BETA-HYDROXYBUTYRYL-COA

DEHYDROGENASE) (BHBD) >gi 1209052 (U32229) HbdA

[Bradyrhizobium japonicum]

Seq. No. 20756

Contig ID 78573 1.R1040

5'-most EST LIB3139-011-P1-N1-B8

Method BLASTX
NCBI GI g3582436
BLAST score 641
E value 5.0e-67
Match length 188
% identity 68

NCBI Description (AB017502) beta-D-glucan exohydrolase [Nicotiana tabacum]

Seq. No. 20757

Contig ID 78583\_1.R1040 5'-most EST leu701153369.h1

Method BLASTX



NCBI GI q3004565 BLAST score 1199 E value 1.0e-132 Match length 280 % identity 37

(AC003673) putative protein kinase [Arabidopsis thaliana] NCBI Description

Seq. No. 20758

78586\_1.R1040 Contig ID kmv700743012.hl 5'-most EST

BLASTX Method NCBI GI q1350522 BLAST score 322 1.0e-29 E value 92 Match length 72 % identity

(L47115) late embryogenesis abundant protein [Picea glauca] NCBI Description

Seq. No.

20759

Contig ID

78594 1.R1040

5'-most EST

jC-gmle01810020b02a1

Seq. No.

20760

Contig ID 5'-most EST 78594 2.R1040

sat701009188.h1

Seq. No.

20761

Contig ID 5'-most EST 78597 1.R1040 zpv700762167.h1

Method BLASTX NCBI GI

q4455359

BLAST score E value

786 4.0e-84

Match length % identity

181 86

NCBI Description

(AL035524) putative protein [Arabidopsis thaliana]

Seq. No.

20762

Contig ID 5'-most EST 78601 1.R1040

Method

awf700841758.hl BLASTX

NCBI GI

g4539291

BLAST score E value

323

66

Match length

4.0e-48

% identity

145

NCBI Description

(AL049480) putative protein [Arabidopsis thaliana]

Seq. No.

20763

Contig ID

78602 1.R1040

5'-most EST

uC-gmflminsoy005c08b1 BLASTX

Method NCBI GI BLAST score

g1076685

E value Match length % identity

336 5.0e-31 153

31



```
NCBI Description SPF1 protein - sweet potato >qi 484261 dbj BAA06278
                 (D30038) SPF1 protein [Ipomoea batatas]
```

78610 1.R1040 Contig ID sat701015303.hl 5'-most EST

Method BLASTX NCBI GI q3643085 BLAST score 452 E value 3.0e-51 Match length 201 56 % identity

NCBI Description (AF075580) protein phosphatase-2C; PP2C [Mesembryanthemum

crystallinum]

20765 Seq. No.

Contig ID 78610 2.R1040

5'-most EST uC-gmrominsoy199c08b1

Method BLASTX NCBI GI q1707015 BLAST score 183 E value 2.0e-13 76 Match length 51 % identity

(U78721) protein phosphatase 2C isolog [Arabidopsis NCBI Description

thaliana]

20766 Seq. No.

Contig ID 78611 1.R1040

5'-most EST LIB3139-011-P1-N1-F9

Method BLASTX NCBI GI q4490706 BLAST score 466 E value 1.0e-46 Match length 121

% identity 72

(AL035680) putative protein [Arabidopsis thaliana] NCBI Description

Seq. No.

20767

78615 1.R1040 Contig ID 5'-most EST wrq700791566.hl

Seq. No.

20768

78616 1.R1040 Contig ID 5'-most EST zhf700961554.h1

Seq. No.

20769

Contig ID

78622 1.R1040

5'-most EST

jC-qmle01810060b09a1

Method BLASTX NCBI GI q3025189 BLAST score 293 E value 3.0e-26 Match length 138 % identity 41

NCBI Description HYPOTHETICAL 67.1 KD PROTEIN SLL1770

>gi\_1652753\_dbj\_BAA17672 (D90908) ABC1-like [Synechocystis



#### sp.]

Seq. No. 20770

Contig ID 78625\_1.R1040

5'-most EST jC-gmst02400072c12a1

Method BLASTX
NCBI GI g1435021
BLAST score 710
E value 1.0e-74
Match length 271
% identity 56

NCBI Description (D26575) DNA-binding protein [Daucus carota]

Seq. No. 20771

Contig ID 78628 1.R1040

5'-most EST LIB3139-011-P1-N1-H9

Method BLASTX
NCBI GI g3413703
BLAST score 178
E value 7.0e-13
Match length 134
% identity 41

NCBI Description (AC004747) unknown protein [Arabidopsis thaliana]

Seq. No. 20772

Contig ID 78649 1.R1040

5'-most EST LIB3139-012-P1-N1-C8

Seq. No. 20773

Contig ID 78650\_1.R1040 5'-most EST eep700866894.h1

Seq. No. 20774

Contig ID 78652 1.R1040

5'-most EST jC-gmst02400042a12a1

Method BLASTX
NCBI GI g2642433
BLAST score 317
E value 5.0e-29
Match length 129
% identity 55

NCBI Description (AC002391) putative receptor protein kinase [Arabidopsis

thaliana]

Seq. No. 20775

Contig ID 78659 1.R1040

5'-most EST LIB3139-012-P1-N1-D9

Method BLASTX
NCBI GI g3688187
BLAST score 652
E value 2.0e-68
Match length 155
% identity 75

NCBI Description (AL031804) putative protein [Arabidopsis thaliana]

Seq. No. 20776

Contig ID 78667\_1.R1040



5'-most EST LIB3139-012-P1-N1-E9

Method BLASTX
NCBI GI g2660670
BLAST score 1002
E value 1.0e-109
Match length 259
% identity 77

NCBI Description (AC002342) putative Cu2+-transporting ATPase [Arabidopsis

thaliana]

Seq. No. 20777

Contig ID 78671 1.R1040

5'-most EST LIB3139-012-P1-N1-F3

Method BLASTN
NCBI GI g4097879
BLAST score 524
E value 0.0e+00
Match length 583
% identity 98

NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein

gene, complete cds

Seq. No. 20778

Contig ID 78678\_1.R1040 5'-most EST hrw701060051.h2

Seq. No. 20779

Contig ID 78686 1.R1040

5'-most EST LIB3139-030-P1-N1-E6

Seq. No. 20780

Contig ID 78700 1.R1040

5'-most EST LIB3139-013-P1-N1-A5

Method BLASTX
NCBI GI g3873408
BLAST score 326
E value 6.0e-30
Match length 172
% identity 46

NCBI Description (L76926) putative zinc finger protein [Arabidopsis

thaliana]

Seq. No. 20781

Contig ID 78701 1.R1040

5'-most EST LIB3139-013-P1-N1-A6

Method BLASTX
NCBI GI g3877655
BLAST score 288
E value 1.0e-25
Match length 143
% identity 41

NCBI Description (Z72511) possible zinc finger protein; cDNA EST EMBL: M89115

comes from this gene; cDNA EST EMBL:D71533 comes from this gene; cDNA EST EMBL:D72314 comes from this gene; cDNA EST

EMBL:D75164 comes from this gene; cDNA EST EMBL:C1

Seq. No. 20782



Contig ID 78712\_1.R1040

5'-most EST jC-gmst02400048h09a1

Seq. No. 20783

Contig ID 78721\_1.R1040 5'-most EST uC-gmropic020c04b1

Method BLASTX
NCBI GI g3023945
BLAST score 199
E value 4.0e-15
Match length 89
% identity 49

NCBI Description HISTONE DEACETYLASE (HD) >gi 2318131 (AF014824) histone

deacetylase [Arabidopsis thaliana]

Seq. No. 20784

Contig ID 78721\_2.R1040 5'-most EST gsv701052906.h1

Seq. No. 20785

Contig ID 78723 1.R1040

5'-most EST uC-gmflminsoy083b11b1

Seq. No. 20786

Contig ID 78743 1.R1040

5'-most EST LIB3139-013-P1-N1-F8

Seq. No. 20787

Contig ID 78755\_1.R1040 5'-most EST pmv700889378.h1

Method BLASTX
NCBI GI g3522942
BLAST score 862
E value 1.0e-92
Match length 222
% identity 74

NCBI Description (AC004411) hypothetical protein [Arabidopsis thaliana]

Seq. No. 20788

Contig ID 78763 1.R1040

5'-most EST jC-gmro02910026g02d1

Method BLASTX
NCBI GI g2245020
BLAST score 269
E value 7.0e-23
Match length 312
% identity 31

NCBI Description (297341) growth regulator homolog [Arabidopsis thaliana]

Seq. No. 20789

Contig ID 78763 2.R1040

5'-most EST jC-gmst02400018b08a1

Seq. No. 20790

Contig ID 78781\_1.R1040 5'-most EST leu701146149.h1

Method BLASTX



NCBI GI g3335366 BLAST score 408 E value 6.0e-40 Match length 109 % identity 72

NCBI Description (AC003028) unknown protein [Arabidopsis thaliana]

20791 Seq. No.

78815 1.R1040 Contig ID

5'-most EST jC-gmf102220089g08a1

20792 Seq. No.

Contig ID 78818 1.R1040 ncj700984740.h1 5'-most EST

Method BLASTX NCBI GI q4190952 BLAST score 881 E value 5.0e-95 Match length 257 % identity 61

NCBI Description (AB022689) similar to hsr203J [Lycopersicon esculentum]

20793 Seq. No.

78819 1.R1040 Contig ID

LIB3139-014-P1-N1-G9 5'-most EST

Method BLASTX NCBI GI g2880042 BLAST score 404 E value 3.0e-39 Match length 179 % identity 50

NCBI Description (AC002340) putative 3-hydroxyisobutyryl-coenzyme A

hydrolase [Arabidopsis thaliana]

Seq. No. 20794

Contig ID 78827 1.R1040

5'-most EST LIB3139-015-P1-N1-A2

Seq. No.

20795 Contig ID 78831 1.R1040 5'-most EST epx701108181.h1

Seq. No. 20796

Contig ID 78833 1.R1040

5'-most EST jC-gmle01810092d04d1

20797 Seq. No.

78835 1.R1040 Contig ID 5'-most EST fde700870806.h1

Method BLASTX NCBI GI g3763925 BLAST score 681 E value 1.0e-71 Match length 152 % identity 86

NCBI Description (AC004450) putative Af10-protein [Arabidopsis thaliana]



```
20798
Seq. No.
                   78835 2.R1040
Contig ID
                   jC-gmle01810061d07a1
5'-most EST
                   BLASTX
Method
                   g3763925
NCBI GI
                   357
BLAST score
                   8.0e-34
E value
Match length
                   80
% identity
                   80
```

NCBI Description (AC004450) putative Af10-protein [Arabidopsis thaliana]

20799 Seq. No. Contig ID

78857 1.R1040 LIB3139-015-P1-N1-E10 5'-most EST

BLASTX Method q4371296 NCBI GI 228 BLAST score

1.0e-18 E value Match length 163 % identity 36

(AC006260) putative receptor protein kinase [Arabidopsis NCBI Description

thaliana]

Seq. No. 20800

78863 1.R1040 Contig ID

LIB3139-015-P1-N1-F2 5'-most EST

20801 Seq. No.

78870 1.R1040 Contig ID

LIB3139-015-P1-N1-F9 5'-most EST

BLASTX Method q2832642 NCBI GI 539 BLAST score 5.0e-55 E value 226 Match length 45 % identity

(AL021710) putative protein [Arabidopsis thaliana] NCBI Description

20802 Seq. No.

78873 1.R1040 Contig ID

LIB3139-015-P1-N1-G12 5'-most EST

BLASTX Method g1176203 NCBI GI BLAST score 301 E value 2.0e-27 117 Match length 52 % identity

HYPOTHETICAL 43.1 KD PROTEIN IN RPLM-HHOA INTERGENIC REGION NCBI Description

(F375) >gi 606171 (U18997) ORF\_f375 [Escherichia coli]

>gi\_1789627 (AE000402) orf, hypothetical protein

[Escherichia coli]

20803 Seq. No.

Contig ID 78884 1.R1040

jC-gmst02400007f06a1 5'-most EST

BLASTN Method NCBI GI g4159703



BLAST score 63 E value 1.0e-26 Match length 211 % identity 87

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K5F14, complete sequence [Arabidopsis thaliana]

Seq. No. 20804

Contig ID 78893\_1.R1040 5'-most EST seb700652450.h1

Method BLASTX
NCBI GI 94115536
BLAST score 382
E value 2.0e-36
Match length 151
% identity 60

NCBI Description (AB012115) UDP-glycose:flavonoid glycosyltransferase [Vigna

mungo]

Seq. No. 20805

Contig ID 78893\_2.R1040

5'-most EST LIB3139-016-P1-N1-B5

Seq. No. 20806

Contig ID 78897\_1.R1040 5'-most EST kl1701213071.h1

Method BLASTX
NCBI GI g4539301
BLAST score 192
E value 8.0e-15
Match length 46
% identity 87

NCBI Description (AL049480) putative mitochondrial protein [Arabidopsis

thaliana]

Seq. No. 20807

Contig ID 78911\_1.R1040 5'-most EST zhf700962791.h1

Method BLASTX
NCBI GI g3757523
BLAST score 455
E value 3.0e-45
Match length 168
% identity 56

NCBI Description (AC005167) putative transportin [Arabidopsis thaliana]

Seq. No. 20808

Contig ID 78913\_1.R1040 5'-most EST uaw700664425.h1

Method BLASTX
NCBI GI g3980378
BLAST score 1032
E value 1.0e-160
Match length 449
% identity 65

NCBI Description (AC004561) putative RNA binding protein [Arabidopsis

thaliana]



```
20809
Seq. No.
Contig ID
                  78913 2.R1040
                  kl1701206574.h1
5'-most EST
                  BLASTX
Method
                  g3980378
NCBI GI
BLAST score
                   679
E value
                  2.0e-71
Match length
                  131
% identity
NCBI Description
                  (AC004561) putative RNA binding protein [Arabidopsis
                  thaliana]
Seq. No.
                   20810
                   78913 3.R1040
Contig ID
5'-most EST
                   dpv701099439.h1
Method
                  BLASTX
NCBI GI
                  g3980378
BLAST score
                  173
E value
                   2.0e-12
                  39
Match length
                   77
% identity
NCBI Description
                  (AC004561) putative RNA binding protein [Arabidopsis
                  thaliana]
                   20811
Seq. No.
Contig ID
                   78913 4.R1040
5'-most EST
                   epx701110408.h1
                   20812
Seq. No.
Contig ID
                  78918 1.R1040
5'-most EST
                  uC-gmropic021d05b1
Method
                  BLASTX
NCBI GI
                   g4467359
BLAST score
                   725
E value
                   7.0e-77
Match length
                   196
                   72
% identity
NCBI Description
                   (AJ002685) Phosphatidylinositol 4-kinase [Arabidopsis
                  thaliana]
Seq. No.
                   20813
                   78941 2.R1040
Contig ID
5'-most EST
                  LIB3139-016-P1-N1-H9
Method
                  BLASTN
NCBI GI
                   q2351070
BLAST score
                   56
E value
                   1.0e-22
Match length
                   282
                   83
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
```

MTH12, complete sequence [Arabidopsis thaliana]
Seq. No. 20814

 Seq. No.
 20814

 Contig ID
 78953\_1.R1040

 5'-most EST
 g5677054

 Method
 BLASTX



NCBI GI g1723125 BLAST score 570 E value 1.0e-58 Match length 195 % identity 58

NCBI Description HYPOTHETICAL 27.8 KD PROTEIN SLL0194

>gi 1001604 dbj BAA10232 (D64000) hypothetical protein

[Synechocystis sp.]

Seq. No. .20815

Contig ID 78954 1.R1040

5'-most EST LIB3139-017-P1-N1-B8

Seq. No. 20816

Contig ID 78959\_1.R1040 5'-most EST zzp700830573.h1

Method BLASTX
NCBI GI g464365
BLAST score 281
E value 3.0e-25
Match length 69
% identity 77

NCBI Description PEROXIDASE P7 >gi 66306 pir OPNB7 peroxidase (EC 1.11.1.7)

- turnip

Seq. No. 20817

Contig ID 78960 1.R1040

5'-most EST LIB3139-017-P1-N1-C8

Seq. No. 20818

Contig ID 78971 1.R1040

5'-most EST LIB3139-017-P1-N1-E5

Method BLASTX
NCBI GI g1084334
BLAST score 358
E value 8.0e-34
Match length 76
% identity 92

NCBI Description calcium-dependent protein kinase (EC 2.7.1.-) 1 -

Arabidopsis thaliana >gi\_604880\_dbj\_BAA04829\_ (D21805) calcium-dependent protein kinase [Arabidopsis thaliana]

Seq. No. 20819

Contig ID 78980 1.R1040 5'-most EST gsv701056023.h1

Seq. No. 20820

Contig ID 78984 1.R1040

5'-most EST LIB3139-017-P1-N1-H12

Seq. No. 20821

Contig ID 78984\_2.R1040

5'-most EST jC-gmle01810093c02a1

Method BLASTX
NCBI GI g1304599
BLAST score 123
E value 2.0e-11



Match length 110 % identity 40

NCBI Description (U41315) ZNF127-Xp [Homo sapiens]

Seq. No. 20822

Contig ID 78988\_2.R1040 5'-most EST zhf700964037.h1

Method BLASTX
NCBI GI g2979554
BLAST score 429
E value 1.0e-42
Match length 91
% identity 85

NCBI Description (AC003680) CDC4 like protein [Arabidopsis thaliana]

Seq. No. 20823

Contig ID 79006 1.R1040

5'-most EST jC-gmfl02220086e03a1

Method BLASTX
NCBI GI g3286691
BLAST score 321
E value 2.0e-29
Match length 230
% identity 36

NCBI Description (AJ007450) auxilin-like protein [Arabidopsis thaliana]

Seq. No. 20824

Contig ID 79007\_1.R1040 5'-most EST uC-gmropic029h07b1

Method BLASTX
NCBI GI g2245060
BLAST score 464
E value 4.0e-46
Match length 201
% identity 46

NCBI Description (Z97342) allergen homolog [Arabidopsis thaliana]

Seq. No. 20825

Contig ID 79027\_1.R1040 5'-most EST taw700659954.h1

Method BLASTX
NCBI GI g3461829
BLAST score 470
E value 4.0e-47
Match length 153
% identity 64

NCBI Description (AC004138) hypothetical protein [Arabidopsis thaliana]

Seq. No. 20826

Contig ID 79035 1.R1040

5'-most EST jC-gmro02800035c08d1

Method BLASTX
NCBI GI g3873408
BLAST score 170
E value 8.0e-12
Match length 104
% identity 39



NCBI Description (L76926) putative zinc finger protein [Arabidopsis thaliana]

Seq. No. 20827

Contig ID 79036 1.R1040

5'-most EST LIB3139-018-P1-N1-G10

Method BLASTX
NCBI GI g1255951
BLAST score 1061
E value 1.0e-116
Match length 306
% identity 65

NCBI Description (X96932) PS60 [Nicotiana tabacum]

Seq. No. 20828

Contig ID 79037 1.R1040

5'-most EST LIB3139-018-P1-N1-G11

Seq. No. 20829

Contig ID 79041\_1.R1040 5'-most EST pcp700994155.h1

Method BLASTX
NCBI GI g3063695
BLAST score 395
E value 3.0e-38
Match length 104
% identity 74

NCBI Description (AL022537) hypothetical protein [Arabidopsis thaliana]

Seq. No. 20830

Contig ID 79048\_1.R1040 5'-most EST rca700996220.h1

Method BLASTX
NCBI GI g4415913
BLAST score 291
E value 6.0e-26
Match length 76
% identity 79

NCBI Description (AC006282) unknown protein [Arabidopsis thaliana]

Seq. No. 20831

Contig ID 79055\_1.R1040 5'-most EST zsg701121327.h1

Seq. No. 20832

Contig ID 79061\_1.R1040

5'-most EST uC-gmflminsoy023a08b1

Seq. No. 20833

Contig ID 79062 1.R1040

5'-most EST jC-gmst02400018a08a1

Method BLASTX
NCBI GI g4371296
BLAST score 992
E value 1.0e-108
Match length 246
% identity 77

3353



```
(AC006260) putative receptor protein kinase [Arabidopsis
NCBI Description
                   thaliana]
                   20834
Seq. No.
                   79065 1.R1040
Contig ID
                   LIB3139-020-P1-N1-B1
5'-most EST
                   BLASTX
Method
                   g1709970
NCBI GI
BLAST score
                   330
                   8.0e-31
E value
                   79
Match length
                   78
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L10A
                   20835
Seq. No.
                   79078 1.R1040
Contig ID
                   seb70\overline{0}652343.h1
5'-most EST
                   20836
Seq. No.
                   79083 1.R1040
Contig ID
                   LIB3139-020-P1-N1-C8
5'-most EST
                   BLASTX
Method
                   q4185855
NCBI GI
                   770
BLAST score
                   3.0e-82
E value
Match length
                   168
                   92
% identity
NCBI Description (AJ132388) Ca2+-ATPase [Arabidopsis thaliana]
                   20837
Seq. No.
                   79087 1.R1040
Contig ID
                   LIB3139-020-P1-N1-D3
5'-most EST
                   BLASTX
Method
                   g3355480
NCBI GI
 BLAST score
                    415
                    2.0e-40
 E value
                    185
 Match length
                    45
 % identity
                    (AC004218) Medicago nodulin N21-like protein [Arabidopsis
 NCBI Description
                    thaliana]
                    20838
 Seq. No.
                    79089 1.R1040
 Contig ID
                    wrg700790915.hl
 5'-most EST
                    BLASTX
 Method
                    g3367596
 NCBI GI
                    333
 BLAST score
                    7.0e-31
 E value
                    192
 Match length
 % identity
                    (AL031135) putative protein [Arabidopsis thaliana]
 NCBI Description
                    20839
```

79094 1.R1040 Contig ID uC-gmronoir046d01b1 5'-most EST

20840 Seq. No.



```
Contig ID
                   79117 1.R1040
5'-most EST
                   gsv701049957.h1
                   20841
Seq. No.
                   79123 1.R1040
Contig ID
                  LIB3139-020-P1-N1-H11
5'-most EST
                  BLASTX
Method
NCBI GI
                  g3510251
BLAST score
                   433
                   6.0e-43
E value
Match length
                  104
                   70
% identity
                  (AC005310) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   20842
Contig ID
                   79131 1.R1040
5'-most EST
                   uC-gmropic114e02b1
Method
                   BLASTX
NCBI GI
                   q3386604
BLAST score
                   173
E value
                   2.0e-12
Match length
                  73
% identity
                   49
NCBI Description
                  (AC004665) putative protein kinase [Arabidopsis thaliana]
Seq. No.
                   20843
                  79138 1.R1040
Contig ID
5'-most EST
                   uC-gmropic039c04b1
                  BLASTX
Method
NCBI GI
                   q3021532
BLAST score
                   194
                   9.0e-15
E value
                   85
Match length
% identity
                   53
NCBI Description
                   (AJ001772) glucose-6-phosphate dehydrogenase [Nicotiana
                   tabacum]
Seq. No.
                   20844
                   79141 1.R1040
Contig ID
                   q5342700
5'-most EST
Method
                  BLASTX
NCBI GI
                   g3757521
BLAST score
                   705
E value
                   4.0e-74
```

Match length 232 % identity

NCBI Description (AC005167) unknown protein [Arabidopsis thaliana]

20845 Seq. No.

79147 1.R1040 Contig ID

5'-most EST LIB3139-021-P1-N1-C3

20846 Seq. No.

79150 1.R1040 Contig ID

LIB3139-099-P1-N1-E6 5'-most EST

Seq. No. 20847

Match length

% identity

109 73



```
Contig ID
                  79150 2.R1040
                  LIB3167-013-P1-K1-H2
5'-most EST
Method
                  BLASTX
NCBI GI
                  q558925
                  208
BLAST score
                  2.0e-16
E value
Match length
                  60
                  75
% identity
NCBI Description
                  (U15778) geranylgeranyl pyrophosphate synthase [Lupinus
                  20848
Seq. No.
Contig ID
                  79152 1.R1040
5'-most EST
                  LIB3139-021-P1-N1-D1
                  BLASTX
Method
NCBI GI
                  g4510344
BLAST score
                  334
E value
                  3.0e-31
Match length
                  128
                  57
% identity
NCBI Description (AC006921) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  20849
Contig ID
                  79160 1.R1040
5'-most EST
                  LIB3139-021-P1-N1-D6
Method
                  BLASTX
NCBI GI
                  g2191136
BLAST score
                  795
E value
                  7.0e-85
Match length
                  290
% identity
                  54
                  (AF007269) Similar to UTP-Glucose Glucosyltransferase;
NCBI Description
                  coded for by A. thaliana cDNA T46230; coded for by A.
                  thaliana cDNA H76538; coded for by A. thaliana cDNA H76290
                   [Arabidopsis thaliana]
Seq. No.
                  20850
                   79163 1.R1040
Contig ID
5'-most EST
                  jC-gmro02910073h12a1
Method
                  BLASTX
NCBI GI
                  g1149569
BLAST score
                  1267
E value
                  1.0e-140
Match length
                  276
% identity
                 (Z50851) HD-zip [Arabidopsis thaliana]
NCBI Description
Seg. No.
                  20851
Contig ID
                  79176 1.R1040
5'-most EST
                  LIB3139-021-P1-N1-F4
Method
                  BLASTX
NCBI GI
                  g4371295
BLAST score
                  404
E value
                  2.0e-39
```

NCBI Description (AC006260) putative CCAAT-binding transcription factor



## [Arabidopsis thaliana]

Seq. No. 20852

Contig ID 79184 1.R1040

5'-most EST LIB3139-092-P1-N1-H11

Seq. No. 20853

Contig ID 79185\_1.R1040 5'-most EST sat701008005.h1

Method BLASTX
NCBI GI g3859696
BLAST score 244
E value 3.0e-20
Match length 223
% identity 26

NCBI Description (AL033497) unknown hypothetical protein [Candida albicans]

Seq. No. 20854

Contig ID 79193\_1.R1040 5'-most EST gsv701047090.h1

Seq. No. 20855

Contig ID 79194 1.R1040

5'-most EST jC-gmle01810021f06a1

Method BLASTX
NCBI GI g4467122
BLAST score 278
E value 1.0e-24
Match length 94
% identity 59

NCBI Description (AL035538) putative protein [Arabidopsis thaliana]

Seq. No. 20856

Contig ID 79195\_1.R1040

5'-most EST LIB3139-114-P1-N1-G12

Method BLASTX
NCBI GI g3367591
BLAST score 331
E value 1.0e-30
Match length 166
% identity 37

NCBI Description (AL031135) putative protein [Arabidopsis thaliana]

Seq. No. 20857

Contig ID 79195\_2.R1040 5'-most EST zsg701118081.h2

Seq. No. 20858

Contig ID 79224 1.R1040

5'-most EST jC-gmf102220142g07a1

Method BLASTX
NCBI GI g2980790
BLAST score 288
E value 9.0e-26
Match length 119
% identity 49

NCBI Description (AL022197) hypothetical protein [Arabidopsis thaliana]



Contig ID 79225 1.R1040

5'-most EST jC-gmle01810062c09a1

Seq. No. 20860

Contig ID 79225 2.R1040

5'-most EST LIB3139-022-P1-N1-D11

Seq. No. 20861

Contig ID 79227 1.R1040 5'-most EST sat701015277.h1

Seq. No. 20862

Contig ID 79248 1.R1040

5'-most EST jC-gmle01810022f07a1

Method BLASTX
NCBI GI g4324470
BLAST score 280
E value 2.0e-24
Match length 173
% identity 38

NCBI Description (AF105010) LAG1Ce-1 [Caenorhabditis elegans]

Seq. No. 20863

Contig ID 79250\_1.R1040

5'-most EST LIB3139-022-P1-N1-G3

Seq. No. 20864

Contig ID 79277\_1.R1040 5'-most EST ncj700986574.h1

Method BLASTX
NCBI GI g4544436
BLAST score 312
E value 2.0e-28
Match length 134
% identity 47

NCBI Description (AC006592) anthocyanidin-3-glucoside rhamnosyltransferase,

3' partial [Arabidopsis thaliana]

Seq. No. 20865

Contig ID 79282\_2.R1040 5'-most EST uC-gmronoir031a09b1

Seq. No. 20866

Contig ID 79285 1.R1040

5'-most EST LIB3139-023-P1-N1-C6

Seq. No. 20867

Contig ID 79298\_1.R1040

5'-most EST LIB3139-023-P1-N1-E11

Method BLASTX
NCBI GI 94204283
BLAST score 615
E value 5.0e-64
Match length 179
% identity 64



NCBI Description (AC004146) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 20868

Contig ID 79314 1.R1040

5'-most EST uC-gmflminsoy005b10b1

Method BLASTX
NCBI GI g2224911
BLAST score 826
E value 1.0e-88
Match length 261
% identity 66

NCBI Description (U93048) somatic embryogenesis receptor-like kinase [Daucus

carota]

Seq. No. 20869

Contig ID 79323\_1.R1040 5'-most EST leu701148586.h1

Method BLASTX
NCBI GI g2224911
BLAST score 286
E value 1.0e-25
Match length 79
% identity 70

NCBI Description (U93048) somatic embryogenesis receptor-like kinase [Daucus

carota]

Seq. No. 20870

Contig ID 79324\_1.R1040

5'-most EST LIB3139-023-P1-N1-H1

Seq. No. 20871

Contig ID 79332\_1.R1040

5'-most EST LIB3139-023-P1-N1-H9

Method BLASTX
NCBI GI g2944180
BLAST score 433
E value 5.0e-68
Match length 256
% identity 61

NCBI Description (AF007779) trehalose-6-phosphate phosphatase [Arabidopsis

thaliana]

Seq. No. 20872

Contig ID 79337\_1.R1040

5'-most EST jC-gmle01810014h08d1

Seq. No. 20873

Contig ID 79348\_1.R1040

5'-most EST LIB3139-024-P1-N1-B9

Method BLASTX
NCBI GI g2062174
BLAST score 198
E value 3.0e-15
Match length 78
% identity 50

NCBI Description (AC001645) transcription factor (TINY) isolog [Arabidopsis

thaliana]



```
Seq. No.
                   20874
Contig ID
                   79348 2.R1040
5'-most EST
                   trc700565484.h1
Method
                   BLASTX
NCBI GI
                   q1246403
BLAST score
                   151
E value
                   5.0e-10
Match length
                   34
% identity
                   76
                   (X94698) TINY [Arabidopsis thaliana] >qi 3406035 (AC005405)
NCBI Description
                   TINY [Arabidopsis thaliana]
Seq. No.
                   20875
                   79361 1.R1040
Contig ID
5'-most EST
                   k1170\overline{1}212190.h1
                   20876
Seq. No.
Contig ID
                   79361 2.R1040
                   ncj700979545.h2
5'-most EST
Seq. No.
                   20877
Contig ID
                   79373 1.R1040
5'-most EST
                   zzp700833542.h1
Method
                   BLASTX
NCBI GI
                   g2689219
BLAST score
                   146
E value
                   3.0e-09
Match length
                   95
% identity
                   39
NCBI Description
                  (X99669) dynamin like protein [Dictyostelium discoideum]
Seq. No.
                   20878
Contig ID
                   79385 1.R1040
5'-most EST
                   LIB3139-024-P1-N1-G11
Method
                   BLASTX
NCBI GI
                   g2181190
BLAST score
                   239
E value
                   4.0e-20
                   107
Match length
% identity
                   52
NCBI Description
                  (Y12531) serine/threonine kinase [Brassica oleracea]
Seq. No.
                   20879
Contig ID
                   79390 1.R1040
5'-most EST
                   fC-gmro700876241d1
Method
                   BLASTX
NCBI GI
                   q3953479
BLAST score
                   207
E value
                   4.0e-16
Match length
                   92
                   7
% identity
                  (AC002328) F2202.24 [Arabidopsis thaliana]
NCBI Description
```

Contig ID 79400\_1.R1040 5'-most EST uC-gmropic078c10b1

NCBI Description



```
Method
                  BLASTX
NCBI GI
                  q4510344
BLAST score
                  196
E value
                  9.0e-15
Match length
                  138
% identity
                  44
NCBI Description (AC006921) hypothetical protein [Arabidopsis thaliana]
                  20881
Seq. No.
                  79400 2.R1040
Contig ID
5'-most EST
                  gsv701053031.h1
Seq. No.
                  20882
                  79401 1.R1040
Contig ID
5'-most EST
                  sat701011730.h1
Seq. No.
                  20883
Contig ID
                  79408 1.R1040
5'-most EST
                  jC-gmle01810059d07a1
                  20884
Seq. No.
Contia ID
                  79412 1.R1040
5'-most EST
                  gsv701056890.hl
Method
                  BLASTX
                  g3406621
NCBI GI
BLAST score
                  153
                  3.0e-10
E value
                  57
Match length
                  47
% identity
NCBI Description (AF078806) unknown [Oryctolagus cuniculus]
                  20885
Seq. No.
                  79424 1.R1040
Contig ID
5'-most EST
                  zhf700964110.h1
Method
                  BLASTX
                  q2444178
NCBI GI
BLAST score
                  458
E value
                  8.0e-46
                  136
Match length
                  69
% identity
NCBI Description (U94784) unconventional myosin [Helianthus annuus]
Seq. No.
                  20886
Contig ID
                  79435 1.R1040
5'-most EST
                  LIB3139-025-P1-N1-E11
                  20887
Seq. No.
                  79443 1.R1040
Contig ID
5'-most EST
                  jC-gmf102220144b12a1
Method
                  BLASTX
NCBI GI
                  g629561
BLAST score
                  275
E value
                  2.0e-24
Match length
                  105
% identity
                  52
```

>gi 479047 emb CAA55654 (X79052) SRG1 [Arabidopsis

SRG1 protein - Arabidopsis thaliana

727



### thaliana]

 Seq. No.
 20888

 Contig ID
 79459 1.R1040

 5'-most EST
 rlr700896402.h1

Method BLASTX
NCBI GI g3176726
BLAST score 819
E value 6.0e-88
Match length 192
% identity 81

NCBI Description (AC002392) putative serine proteinase [Arabidopsis

thaliana]

Seq. No. 20889

Contig ID 79464 1.R1040

5'-most EST uC-gmrominsoy125e11b1

Seq. No. 20890

Contig ID 79465 1.R1040

5'-most EST LIB3139-026-P1-N1-A12

Method BLASTX
NCBI GI g1703201
BLAST score 457
E value 9.0e-46
Match length 117
% identity 77

NCBI Description PROTEIN KINASE AFC3 >gi 601791 (U16178) protein kinase

[Arabidopsis thaliana]

Seq. No. 20891

Contig ID 79476\_1.R1040

5'-most EST LIB3139-026-P1-N1-B5

Method BLASTX
NCBI GI 94204276
BLAST score 418
E value 3.0e-41
Match length 120
% identity 68

NCBI Description (AC004146) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 20892

Contig ID 79492 1.R1040 5'-most EST bnh700764650.h1

Method BLASTX
NCBI GI g3549669
BLAST score 249
E value 3.0e-21
Match length 69
% identity 74

NCBI Description (AL031394) putative protein [Arabidopsis thaliana]

Seq. No. 20893

Contig ID 79494\_1.R1040

5'-most EST LIB3139-026-P1-N1-D4

Method BLASTX NCBI GI g2160156

3362



BLAST score 306 E value 5.0e-28 Match length 94 % identity 65

NCBI Description (AC000132) Strong similarity to S. pombe leucyl-tRNA

synthetase (gb Z73100). [Arabidopsis thaliana]

Seq. No. 20894

Contig ID 79495\_1.R1040 5'-most EST ary700764420.h1

Seq. No. 20895

Contig ID 79496 1.R1040

5'-most EST LIB3139-026-P1-N1-D7

Method BLASTX
NCBI GI g3395440
BLAST score 403
E value 2.0e-39
Match length 126
% identity 56

NCBI Description (AC004683) hypothetical protein [Arabidopsis thaliana]

Seq. No. 20896

Contig ID 79499 1.R1040

5'-most EST LIB3139-026-P1-N1-E12

Method BLASTX
NCBI GI g2586082
BLAST score 259
E value 3.0e-22
Match length 153
% identity 45

NCBI Description (U72725) retrofit [Oryza longistaminata]

Seq. No. 20897

Contig ID 79504 1.R1040

5'-most EST jC-gmro02910050c08d1

Seq. No. 20898

Contig ID 79510\_1.R1040 5'-most EST ssr700555962.h1

Method BLASTX
NCBI GI g4510350
BLAST score 365
E value 9.0e-35
Match length 109
% identity 64

NCBI Description (AC006921) hypothetical protein [Arabidopsis thaliana]

Seq. No. 20899

Contig ID 79521 1.R1040

5'-most EST uC-gmrominsoy174h02b1

Method BLASTN
NCBI GI g3821780
BLAST score 38
E value 8.0e-12
Match length 46
% identity 96



## NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 20900

Contig ID 79538\_1.R1040 5'-most EST awf700839205.h1

Method BLASTX
NCBI GI g1169128
BLAST score 868
E value 3.0e-93
Match length 293
% identity 84

NCBI Description SERINE/THREONINE-PROTEIN KINASE CTR1 >gi\_166680 (L08789)

protein kinase [Arabidopsis thaliana] >gi\_166682 (L08790)

protein kinase [Arabidopsis thaliana]

Seq. No. 20901

Contig ID 79539 1.R1040 5'-most EST g5057836 Method BLASTX q4490737 NCBI GI BLAST score 347 2.0e-32 E value Match length 91 75 % identity

NCBI Description (AL035708) putative protein [Arabidopsis thaliana]

Seq. No. 20902

Contig ID 79541\_1.R1040 5'-most EST ssr700557649.h1

Seq. No. 20903

Contig ID 79555\_1.R1040 5'-most EST dpv701102359.h1

Method BLASTX
NCBI GI g4455184
BLAST score 442
E value 9.0e-44
Match length 175
% identity 55

NCBI Description (AL035521) extra-large G-protein-like [Arabidopsis

thaliana]

Seq. No. 20904

Contig ID 79574 1.R1040 5'-most EST hyd700730174.h1

Method BLASTX
NCBI GI g2760839
BLAST score 518
E value 3.0e-52
Match length 247
% identity 51

NCBI Description (AC003105) putative receptor kinase [Arabidopsis thaliana]

Seq. No. 20905

Contig ID 79578\_1.R1040 5'-most EST zhf700953640.h1

Method BLASTX



```
NCBI GI
                  q4538935
BLAST score
                  295
                  1.0e-26
E value
Match length
                  71
                  73
% identity
NCBI Description
                  (AL049483) putative protein [Arabidopsis thaliana]
Seq. No.
                  20906
Contig ID
                  79585 1.R1040
5'-most EST
                  zzp700832036.h1
Method ,
                  BLASTX
NCBI GI
                  g2245136
BLAST score
                  1250
E value
                  1.0e-138
Match length
                  331
% identity
                  77
                  (Z97344) trehalose-6-phosphate synthase homolog
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  20907
Contig ID
                  79596 1.R1040
5'-most EST
                  pxt700944555.h1
Method
                  BLASTX
NCBI GI
                  g3335378
BLAST score
                  289
                  6.0e-35
E value
Match length
                  129
% identity
                  51
                  (AC003028) Myb-related transcription activator [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  20908
Contig ID
                  79603 1.R1040
5'-most EST
                  zhf700960159.hl
Method
                  BLASTX
NCBI GI
                  q3193330
BLAST score
                   463
E value
                  3.0e-46
                                                    Ē
Match length
                  133
% identity
                   71
                  (AF069299) contains similarity to Medicago sativa corC
NCBI Description
                   (GB:L22305) [Arabidopsis thaliana]
Seq. No.
                  20909
                  79606 1.R1040
Contig ID
5'-most EST
                  zhf700958264.h1
                  20910
Seq. No.
                  79616 1.R1040
Contig ID
5'-most EST
                  uC-gmropic042a11b1
                  20911
Seq. No.
```

Contig ID 79639 1.R1040 5'-most EST zsq701118922.h1

Method BLASTX NCBI GI g4539322 BLAST score 283



E value 1.0e-27 Match length 100 69 % identity

(AL035679) putative protein [Arabidopsis thaliana] NCBI Description

20912 Seq. No.

Contig ID 79646 1.R1040

5'-most EST jC-qmst02400052a03a1

Method BLASTX NCBI GI q4539006 BLAST score 193 9.0e-16 E value 190 Match length 32 % identity

(AL049481) putative protein [Arabidopsis thaliana] NCBI Description

Seq. No.

20913 Contig ID 79653 1.R1040 5'-most EST zzp700836001.hl

Seq. No.

20914 Contig ID 79654 1.R1040

5'-most EST LIB3139-118-P1-N1-B8

Seq. No. 20915

Contig ID 79657 1.R1040 5'-most EST asn701131789.h1

Method BLASTX g4539401 NCBI GI BLAST score 353 E value 3.0e-33 Match length 172 % identity

(AL035526) putative protein [Arabidopsis thaliana] NCBI Description

20916 Seq. No.

79657 2.R1040 Contig ID

5'-most EST LIB3139-028-P1-N1-G2

BLASTX Method g4539401 NCBI GI BLAST score 441 8.0e-44 E value Match length 119 70 % identity

NCBI Description (AL035526) putative protein [Arabidopsis thaliana]

20917 Seq. No.

Contig ID 79662 1.R1040

5'-most EST uC-gmronoir063b03b1

Method BLASTX NCBI GI g4510376 BLAST score 333 E value 7.0e-31 Match length 142 47 % identity

(AC007017) unknown protein [Arabidopsis thaliana] NCBI Description



```
20918
Seq. No.
Contig ID
                  79669 1.R1040
                  epx701106551.hl
5'-most EST
                  20919
Seq. No.
                  79683 1.R1040
Contig ID
5'-most EST
                  LIB3139-029-P1-N1-C3
Method
                  BLASTX
NCBI GI
                  g3063455
BLAST score
                  436
                  2.0e-42
E value
Match length
                  102
                  76
% identity
                 (AC003981) F22013.17 [Arabidopsis thaliana]
NCBI Description
                  20920
Seq. No.
Contig ID
                  79724 1.R1040
5'-most EST
                  trc700561179.h1
Seq. No.
                  20921
                  79728 1.R1040
Contig ID
5'-most EST
                  uxk700668456.h1
                  BLASTX
Method
NCBI GI
                  g2780192
BLAST score
                  655
E value
                  9.0e-69
                  131
Match length
% identity
                  88
                  (AJ222713) unnamed protein product [Arabidopsis thaliana]
NCBI Description
                  20922
Seq. No.
Contig ID
                  79729_1.R1040
5'-most EST
                  LIB3139-029-P1-N1-H10
Method
                  BLASTX
NCBI GI
                  g2760830
                  508
BLAST score
                  9.0e-52
E value
                  118
Match length
% identity
                  84
                  (ACO03105) putative beta-ketoacyl-CoA synthase [Arabidopsis
NCBI Description
                  thaliana]
                  20923
Seq. No.
                  79731 1.R1040
Contig ID
5'-most EST
                  jC-gmst02400046g05a1
Method
                  BLASTN
NCBI GI
                  g2351064
BLAST score
                  40
                  5.0e-13
E value
Match length
                  44
                  98
% identity
                 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
```

Seq. No. 20924

Contig ID 79742\_1.R1040 5'-most EST kmv700742804.h1

MDJ22, complete sequence [Arabidopsis thaliana]



Method BLASTX
NCBI GI g1871182
BLAST score 690
E value 7.0e-73
Match length 169
% identity 77

NCBI Description (U90439) phospholipase D isolog [Arabidopsis thaliana]

Seq. No. 20925

Contig ID 79748 1.R1040

5'-most EST uC-gmrominsoy169c11b1

Seq. No. 20926

Contig ID 79748\_2.R1040 5'-most EST leu701152554.h1

Seq. No. 20927

Contig ID 79749 1.R1040 5'-most EST kl1701206380.h1

Method BLASTX
NCBI GI g2829923
BLAST score 339
E value 1.0e-31
Match length 75
% identity 48

NCBI Description (AC002291) Similar to uridylyl transferases [Arabidopsis

thaliana]

Seq. No. 20928

Contig ID 79764\_1.R1040

5'-most EST LIB3139-030-P1-N1-D2

Seq. No. 20929

Contig ID 79766\_1.R1040

5'-most EST LIB3139-030-P1-N1-D4

Seq. No. 20930

Contig ID 79767 1.R1040

5'-most EST LIB3139-030-P1-N1-D6

Method BLASTX
NCBI GI g2088657
BLAST score 149
E value 1.0e-09
Match length 87
% identity 33

NCBI Description (AF002109) unknown protein [Arabidopsis thaliana]

Seq. No. 20931

Contig ID 79773 1.R1040

5'-most EST LIB3139-030-P1-N1-E3

Seq. No. 20932

Contig ID 79786 1.R1040

5'-most EST LIB3139-030-P1-N1-F9

Method BLASTX
NCBI GI g2465923
BLAST score 157

E value 2.0e-10
Match length 100
% identity 35

NCBI Description (AF024648) receptor-like serine/threonine kinase

[Arabidopsis thaliana]

Seq. No. 20933

Contig ID 79791\_1.R1040 5'-most EST xpa700793503.h1

Method BLASTX
NCBI GI g1369981
BLAST score 176
E value 1.0e-12
Match length 86
% identity 21

NCBI Description (X95609) mec-8 [Caenorhabditis elegans]

>gi\_3874374\_emb\_CAB02754\_ (Z81037) similar to mecanosensory gene mec-8; cDNA EST EMBL:T00424 comes from this gene; cDNA EST yk494a10.3 comes from this gene; cDNA EST yk333a11.3 comes from this gene; cDNA EST yk505h10.3 comes from this gene; cDNA EST yk2... >gi\_3877217\_emb\_CAB03111\_ (Z81084) similar to mecanosensory gene mec-8; cDNA EST EMBL:T00424 comes from this gene; cDNA EST yk333a11.3 comes from this gene; cDNA EST yk333a11.3 comes from this gene; cDNA EST

yk505h10.3 comes from this gene; cDNA EST yk2

Seq. No. 20934

Contig ID 79792 1.R1040

5'-most EST LIB3139-030-P1-N1-G5

Seq. No. 20935

Contig ID 79793 1.R1040

5'-most EST LIB3139-030-P1-N1-G7

Method BLASTN
NCBI GI g4097879
BLAST score 116
E value 1.0e-58
Match length 340
% identity 84

NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein

gene, complete cds

Seq. No. 20936

Contig ID 79800 1.R1040

5'-most EST LIB3139-030-P1-N1-H5

Seq. No. 20937

Contig ID 79808 1.R1040

5'-most EST LIB3139-031-P1-N1-A4

Seq. No. 20938

Contig ID 79823 1.R1040

5'-most EST LIB3139-031-P1-N1-C12

Seq. No. 20939

Contig ID 79829\_1.R1040

5'-most EST LIB3139-031-P1-N1-D1



Seq. No. 20940

Contig ID 79832 1.R1040

5'-most EST LIB3170-061-Q1-J1-G8

Seq. No. 20941

Contig ID 79834\_1.R1040 5'-most EST fC-gmse700672004f2

Method BLASTX
NCBI GI g4218011
BLAST score 629
E value 9.0e-66
Match length 159
% identity 75

NCBI Description (AC006135) putative protein kinase [Arabidopsis thaliana]

>gi\_4309721\_gb\_AAD15491\_ (AC006439) putative

serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No. 20942

Contig ID 79839\_1.R1040

5'-most EST uC-gmrominsoy053h10b1

Method BLASTX
NCBI GI g3367591
BLAST score 503
E value 1.0e-50
Match length 151
% identity 63

NCBI Description (AL031135) putative protein [Arabidopsis thaliana]

Seq. No. 20943

Contig ID 79839 2.R1040

5'-most EST uC-gmrominsoy120g04b1

Method BLASTX
NCBI GI g3367591
BLAST score 184
E value 7.0e-14
Match length 54
% identity 67

NCBI Description (AL031135) putative protein [Arabidopsis thaliana]

Seq. No. 20944

Contig ID 79839 3.R1040 5'-most EST hrw701060749.h1

Seq. No. 20945

Contig ID 79851 1.R1040

5'-most EST LIB3139-031-P1-N1-F4

Method BLASTX
NCBI GI g3135251
BLAST score 147
E value 2.0e-09
Match length 123
% identity 37

NCBI Description (AC003058) putative receptor protein kinase [Arabidopsis

thaliana] >gi 3176719 (AC002392) putative protein kinase

[Arabidopsis thaliana]



Seq. No. 20946

Contig ID 79852 1.R1040

LIB3139-070-P1-N1-E10 5'-most EST

20947 Seq. No.

79865 1.R1040 Contig ID 5'-most EST pcp700995780.hl

Method BLASTX NCBI GI g3873823 BLAST score 166 1.0e-11 E value 82 Match length % identity 43

(Z73422) predicted using Genefinder [Caenorhabditis NCBI Description

elegans]

20948 Seq. No.

Contig ID 79865 2.R1040  $uaw70\overline{0}665457.h1$ 5'-most EST

20949 Seq. No.

79867\_1.R1040 Contig ID 5'-most EST g4285361

Seq. No. 20950

79887 1.R1040 Contig ID pxt700944223.hl 5'-most EST

Method BLASTX NCBI GI q4539386 284 BLAST score 2.0e-25 E value Match length 101

% identity

(AL035526) extensin-like protein [Arabidopsis thaliana] NCBI Description

20951 Seq. No.

79889 1.R1040 Contig ID

jC-gmle01810091e03a1 5'-most EST

BLASTX Method g732311 NCBI GI 248 BLAST score 8.0e-21 E value 122 Match length 42 % identity

HYPOTHETICAL 15.7 KD PROTEIN IN PBPD-COMA INTERGENIC REGION NCBI Description

(ORF2) >gi 1075880 pir B55220 pbpD 3'-region hypothetical protein - Bacillus subtilis >gi\_520537 (U11882) unknown [Bacillus subtilis] >gi\_1934785\_emb\_CAB07916 (Z93933) unknown [Bacillus subtilis] >gi 2635646 emb CAB15139 (Z99120) alternate gene name: yugD [Bacillus subtilis]

20952 Seq. No.

79895 1.R1040 Contig ID 5'-most EST pmv700889465.hl

BLASTX Method g3738296 NCBI GI 476 BLAST score



E value 1.0e-47 Match length 157 % identity 61

NCBI Description (AC005309) hypothetical protein [Arabidopsis thaliana]

Seq. No.

20953

Contig ID

79896 1.R1040

5'-most EST

LIB3139-032-P1-N1-C12

Seq. No.

20954

Contig ID 5'-most EST

79903\_1.R1040 jex700908215.h1

Seq. No.

20955

Contig ID 5'-most EST

79907\_1.R1040 rca701001570.h1

Method NCBI GI BLASTX g3790567

BLAST score E value

179 6.0e-13

Match length % identity

133 35

NCBI Description

(AF078821) RING-H2 finger protein RHA1b [Arabidopsis

thaliana]

Seq. No.

20956

Contig ID 5'-most EST

79921\_1.R1040 vzy700753611.h1

Method NCBI GI

BLASTX g3695389

BLAST score E value

158 1.0e-10

Match length % identity

65 34

NCBI Description

(AF096371) contains similarity to D-isomer specific

2-hydroxyacid dehydrogenases (Pfam: 2-Hacid DH.hmm, score:

19.11) [Arabidopsis thaliana]

Seq. No.

20957

Contig ID

79938 1.R1040

5'-most EST

LIB3139-089-P1-N1-G3

Method NCBI GI BLASTX g4455186

BLAST score

304

E value

3.0e-27

Match length

144

% identity

56

NCBI Description

(AL035521) putative protein [Arabidopsis thaliana]

Seq. No.

20958

Contig ID

79943 1.R1040

5'-most EST

jC-gmf102220052h07a1

Seq. No.

20959

Contig ID

79943 2.R1040

5'-most EST

LIB3139-032-P1-N1-G9

Method

BLASTX



q3-927830 NCBI GI BLAST score 150 1.0e-09 E value 93 Match length % identity

(AC005727) hypothetical protein [Arabidopsis thaliana] NCBI Description

20960 Seq. No.

79959 1.R1040 Contig ID crh700852977.h1 5'-most EST

Method BLASTX g3413716 NCBI GI BLAST score 397 2.0e-49 E value 235 Match length % identity

(AC004747) unknown protein [Arabidopsis thaliana] NCBI Description

>gi 3643589 (AC005395) unknown protein [Arabidopsis

thaliana]

20961 Seq. No.

79968 1.R1040 Contig ID

jC-gmst02400077b04a1 5'-most EST

20962 Seq. No.

79970 1.R1040 Contig ID

LIB3139-039-P1-N1-B2 5'-most EST

BLASTN Method g4558461 NCBI GI BLAST score 408 0.0e+00E value Match length 620 91 % identity

Medicago sativa subsp. X varia cell cycle switch protein NCBI Description

(ccs52) mRNA, complete cds

20963 Seq. No.

79973 1.R1040 Contig ID kl1701213853.hl 5'-most EST

BLASTX Method g3249105 NCBI GI 779 BLAST score 4.0e-83 E value 187 Match length 80 % identity

(AC003114) Contains similarity to protein phosphatase 2C NCBI Description

(ABI1) gb\_X78886 from A. thaliana. [Arabidopsis thaliana]

20964 Seq. No.

79973 2.R1040 Contig ID 5'-most EST uC-gmropic031e05b1

BLASTX Method q3249105 NCBI GI 262 BLAST score 7.0e-46E value Match length 140 % identity 72

3373



NCBI Description (ACO03114) Contains similarity to protein phosphatase 2C (ABI1) gb X78886 from A. thaliana. [Arabidopsis thaliana]

20965 Seq. No.

79977 1.R1040 Contig ID 5'-most EST zsg701123729.h1

BLASTX Method a3548810 NCBI GI BLAST score 225 4.0e-18 E value Match length 86 41 % identity

NCBI Description (AC005313) putative chloroplast nucleoid DNA binding

protein [Arabidopsis thaliana]

Seq. No. 20966

79982 1.R1040 Contig ID 5'-most EST dpv701101511.h1

BLASTX Method NCBI GI q3641252 275 BLAST score 4.0e-24 E value 102 Match length % identity 55

NCBI Description (AF053127) leucine-rich receptor-like protein kinase [Malus

domestica]

20967 Seq. No.

79986 1.R1040 Contig ID

5'-most EST LIB3139-033-P1-N1-D7

Method BLASTX NCBI GI g4539335 BLAST score 399 1.0e-38 E value 138 Match length

% identity 48

(AL035539) putative protein [Arabidopsis thaliana] NCBI Description

20968 Seq. No.

Contig ID 79990 1.R1040

5'-most EST LIB3139-033-P1-N1-E10

Method BLASTX NCBI GI q3395938 BLAST score 495 E value 5.0e-50 Match length 121 80 % identity

(AF076924) polypyrimidine tract-binding protein homolog NCBI Description

[Arabidopsis thaliana]

Seq. No. 20969

Contig ID 79995 1.R1040 5'-most EST uC-qmropic089c07b1

20970 Seq. No.

80003 1.R1040 Contig ID 5'-most EST pmv700894224.h1



Seq. No. 20971

80005 1.R1040 Contig ID

LIB3139-033-P1-N1-G10 5'-most EST

BLASTX Method NCBI GI g1850546 BLAST score 199 2.0e-15 E value 58 Match length 72 % identity

(U88045) syntaxin related protein AtVam3p [Arabidopsis NCBI Description

thaliana]

20972 Seq. No.

Contig ID 80012 1.R1040

5'-most EST jC-qmro02800043c06a1

Method BLASTX NCBI GI g4559331 BLAST score 612 E value 1.0e-63 Match length 134 % identity 83

(AC007087) unknown protein [Arabidopsis thaliana] NCBI Description

Seq. No.

Contig ID 80026 1.R1040

5'-most EST LIB3139-105-P1-N1-D4

20973

Seq. No. 20974

Contig ID 80029 1.R1040

5'-most EST jC-gmro02910009e01a1

Method BLASTX NCBI GI q3927830 BLAST score 200 E value 5.0e-33 262 Match length % identity

(AC005727) hypothetical protein [Arabidopsis thaliana] NCBI Description

Seq. No. 20975

Contig ID 80040 1.R1040

5'-most EST LIB3139-034-P1-N1-C1

Method BLASTN NCBI GI g595956 BLAST score 34 1.0e-09 E value 46 Match length 93 % identity

Brassica rapa acyl-ACP thioesterase Br FatA1 (FatA1) mRNA, NCBI Description

complete cds >gi\_1249747\_gb\_I14838\_I14838 Sequence 6 from patent US 5455167 >gi 2471012\_gb\_I47047\_I47047 Sequence 8

from patent US 5639790 >gi\_2482072\_gb\_165502\_165502 Sequence 12 from patent US 5667997

>gi\_3410286 gb I90346 I90346 Sequence 11 from patent US

Seq. No. 20976

Contig ID 80048 1.R1040

1385



```
5'-most EST
                  bth700848427.h1
Method
                  BLASTX
NCBI GI
                  g4115341
BLAST score
                  148
E value
                  2.0e-09
Match length
                  101
% identity
                  32
NCBI Description (U51100) chromaffin granule ATPase II [Bos taurus]
                  20977
Seq. No.
Contig ID
                  80054 1.R1040
5'-most EST
                  LIB3139-120-P1-N1-H9
Method
                  BLASTX
NCBI GI
                  g3914359
BLAST score
                  1096
E value
                  1.0e-120
Match length
                  242
% identity
                  84
NCBI Description
                  PHOSPHOLIPASE D PRECURSOR (PLD) (CHOLINE PHOSPHATASE)
                  (PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D)
                  >gi 1928979 (U92656) phospholipase D [Vigna unguiculata]
                  20978
Seq. No.
Contig ID
                  80067 1.R1040
5'-most EST
                  jC-gmro02800035c03a1
Method
                  BLASTX
NCBI GI
                  q3941472
                  470
BLAST score
E value
                  3.0e-47
Match length
                  100
% identity
NCBI Description
                  (AF062890) putative transcription factor [Arabidopsis
                  thaliana]
                  20979
Seq. No.
                  80068 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy302f08b1
Method
                  BLASTX
NCBI GI
                  g3258571
                  358
BLAST score
E value
                  3.0e-34
Match length
                  95
% identity
                  78
NCBI Description
                  (U89959) Hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  20980
                  80076 1.R1040
Contig ID
5'-most EST
                  LIB3139-054-P1-N1-B1
                  20981
Seq. No.
                  80091 1.R1040
Contig ID
5'-most EST
                  LIB3139-034-P1-N1-H6
```

Method BLASTX

NCBI GI g129248
BLAST score 152
E value 7.0e-10
Match length 113

3376



% identity 33

NCBI Description ORGAN SPECIFIC PROTEIN S2 >gi\_72318\_pir\_\_KNPMS2 protein S2

- garden pea >gi 295831 emb CAA35944 (X51595) S2 protein

[Pisum sativum]

Seq. No. 20982

Contig ID 80092 1.R1040

5'-most EST jC-qmro02910026b04a1

Method BLASTX
NCBI GI g3876927
BLAST score 307
E value 6.0e-28
Match length 92
% identity 24

NCBI Description (Z68342) Similarity to Human Coatomer beta' subunit

(SW:COPP HUMAN); cDNA EST EMBL:T00205 comes from this gene;

cDNA EST EMBL:D33984 comes from this gene; cDNA EST EMBL:D36965 comes from this gene; cDNA EST EMBL:D67413

comes fr

Seq. No. 20983

Contig ID 80115 1.R1040

5'-most EST uC-gmrominsoy298c01b1

Method BLASTX
NCBI GI g3249064
BLAST score 371
E value 2.0e-35
Match length 109
% identity 71

NCBI Description (AC004473) Strong similarity to trehalose-6-phosphate

synthase homolog gb 2245136 from A. thaliana chromosome 4

contig gb\_Z97344. [Arabidopsis thaliana]

Seq. No. 20984

Contig ID 80115\_2.R1040 5'-most EST dpv701099739.h1

Method BLASTX
NCBI GI g3249064
BLAST score 154
E value 3.0e-10
Match length 65
% identity 54

NCBI Description (AC004473) Strong similarity to trehalose-6-phosphate

synthase homolog gb 2245136 from A. thaliana chromosome 4

contig gb Z97344. [Arabidopsis thaliana]

Seq. No. 20985

Contig ID 80120\_1.R1040

5'-most EST LIB3139-035-P1-N1-C3

Seq. No. 20986

Contig ID 80125\_1.R1040 5'-most EST g5688015

Seq. No. 20987

Contig ID 80125\_2.R1040 5'-most EST epx701107023.h1



Method BLASTX
NCBI GI g4512659
BLAST score 376
E value 3.0e-54
Match length 141
% identity 80

NCBI Description (AC006931) putative protein kinase [Arabidopsis thaliana] >gi\_4544465 gb\_AAD22372.1\_AC006580\_4 (AC006580) putative

protein kinase [Arabidopsis thaliana]

Seq. No. 20988

Contig ID 80130\_1.R1040 5'-most EST zhf700953380.h1

Method BLASTX
NCBI GI g3341747
BLAST score 579
E value 3.0e-59
Match length 175
% identity 64

NCBI Description (AF077130) receptor-like protein kinase [Oryza sativa]

Seq. No. 20989

Contig ID 80134\_1.R1040 5'-most EST sat701006288.h2

Seq. No. 20990

Contig ID 80139 1.R1040

5'-most EST LIB3139-035-P1-N1-E3

Seq. No. 20991

Contig ID 80169 1.R1040

5'-most EST jC-gmro02800028h09a1

Method BLASTX
NCBI GI g4263716
BLAST score 220
E value 2.0e-23
Match length 135
% identity 48

NCBI Description (AC006223) putative alanine acetyl transferase [Arabidopsis

thaliana]

Seq. No. 20992

Contig ID 80181 1.R1040

5'-most EST LIB3139-036-P1-N1-B12

Seq. No. 20993

Contig ID 80186 1.R1040

5'-most EST LIB3139-048-P1-N1-C8

Seq. No. 20994

Contig ID 80200 1.R1040

5'-most EST LIB3139-036-P1-N1-E10

Seq. No. 20995

Contig ID 80205\_1.R1040

5'-most EST LIB3139-036-P1-N1-E5



```
20996
Seq. No.
                  80209 1.R1040
Contig ID
                  jC-gm\overline{l}e01810027c12d1
5'-most EST
                  20997
Seq. No.
                  80222 1.R1040
Contig ID
                  uC-gmropic110g12b1
5'-most EST
                   20998
Seq. No.
                   80223 1.R1040
Contig ID
                   eep700868607.hl
5'-most EST
                   BLASTX
Method
                   g4490311
NCBI GI
                   183
BLAST score
                   2.0e-13
E value
                   59
Match length
% identity
                  (AL035678) putative protein [Arabidopsis thaliana]
NCBI Description
                   20999
Seq. No.
                   80241 1.R1040
Contig ID
                   epx701109166.hl
5'-most EST
                   21000
Seq. No.
                   80268 1.R1040
Contig ID
5'-most EST
                   kl1701214348.hl
                   21001
Seq. No.
                   80269 2.R1040
Contig ID
                   LIB3139-037-P1-N1-D11
5'-most EST
                   BLASTX
Method
                   q1706482
NCBI GI
                   210
BLAST score
                   2.0e-16
E value
                   206
Match length
                    27
 % identity
                   DNA LIGASE IV (POLYDEOXYRIBONUCLEOTIDE SYNTHASE (ATP))
 NCBI Description
                                             (X83441) DNA ligase IV [Homo
                    >qi 860937 emb_CAA58467_
                    sapiens] >gi_4504997_ref_NP_002303.1_pLIG4_ ligase IV, DNA,
                    ATP-dependent
                    21002
 Seq. No.
                    80273 1.R1040
 Contig ID
                    LIB3139-037-P1-N1-D4
 5'-most EST
                    BLASTX
 Method
                    g4115379
 NCBI GI
                    286
 BLAST score
```

1.0e-25 E value 92 Match length 62 % identity

(AC005967) putative carbonyl reductase [Arabidopsis NCBI Description

thaliana]

21003 Seq. No.

80276 1.R1040 Contig ID

LIB3139-037-P1-N1-D8 5'-most EST

BLASTX Method



```
NCBI GI
                  q2499115
BLAST score
                  321
E value
                  8.0e-30
                  72
Match length
                  82
% identity
NCBI Description VACUOLAR ASSEMBLY PROTEIN VPS41 HOMOLOG >gi 1835788
                  (U86662) VPS41 [Lycopersicon esculentum]
                  21004
Seq. No.
Contig ID
                  80280 1.R1040
                  eep700869664.hl
5'-most EST
Method
                  BLASTX
                  q3402686
NCBI GI
BLAST score
                  146
E value
                  6.0e-09
Match length
                  127
% identity
NCBI Description (AC004697) putative serine/threonine protein kinase
                  [Arabidopsis thaliana]
Seq. No.
                  21005
                  80281 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy142b10b1
Method
                  BLASTX
NCBI GI
                  g3850569
BLAST score
                  532
E value
                  3.0e-54
Match length
                  196
% identity
                  56
NCBI Description
                 (AC005278) ESTs gb T21276, gb T45403, and gb AA586113 come
                  from this gene. [Arabidopsis thaliana]
Seq. No.
                  21006
Contig ID
                  80286 1.R1040
5'-most EST
                  LIB3139-037-P1-N1-E6
Method
                  BLASTX
NCBI GI
                  g4490297
BLAST score
                  384
E value
                  1.0e-36
Match length
                  271
% identity
NCBI Description (AL035678) putative protein [Arabidopsis thaliana]
                  21007
Seq. No.
Contig ID
                  80287 1.R1040
5'-most EST
                  LIB3170-082-Q1-J1-H12
                  21008
Seq. No.
Contig ID
                  80299 1.R1040
5'-most EST
                  jC-gmst02400045f05a1
Method
                  BLASTX
```

Method BLASTX
NCBI GI g2191135
BLAST score 569
E value 3.0e-58
Match length 244
% identity 43

NCBI Description (AF007269) A\_IG002N01.14 gene product [Arabidopsis



## thaliana]

```
Seq. No.
                  21009
                  80307 1.R1040
Contig ID
5'-most EST
                  g4291063
Method
                  BLASTX
NCBI GI
                  q4234955
BLAST score
                  229
                  7.0e-19
E value
                  146
Match length
                  24
% identity
NCBI Description (AF098971) NBS-LRR-like protein cD8 [Phaseolus vulgaris]
                  21010
Seq. No.
Contig ID
                  80309 1.R1040
5'-most EST
                  uC-gmrominsoy310c10b1
Seq. No.
                  21011
Contig ID
                  80309 2.R1040
5'-most EST
                  uC-gmronoir034d01b1
                  21012
Seq. No.
Contig ID
                  80312 1.R1040
5'-most EST
                  fua701039992.hl
Method
                  BLASTX
NCBI GI
                  q3831441
BLAST score
                  153
                  2.0e-09
E value
Match length
                  43
                  79
% identity
NCBI Description (AC005819) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  21013
                  80314 1.R1040
Contig ID
5'-most EST
                  k11701207344.h1
                  BLASTX
Method
NCBI GI
                  g113292
BLAST score
                  209
                  2.0e-16
E value
Match length
                   139
% identity
                   38
NCBI Description
                  ACTIN >qi 83899 pir S07639 actin - yeast (Candida
                  albicans) >gi 295923 emb CAA34413 (X16377) actin [Candida
                  albicans
Seq. No.
                  21014
                  80317 1.R1040
Contig ID
5'-most EST
                  LIB3139-038-P1-N1-A1
Method
                  BLASTX
NCBI GI
                  g2145356
BLAST score
                   470
E value
                   3.0e-74
Match length
                  212
% identity
                   69
```

NCBI Description (Y11122) HD-Zip protein [Arabidopsis thaliana] >gi\_3132474

(AC003096) homeobox protein, ATHB-14 [Arabidopsis thaliana]



Seq. No. 21015

Contig ID 80327\_1.R1040 5'-most EST fde700876028.h1

Method BLASTX
NCBI GI g4056506
BLAST score 235
E value 2.0e-19
Match length 124
% identity 40

NCBI Description (AC005896) nodulin-like protein [Arabidopsis thaliana]

Seq. No. 21016

Contig ID 80336 1.R1040

5'-most EST LIB3139-038-P1-N1-C6

Method BLASTX
NCBI GI g4580531
BLAST score 262
E value 1.0e-22
Match length 154
% identity 43

NCBI Description (AF036309) scarecrow-like 14 [Arabidopsis thaliana]

Seq. No. 21017

Contig ID 80347\_1.R1040 5'-most EST pmv700889539.h1

Method BLASTX
NCBI GI g3746060
BLAST score 282
E value 5.0e-25
Match length 51
% identity 100

NCBI Description (AC005311) unknown protein [Arabidopsis thaliana]

Seq. No. 21018

Contig ID 80347 2.R1040

5'-most EST uC-gmrominsoy302d10b1

Seq. No. 21019

Contig ID 80347\_3.R1040 5'-most EST pxt700944858.h1

Method BLASTX
NCBI GI g3746060
BLAST score 291
E value 6.0e-26
Match length 99
% identity 58

NCBI Description (AC005311) unknown protein [Arabidopsis thaliana]

Seq. No. 21020

Contig ID 80360\_1.R1040 5'-most EST fde700873967.h1

Seq. No. 21021

Contig ID 80375\_1.R1040 5'-most EST rlr700899693.h1

Method BLASTX NCBI GI g3880563



BLAST score 8.0e-18 E value 111 Match length 43 % identity

(278018) predicted using Genefinder; similar to NCBI Description

serine/threonine kinase; cDNA EST yk353d10.5 comes from

this gene [Caenorhabditis elegans]

21022 Seq. No.

80383 1.R1040 Contig ID zhf700954392.h1 5'-most EST

BLASTX Method g4415924 NCBI GI BLAST score 500 1.0e-50 E value 143 Match length % identity

(AC006282) putative glucosyl transferase [Arabidopsis NCBI Description

thaliana]

21023 Seq. No.

80390 1.R1040 Contig ID  $seb70\overline{0}653756.h1$ 5'-most EST

BLASTX Method g4115913 NCBI GI 405 BLAST score 2.0e-39 E value 146 Match length 53 % identity

NCBI Description

(AF118222) contains similarity to Iron/Ascorbate family of oxidoreductases (Pfam: PF00671, Score=307.1, E=2.2e-88, N=1) [Arabidopsis thaliana] >gi\_4539409\_emb\_CAB40042.1\_

(AL049524) putative flavanone 3-beta-hydroxylase

[Arabidopsis thaliana]

21024 Seq. No.

80390 2.R1040 Contig ID

uC-gmflminsoy089a12b1 5'-most EST

21025 Seq. No.

80396 1.R1040 Contig ID seb700651303.h1 5'-most EST

BLASTX Method q464777 NCBI GI BLAST score 517 3.0e-52 E value 261 Match length 39 % identity

SOF1 PROTEIN >gi\_486774\_pir\_\_S35323 SOF1 protein - yeast NCBI Description

(Saccharomyces cerevisiae) >gi 312015 emb CAA49658

(X70052) SOF1 [Saccharomyces cerevisiae]

>gi 1360177 emb CAA97455 (Z73116) ORF YLL011w [Saccharomyces cerevisiae] >gi\_1495213\_emb\_CAA62781 (X91488) L1339/SOF1 protein [Saccharomyces cerevisiae]

21026 Seq. No.

80403 1.R1040 Contig ID



5'-most EST sat701006553.h1

Method BLASTX
NCBI GI g4206196
BLAST score 154
E value 6.0e-10
Match length 72
% identity 49

NCBI Description (AF071527) hypothetical protein [Arabidopsis thaliana]

Seq. No. 21027

Contig ID 80410 1.R1040

5'-most EST LIB3139-039-P1-N1-C8

Seq. No. 21028

Contig ID 80415\_1.R1040 5'-most EST fC-gmle700686670a1

Method BLASTX
NCBI GI g1495804
BLAST score 901
E value 2.0e-97
Match length 234
% identity 76

NCBI Description (X96406) 13-lipoxygenase [Solanum tuberosum]

Seq. No. 21029

Contig ID 80422\_1.R1040 5'-most EST uC-gmropic115g03b1

Method BLASTX

NCBI GI 94559331

BLAST score 357

E value 7.0e-34

Match length 73

% identity 84

NCBI Description (AC007087) unknown protein [Arabidopsis thaliana]

Seq. No. 21030

Contig ID 80429 2.R1040

5'-most EST LIB3139-039-P1-N1-F12

Method BLASTX
NCBI GI g1063400
BLAST score 388
E value 2.0e-37
Match length 84
% identity 87

NCBI Description (X92888) glycolate oxidase [Lycopersicon esculentum]

Seq. No. 21031

Contig ID 80457 1.R1040

5'-most EST LIB3139-040-P1-N1-A7

Seq. No. 21032

Contig ID 80463 1.R1040

5'-most EST LIB3139-040-P1-N1-B2

Seq. No. 21033

Contig ID 80467\_1.R1040 5'-most EST ncj700977282.h1



Method BLASTX
NCBI GI g2462749
BLAST score 795
E value 4.0e-85
Match length 175
% identity 87

NCBI Description (AC002292) Putative Serine/Threonine protein kinase

[Arabidopsis thaliana]

Seq. No. 21034

Contig ID 80479\_1.R1040 5'-most EST wrg700789061.h2

Method BLASTX
NCBI GI g3482967
BLAST score 700
E value 7.0e-74
Match length 179
% identity 72

NCBI Description (AL031369) Protein phosphatase 2C-like protein [Arabidopsis

thaliana] >gi 4559345 gb AAD23006.1\_AC006585\_1 (AC006585)

protein phosphatase 2C [Arabidopsis thaliana]

Seq. No. 21035

Contig ID 80480\_1.R1040 5'-most EST pmv700890946.h1

Method BLASTX
NCBI GI g2275215
BLAST score 624
E value 6.0e-65
Match length 225
% identity 56

NCBI Description (AC002337) hypothetical protein [Arabidopsis thaliana]

Seq. No. 21036

Contig ID 80490\_1.R1040

5'-most EST LIB3139-040-P1-N1-E6

Seq. No. 21037

Contig ID 80501\_1.R1040 5'-most EST dpv701103439.h1

Seq. No. 21038

Contig ID 80501\_2.R1040 5'-most EST seb700652190.h1

Seq. No. 21039

Contig ID 80502\_1.R1040

5'-most EST LIB3139-040-P1-N1-G11

Method BLASTX
NCBI GI 94580461
BLAST score 335
E value 5.0e-31
Match length 80
% identity 80

NCBI Description (AC006081) unknown protein [Arabidopsis thaliana]

Seq. No. 21040



```
Contig ID
                  80504 1.R1040
5'-most EST
                  LIB3139-040-P1-N1-G4
                  21041
Seq. No.
                  80505 1.R1040
Contig ID
                  sat701002993.h1
5'-most EST
                  BLASTX
Method
                  g2894599
NCBI GI
                  179
BLAST score
                  4.0e-13
E value
                  86
Match length
                  41
% identity
                  (AL021889) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  21042
                  80507 1.R1040
Contig ID
                  xpa700796263.h1
5'-most EST
                  BLASTN
Method
                  g3462613
NCBI GI
BLAST score
                  129
                  3.0e-66
E value
                  269
Match length
                  87
% identity
                  Pisum sativum knotted I class homeodomain protein (Kn284)
NCBI Description
                  mRNA, partial cds
Seq. No.
                  21043
                  80509 1.R1040
Contig ID
                  LIB3139-040-P1-N1-G9
5'-most EST
                  BLASTX
Method
                  g2232354
NCBI GI
BLAST score
                  242
E value
                  1.0e-20
Match length
                  115
% identity
                  48
                  (AF006081) UDPG glucosyltransferase [Solanum berthaultii]
NCBI Description
                  21044
Seq. No.
                  80510 1.R1040
Contig ID
5'-most EST
                  rlr700900930.h1
Method
                  BLASTX
NCBI GI
                   q3036805
BLAST score
                   182
E value
                   3.0e-13
Match length
                  52
                   75
% identity
NCBI Description
                  (AL022373) thaumatin-like protein [Arabidopsis thaliana]
Seq. No.
                   21045
Contig ID
                  80513 1.R1040
```

LIB3139-040-P1-N1-H12 5'-most EST

BLASTX Method g130759 NCBI GI 371 BLAST score 2.0e-35 E value 138 Match length % identity 51



NCBI Description PROLYL ENDOPEPTIDASE (POST-PROLINE CLEAVING ENZYME) (PE) >gi\_108383\_pir\_\_A37942 prolyl oligopeptidase (EC 3.4.21.26) - pig >gi\_164621 (M64227) prolyl endopeptidase [Sus scrofa] Seq. No. 21046

Contig ID 80519\_1.R1040 5'-most EST uaw700666764.h1

Seq. No. 21047

Contig ID 80520\_1.R1040

5'-most EST LIB3139-041-P1-N1-A1

Method BLASTX
NCBI GI g117188
BLAST score 332
E value 1.0e-30
Match length 224
% identity 35

NCBI Description CYTOCHROME P450 71A1 (CYPLXXIA1) (ARP-2)

>gi\_81423\_pir\_\_A35867 cytochrome P450 71A1 - avocado

Seq. No. 21048

Contig ID 80522 1.R1040

5'-most EST LIB3139-041-P1-N1-A12

Method BLASTX
NCBI GI g3548810
BLAST score 1251
E value 1.0e-138
Match length 426
% identity 58

NCBI Description (AC005313) putative chloroplast nucleoid DNA binding

protein [Arabidopsis thaliana]

Seq. No. 21049

Contig ID 80522\_2.R1040 5'-most EST pxt700943758.h1

Seq. No. 21050

Contig ID 80523\_1.R1040

5'-most EST LIB3139-041-P1-N1-A2

Method BLASTX
NCBI GI g4539001
BLAST score 519
E value 3.0e-67
Match length 234
% identity 63

NCBI Description (AL049481) putative protein [Arabidopsis thaliana]

Seq. No. 21051

Contig ID 80526\_1.R1040

5'-most EST LIB3139-041-P1-N1-A5

Method BLASTX
NCBI GI 94539326
BLAST score 394
E value 2.0e-38
Match length 102
% identity 70

NCBI Description (AL035679) putative zinc finger protein [Arabidopsis



## thaliana]

```
21052
Seq. No.
                  80526 2.R1040
Contig ID
                  leu70\overline{1}145669.h1
5'-most EST
                  BLASTX
Method
                  q4539326
NCBI GI
                  154
BLAST score
                   4.0e-10
E value
                   52
Match length
% identity
                  (AL035679) putative zinc finger protein [Arabidopsis
NCBI Description
                   thaliana]
                   21053
Seq. No.
                   80552 1.R1040
Contig ID
                   LIB3139-044-P1-N1-F11
5'-most EST
                   BLASTX
Method
                   g2576361
NCBI GI
                   305
BLAST score
                   6.0e-28
E value
                   75
Match length
% identity
                   67
                  (U39782) lysine and histidine specific transporter
NCBI Description
                   [Arabidopsis thaliana]
                   21054
Seq. No.
                   80564 1.R1040
Contig ID
                   zhf700964785.h1
5'-most EST
                   BLASTX
Method
                   g4204296
NCBI GI
                   694
BLAST score
                   1.0e-75
E value
                   249
Match length
                   63
 % identity
                   (AC003027) lcl prt_seq No definition line found
NCBI Description
                   [Arabidopsis thaliana]
                   21055
 Seq. No.
                   80564 2.R1040
 Contig ID
                   LIB3139-041-P1-N1-E9
 5'-most EST
                   BLASTX
 Method
                   g541824
 NCBI GI
                   437
 BLAST score
 E value
                   2.0e-43
                   130
 Match length
                   65
 % identity
 NCBI Description protein kinase - spinach >gi_457709_emb_CAA82991_ (Z30330)
                   protein kinase [Spinacia oleracea]
 Seq. No.
                   21056
                   80567 1.R1040
 Contig ID
                   LIB3139-041-P1-N1-F2
 5'-most EST
                   BLASTX
 Method
 NCBI GI
                   g3582333
```

167

1.0e-11

BLAST score

E value



Match length 100 % identity 36

NCBI Description (AC005496) hypothetical protein [Arabidopsis thaliana]

Seq. No. 21057

Contig ID 80576 1.R1040

5'-most EST jC-gmst02400056a10d1

Method BLASTX
NCBI GI g2129932
BLAST score 611
E value 2.0e-63
Match length 217
% identity 60

NCBI Description myb-related transcription factor TMH1 - tomato

>gi\_1167486\_emb\_CAA64615\_ (X95297) transcription factor

[Lycopersicon esculentum]

Seq. No. 21058

Contig ID 80585 1.R1040

5'-most EST jC-gmst02400040c10d1

Seq. No. 21059

Contig ID 80586\_1.R1040

5'-most EST jC-gmst02400045e11a1

Seq. No. 21060

Contig ID 80598\_1.R1040 5'-most EST ncj700985793.h1

Seq. No. 21061

Contig ID 80600\_1.R1040

5'-most EST LIB31 $\overline{3}$ 9-065-P1-N1-D7

Method BLASTX
NCBI GI g2982434
BLAST score 562
E value 9.0e-58
Match length 177
% identity 62

NCBI Description (AL022224) putative protein [Arabidopsis thaliana]

Seq. No. 21062

Contig ID 80607\_1.R1040

5'-most EST LIB3139-042-P1-N1-C10

Method BLASTX
NCBI GI g3647183
BLAST score 195
E value 7.0e-15
Match length 117
% identity 37

NCBI Description (AL031178) dJ341E18.2.2 (novel PUTATIVE protein) (PUTATIVE

isoform 2) [Homo sapiens]

Seq. No. 21063

Contig ID 80617\_1.R1040 5'-most EST gsv701051693.h1

Method BLASTX NCBI GI g4220533

```
T score 269 4.0e-2
```

BLAST score 269
E value 4.0e-24
Match length 77
% identity 75

NCBI Description (AL035356) putative mitochondrial uncoupling protein

[Arabidopsis thaliana]

Seq. No. 21064

Contig ID 80623\_1.R1040

5'-most EST LIB3139-042-P1-N1-D8

Method BLASTX
NCBI GI g2642165
BLAST score 236
E value 7.0e-20
Match length 105
% identity 44

NCBI Description (AC003000) hypothetical protein [Arabidopsis thaliana]

Seq. No. 21065

Contig ID 80632 1.R1040

5'-most EST LIB31 $\overline{3}$ 9-042-P1-N1-E6

Method BLASTX
NCBI GI g1001955
BLAST score 127
E value 6.0e-15
Match length 70
% identity 56

NCBI Description (U19099) unknown protein [Lycopersicon chilense ]

Seq. No. 21066

Contig ID 80636\_1.R1040 5'-most EST hyd700725928.h1

Method BLASTX
NCBI GI g3913366
BLAST score 351
E value 7.0e-33
Match length 181
% identity 43

NCBI Description PUTATIVE RECEPTOR PROTEIN KINASE CRINKLY4 PRECURSOR >gi\_1597723 (U67422) CRINKLY4 precursor [Zea mays]

Seq. No. 21067

Contig ID 80641\_1.R1040 5'-most EST fua701039334.h1

Method BLASTX
NCBI GI g2911055
BLAST score 418
E value 7.0e-41
Match length 153
% identity 55

NCBI Description (AL021961) putative protein [Arabidopsis thaliana]

Seq. No. 21068

Contig ID 80669\_1.R1040

5'-most EST uC-gmrominsoy157c01b1

Method BLASTX NCBI GI g3643085

```
BLAST score
                   1284
E value
                   1.0e-142
Match length
                   351
% identity
                   70
NCBI Description
                   (AF075580) protein phosphatase-2C; PP2C [Mesembryanthemum
                   crystallinum]
Seq. No.
                   21069
Contig ID
                   80669 4.R1040
5'-most EST
                   LIB3170-077-Q1-K1-D3
Seq. No.
                   21070
                   80671 1.R1040
Contig ID
5'-most EST
                   LIB3139-043-P1-N1-B12
Seq. No.
                   21071
Contig ID
                   80674 1.R1040
5'-most EST
                   LIB3139-043-P1-N1-B4
Method
                   BLASTN
NCBI GI
                   q3941447
BLAST score
                   35
E value
                   5.0e-10
Match length
                   59
% identity
                   90
NCBI Description Arabidopsis thaliana putative transcription factor (MYB36)
                  mRNA, complete cds
Seq. No.
                   21072
                   80676 1.R1040
Contig ID
5'-most EST
                   asn701132886.h1
Seq. No.
                   21073
Contig ID
                   80685 1.R1040
5'-most EST
                  LIB3139-043-P1-N1-C5
Method
                  BLASTX
NCBI GI
                  g4539335
                   <u>2</u>73
BLAST score
                   6.0e-24
E value
Match length
                  147
% identity
                  38
NCBI Description (AL035539) putative protein [Arabidopsis thaliana]
Seq. No.
                  21074
Contig ID
                  80686 1.R1040
5'-most EST
                  sat701006228.h2
Seq. No.
                  21075
                  80689 1.R1040
Contig ID
5'-most EST
                  dpv701098482.h1
```

Method BLASTX
NCBI GI g3882183
BLAST score 534
E value 2.0e-54
Match length 165
% identity 61

NCBI Description (AB018274) KIAA0731 protein [Homo sapiens]

Seq. No. 21076 Contig ID 80706 1.R1040 5'-most EST LIB3139-043-P1-N1-F10 Seq. No. 21077 Contig ID 80726 1.R1040 5'-most EST zhf700960432.h1 Method BLASTX NCBI GI q3757522 BLAST score 770 E value 7.0e-82 Match length 268 % identity (AC005167) putative splicing factor [Arabidopsis thaliana] NCBI Description Seq. No. 21078 Contig ID 80727 1.R1040 5'-most EST pmv700893752.h1 Seq. No. 21079 Contig ID 80755 2.R1040 5'-most EST seb700651885.hl Seq. No. 21080 Contig ID 80765 1.R1040 5'-most EST pcp700992731.h1Method BLASTX NCBI GI q1170409 BLAST score 231 E value 5.0e-19 Match length 106 % identity 56 NCBI Description HOMEOBOX-LEUCINE ZIPPER PROTEIN HAT22 (HD-ZIP PROTEIN 22) >gi\_549887 (U09336) homeobox protein [Arabidopsis thaliana] 549888 (U09337) homeobox protein [Arabidopsis thaliana] >gi\_4490724\_emb\_CAB38927.1\_ (AL035709) homeobox protein HAT22 [Arabidopsis thaliana] 21081 Seq. No. Contig ID 80769 1.R1040 5'-most EST LIB3139-044-P1-N1-D8 Method BLASTX NCBI GI g3482933

BLAST score 788 E value 4.0e-84 Match length 206 % identity 70

NCBI Description (AC003970) Similar to cdc2 protein kinases [Arabidopsis thaliana]

Seq. No. 21082

80780 1.R1040 Contig ID 5'-most EST txt700734549.h1

Seq. No. 21083

Contig ID 80781 1.R1040

5'-most EST LIB3139-044-P1-N1-E8



Method BLASTX
NCBI GI g3021280
BLAST score 230
E value 8.0e-19
Match length 191
% identity 25

NCBI Description (AL022347) serine /threonine kinase - like protein

[Arabidopsis thaliana]

Seq. No. 21084

Contig ID 80794 1.R1040 5'-most EST g5058112

Seq. No. 21085

Contig ID 80794 2.R1040

5'-most EST jC-gmro02910052c12a1

Method BLASTX
NCBI GI g2347199
BLAST score 595
E value 7.0e-62
Match length 135
% identity 83

NCBI Description (AC002338) protein kinase isolog [Arabidopsis thaliana]

Seq. No. 21086

Contig ID 80809\_1.R1040 5'-most EST bth700843525.h1

Seq. No. 21087

Contig ID 80812\_1.R1040

5'-most EST LIB3139-045-P1-N1-A2

Method BLASTX
NCBI GI g179462
BLAST score 249
E value 6.0e-21
Match length 187
% identity 41

NCBI Description (M13519) N-acetyl-beta-glucosaminidase prepro-polypeptide

[Homo sapiens]

Seq. No. 21088

Contig ID 80814\_1.R1040

5'-most EST LIB3139-045-P1-N1-A4

Method BLASTX
NCBI GI g3549681
BLAST score 950
E value 1.0e-103
Match length 292
% identity 59

NCBI Description (AL031394) male sterility 2-like protein [Arabidopsis

thaliana]

Seq. No. 21089

Contig ID 80835 1.R1040

5'-most EST jC-gmf102220077d12a1

Seq. No. 21090



Contig ID 80836\_1.R1040 5'-most EST LIB3139-045-P1-N1-C5

Method BLASTX
NCBI GI g4539386
BLAST score 234
E value 1.0e-19
Match length 62
% identity 65

NCBI Description (AL035526) extensin-like protein [Arabidopsis thaliana]

Seq. No. 21091

Contig ID 80840\_1.R1040 5'-most EST rca700998162.h1

Seq. No. 21092

Contig ID 80843\_1.R1040 5'-most EST jex700907819.h1

Method BLASTX
NCBI GI g3894193
BLAST score 206
E value 2.0e-16
Match length 114
% identity 39

NCBI Description (AC005662) putative strictosidine synthase [Arabidopsis

thaliana]

Seq. No. 21093

Contig ID 80846 1.R1040 5'-most EST bnu700967565.h1

Method BLASTX
NCBI GI g1272349
BLAST score 452
E value 6.0e-45
Match length 168
% identity 55

NCBI Description (U51740) secreted glycoprotein 3 [Ipomoea trifida]

Seq. No. 21094

Contig ID 80870 1.R1040

5'-most EST uC-gmflminsoy061h05b1

Method BLASTX
NCBI GI g2244834
BLAST score 601
E value 1.0e-66
Match length 231
% identity 49

NCBI Description (297337) hypothetical protein [Arabidopsis thaliana]

Seq. No. 21095

Contig ID 80885\_1.R1040

5'-most EST LIB3139-046-P1-N1-A10

Method BLASTX
NCBI GI g3880563
BLAST score 199
E value 3.0e-15
Match length 189
% identity 31



(Z78018) predicted using Genefinder; similar to

serine/threonine kinase; cDNA EST yk353d10.5 comes from

this gene [Caenorhabditis elegans]

Seq. No. 21096

NCBI Description

Contig ID 80888 1.R1040

5'-most EST uC-gmrominsoy298g11b1

Method BLASTX
NCBI GI g2244754
BLAST score 244
E value 2.0e-20
Match length 86
% identity 55

NCBI Description (Z97335) heat shock transcription factor homolog

[Arabidopsis thaliana]

Seq. No. 21097

Contig ID 80889\_1.R1040 5'-most EST epx701104732.h1

Method BLASTX
NCBI GI g4558673
BLAST score 190
E value 2.0e-14
Match length 84
% identity 50

NCBI Description (AC007063) hypothetical protein [Arabidopsis thaliana]

Seq. No. 21098

Contig ID 80895\_1.R1040 5'-most EST wvk700684491.h1

Seq. No. 21099

Contig ID 80905\_1.R1040

5'-most EST uC-gmflminsoy098c10b1

Seq. No. 21100

Contig ID 80905 2.R1040

5'-most EST LIB3167-077-P1-K2-G9

Seq. No. 21101

Contig ID 80905\_3.R1040 5'-most EST jex700907589.h1

Seq. No. 21102

Contig ID 80905\_4.R1040 5'-most EST pmv700892605.h1

Seq. No. 21103

Contig ID 80918 1.R1040

5'-most EST LIB3139-046-P1-N1-D4

Seq. No. 21104

Contig ID 80928\_1.R1040 5'-most EST fua701039007.h1

Method BLASTX NCBI GI g2462834 BLAST score 153

```
E value
                   7.0e-10
Match length
                   78
% identity
                   40
NCBI Description
                  (AF000657) hypothetical protein [Arabidopsis thaliana]
                  21105
Seq. No.
Contig ID
                  80939 1.R1040
5'-most EST
                  jC-gmf102220071h01a1
Seq. No.
                  21106
Contig ID
                  80961_1.R1040
5'-most EST
                  ncj700983457.h1
Method
                  BLASTX
NCBI GI
                  q627580
BLAST score
                  186
E value
                  1.0e-24
Match length
                  110
% identity
                  52
NCBI Description
                  prolyl oligopeptidase (EC 3.4.21.26) - human
                  >gi_904214_dbj_BAA04661 (D21102) prolyl endopeptidase
                   [Homo sapiens]
Seq. No.
                  21107
Contig ID
                  80980 1.R1040
5'-most EST
                  LIB3139-047-P1-N1-C7
Method
                  BLASTX
NCBI GI
                  q3023956
                  207
BLAST score
E value
                  3.0e-16
Match length
                  108
% identity
                 VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1 >gi_607003
NCBI Description
                  (L28125) beta transducin-like protein [Podospora anserina]
Seq. No.
                  21108
Contig ID
                  80988 1.R1040
5'-most EST
                  fua701040632.h1
Method
                  BLASTN
NCBI GI
                  g2760170
BLAST score
                  41
E value
                  1.0e-13
Match length
                  77
% identity
                  88
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MIO24, complete sequence [Arabidopsis thaliana]
Seq. No.
                  21109
```

Contig ID 81003 1.R1040

5'-most EST LIB3139-047-P1-N1-F6 BLASTN Method NCBI GI g4519193 BLAST score 35 E value 5.0e-10 Match length 130

% identity 87 Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: NCBI Description MDC11, complete sequence



Seq. No. 21110

Contig ID 81007\_1.R1040 5'-most EST trc700563576.h1

Method BLASTX
NCBI GI 94335742
BLAST score 203
E value 5.0e-16
Match length 98
% identity 53

NCBI Description (AC006248) putative AR781 [Arabidopsis thaliana]

Seq. No. 21111

Contig ID 81009\_1.R1040 5'-most EST uC-gmropic016a06b1

Seq. No. 21112

Contig ID 81010 1.R1040

5'-most EST jC-gmst02400050h02a1

Seq. No. 21113

Contig ID 81012 1.R1040

5'-most EST jC-gmf102220053g08a1

Method BLASTX
NCBI GI g3047085
BLAST score 231
E value 5.0e-19
Match length 94
% identity 52

NCBI Description (AF058914) No definition line found [Arabidopsis thaliana]

Seq. No. 21114

Contig ID 81019 1.R1040

5'-most EST LIB3139-047-P1-N1-H8

Seq. No. 21115

Contig ID 81032\_1.R1040 5'-most EST eep700868336.h1

Seq. No. 21116

Contig ID 81049 1.R1040

5'-most EST LIB3139-048-P1-N1-D6

Method BLASTX
NCBI GI 94335773
BLAST score 247
E value 6.0e-21
Match length 93
% identity 61

NCBI Description (AC006284) unknown protein [Arabidopsis thaliana]

Seq. No. 21117

Contig ID 81054\_1.R1040 5'-most EST epx701104156.h1

Method BLASTN
NCBI GI g3046856
BLAST score 36
E value 2.0e-10



Match length 280
% identity 83
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
MXI22, complete sequence [Arabidopsis thaliana]

Contig ID 81054 2.R1040 5'-most EST kl1701208021.h1

Seq. No. 21119

Seq. No.

Contig ID 81055 1.R1040

5'-most EST  $jC-gm\overline{f}1022220101d01d1$ 

21118

Seq. No. 21120

Contig ID 81067 1.R1040

5'-most EST LIB3139-048-P1-N1-F4

Seq. No. 21121

Contig ID 81069 1.R1040

5'-most EST LIB3139-048-P1-N1-F7

Method BLASTX
NCBI GI g2826786
BLAST score 185
E value 1.0e-13
Match length 87
% identity 47

NCBI Description (Y10905) RAPB protein [Oryza sativa]

Seq. No.

Contig ID 81069 3.R1040

5'-most EST uC-gmrominsoy223c10b1

21122

Seq. No. 21123

Contig ID 81072\_1.R1040

5'-most EST LIB3139-048-P1-N1-G1

Method BLASTX
NCBI GI g1752734
BLAST score 576
E value 3.0e-59
Match length 178
% identity 60

NCBI Description (D78510) beta-glucan-elicitor receptor [Glycine max]

Seq. No. 21124

Contig ID 81083\_1.R1040

5'-most EST LIB3139-048-P1-N1-H10

Seq. No. 21125

Contig ID 81086\_1.R1040

5'-most EST LIB3139-048-P1-N1-H5

Method BLASTX
NCBI GI g3738298
BLAST score 409
E value 1.0e-39
Match length 195
% identity 46

NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]



>gi 4249394 (AC006072) unknown protein [Arabidopsis thaliana]

21126 Seq. No.

81094\_1.R1040 Contig ID uC-gmropic049d02b1 5'-most EST

BLASTX Method q4455202 NCBI GI 230 BLAST score 5.0e-19 E value Match length 75

59 % identity

(AL035440) putative APG protein [Arabidopsis thaliana] NCBI Description

Seq. No. 21127

81098 1.R1040 Contig ID uC-gmropic059b11b1 5'-most EST

21128 Seq. No.

81101 1.R1040 Contig ID

LIB3139-049-P1-N1-B3 5'-most EST

Seq. No. 21129

81103 1.R1040 Contig ID

LIB3139-049-P1-N1-B5 5'-most EST

21130 Seq. No.

81107 1.R1040 Contig ID

LIB3139-049-P1-N1-B9 5'-most EST

BLASTX Method g2827141 NCBI GI 334 BLAST score 4.0e-31 E value 139 Match length 47 % identity

(AF027173) cellulose synthase catalytic subunit NCBI Description

[Arabidopsis thaliana]

21131 Seq. No.

81109 1.R1040 Contig ID zhf700965274.h1 5'-most EST

21132 Seq. No.

81123 1.R1040 Contig ID ssr700560929.h1 5'-most EST

BLASTX Method g2980772 NCBI GI 157 BLAST score 4.0e-10 E value Match length 154 % identity

NCBI Description (AL022198) putative protein [Arabidopsis thaliana]

21133 Seq. No.

81127 1.R1040 Contig ID

jC-gmst02400007c05a1 5'-most EST

BLASTX Method

3399



```
q2129473
NCBI GI
                  223
BLAST score
                  2.0e-30
E value
                  169
Match length
                   45
% identity
                  arabinogalactan-like protein - loblolly pine >gi_607774
NCBI Description
                   (U09556) arabinogalactan-like protein [Pinus taeda]
                   21134
Seq. No.
                   81127 2.R1040
Contig ID
5'-most EST
                   jC-gmst02400011d04d1
                   21135
Seq. No.
                   81127 3.R1040
Contig ID
                   sat701006505.h1
5'-most EST
                   21136
Seq. No.
                   81127 4.R1040
Contig ID
                   pxt700944173.h1
5'-most EST
                   21137
Seq. No.
                   81128 1.R1040
Contig ID
5'-most EST
                   sat701010927.hl
Method
                   BLASTX
                   q3695023
NCBI GI
BLAST score
                   314
                   9.0e-29
E value
                   120
Match length
                   54
% identity
                   (AF055850) unknown [Arabidopsis thaliana]
NCBI Description
                   21138
Seq. No.
                   81129 1.R1040
Contig ID
5'-most EST
                   LIB3139-049-P1-N1-E3
Seq. No.
                   21139
                   81139 1.R1040
Contig ID
                   vzy700751455.hl
5'-most EST
                   BLASTX
Method
                   q4186184
NCBI GI
                   287
BLAST score
                   1.0e-25
E value
Match length
                   135
                   44
% identity
NCBI Description (AF111168) unknown [Homo sapiens]
                   21140
Seq. No.
                   81140 1.R1040
Contig ID
                   fC-gmf1700902387a1
5'-most EST
                   21141
Seq. No.
                   81153 1.R1040
Contig ID
                   jsh70\overline{1}064821.h1
```

5'-most EST jsh701064 Method BLASTX NCBI GI g3386595

NCBI GI g3386595 BLAST score 169 E value 6.0e-12

5'-most EST

```
Match length
                   86
% identity
                   44
NCBI Description
                   (AC004665) hypothetical protein [Arabidopsis thaliana]
                   >gi_3702345 (AC005397) hypothetical protein [Arabidopsis
                   thaliana]
Seq. No.
                   21142
Contig ID
                   81159 1.R1040
5'-most EST
                   LIB3139-102-P1-N1-H1
Method
                   BLASTX
NCBI GI
                   q3540188
BLAST score
                   694
E value
                   7.0e-73
Match length
                   235
% identity
NCBI Description (AC004122) Hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   21143
Contig ID
                   81159 3.R1040
5'-most EST
                   zzp700833157.h1
Method
                   BLASTX
NCBI GI
                   q3540188
BLAST score
                   307
E value
                   7.0e-31
Match length
                   115
% identity
                   66
                  (AC004122) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   21144
Contig ID
                   81164 1.R1040
5'-most EST
                   uC-gmropic043c03b1
Method
                   BLASTX
NCBI GI
                   g2245082
BLAST score
                   1071
E value
                   1.0e-117
Match length
                   282
% identity
                  73
NCBI Description
                  (Z97343) SCARECROW homolog [Arabidopsis thaliana]
Seq. No.
                   21145
Contig ID
                  81166 1.R1040
5'-most EST
                  LIB3139-050-P1-N1-B2
Seq. No.
                  21146
                  81219 1.R1040
Contig ID
5'-most EST
                  LIB3139-050-P1-N1-G6
Method
                  BLASTX
NCBI GI
                  q4417287
BLAST score
                  334
E value
                  4.0e-31
Match length
                  110
% identity
                  56
NCBI Description (AC007019) unknown protein [Arabidopsis thaliana]
Seq. No.
                  21147
Contig ID
                  81224 1.R1040
```

3401

zhf700955438.h1

```
Seq. No.
                   21148
Contig ID
                   81226 1.R1040
5'-most EST
                   jC-gmro02910002a09d1
Seq. No.
                   21149
Contig ID
                   81231 1.R1040
5'-most EST
                   g5666705
Method
                   BLASTX
NCBI GI
                   g2398525
BLAST score
                   226
E value
                   2.0e-18
Match length
                   105
% identity
                   52
NCBI Description
                  (Y13722) Transcription factor [Arabidopsis thaliana]
Seq. No.
                   21150
Contig ID
                   81244 1.R1040
5'-most EST
                   LIB3139-051-P1-N1-C5
Seq. No.
                   21151
Contig ID
                   81251 1.R1040
5'-most EST
                   LIB3139-051-P1-N1-D7
Method
                   BLASTN
NCBI GI
                   q1022364
BLAST score
                   143
E value
                   3.0e-74
Match length
                   375
% identity
                   90
NCBI Description V.faba mRNA for sucrose phosphate synthase
Seq. No.
                   21152
Contig ID
                   81251 2.R1040
5'-most EST
                   g5606920
Method
                   BLASTN
NCBI GI
                   g1022364
BLAST score
                   131
E value
                   2.0e-67
Match length
                   260
% identity
                   90
NCBI Description V.faba mRNA for sucrose phosphate synthase
Seq. No.
                   21153
                   81252 1.R1040
Contig ID
                  LIB3139-051-P1-N1-D8
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3142298
BLAST score
                   608
                  3.0e-63
E value
Match length
                  164
% identity
NCBI Description
                  (AC002411) Strong similarity to protein SBT1 gb X98929 from
                  Lycopersicum esculentum. [Arabidopsis thaliana]
Seq. No.
                  21154
Contig ID
```

81256 1.R1040

LIB3139-051-P1-N1-E2

5'-most EST

E value

Match length

% identity

1.0e-39

123

62

Seq. No. 21155 Contig ID 81264 1.R1040 5'-most EST wvk700681715.h1 Seq. No. 21156 Contig ID 81283 1.R1040 5'-most EST fC-gmst700664459f2 Method BLASTX NCBI GI q3242708 BLAST score 486 E value 2.0e-48 Match length 178 % identity 54 (AC003040) putative serine/threonine protein kinase NCBI Description [Arabidopsis thaliana] Seq. No. 21157 Contig ID 81287 1.R1040 5'-most EST zsg701124368.h1 Method BLASTX NCBI GI q4455330 BLAST score 313 E value 1.0e-28 Match length 95 % identity 65 NCBI Description (AL035525) contains EST gb:T44002 [Arabidopsis thaliana] Seq. No. 21158 Contig ID 81288 1.R1040 5'-most EST  $jsh70\overline{1}064646.h1$ Seq. No. 21159 81288 2.R1040 Contig ID 5'-most EST zhf700960346.h1 Seq. No. 21160 Contig ID 81291 1.R1040 5'-most EST jC-gmf102220143h05d1 Seq. No. 21161 Contig ID 81291 2.R1040 5'-most EST LIB3139-052-P1-N1-A3 Seq. No. 21162 Contig ID 81295 1.R1040 LIB3139-052-P1-N1-A7 5'-most EST Seq. No. 21163 Contig ID 81309 1.R1040 5'-most EST fC-gmro700747038a2 Method BLASTX NCBI GI g1781330 BLAST score 408

5'-most EST

Method

```
NCBI Description (Y10466) peroxidase [Spinacia oleracea]
 Seq. No.
                   21164
                   81319 1.R1040
Contig ID
 5'-most EST
                   gsv701052812.h1
Method
                   BLASTX
NCBI GI
                   g3522937
BLAST score
                   295
E value
                   1.0e-26
Match length
                   125
% identity
                   50
NCBI Description
                  (AC004411) unknown protein [Arabidopsis thaliana]
Seq. No.
                   21165
Contig ID
                   81327 1.R1040
5'-most EST
                   zzp700835089.h1
Seq. No.
                   21166
Contig ID
                   81333 1.R1040
5'-most EST
                   LIB3139-052-P1-N1-E9
Method
                   BLASTX
NCBI GI
                   g3426039
BLAST score
                   571
E value
                   6.0e-59
Match length
                   149
% identity
                   69
NCBI Description
                  (AC005168) unknown protein [Arabidopsis thaliana]
Seq. No.
                   21167
Contig ID
                   81349 1.R1040
5'-most EST
                   uC-gmrominsoy029f03b1
Seq. No.
                   21168
Contig ID
                   81349 2.R1040
5'-most EST
                   LIB3139-052-P1-N1-G9
Seq. No.
                   21169
Contig ID
                   81351 1.R1040
5'-most EST
                  LIB3139-052-P1-N1-H11
Seq. No.
                   21170
Contig ID
                   81362 1.R1040
5'-most EST
                   jC-gmro02800029e11a1
Method
                  BLASTX
NCBI GI
                  g3236238
BLAST score
                  508
                  5.0e-51
E value
Match length
                  253
% identity
NCBI Description
                   (AC004684) putative ARF1 GTPase activating protein
                   [Arabidopsis thaliana] >gi_4519792_dbj_BAA75744.1_
                   (AB017876) Asp1 [Arabidopsis thaliana]
Seq. No.
                  21171
Contig ID
                  81364 1.R1040
```

3404

uC-gmropic106e06b1

BLASTX

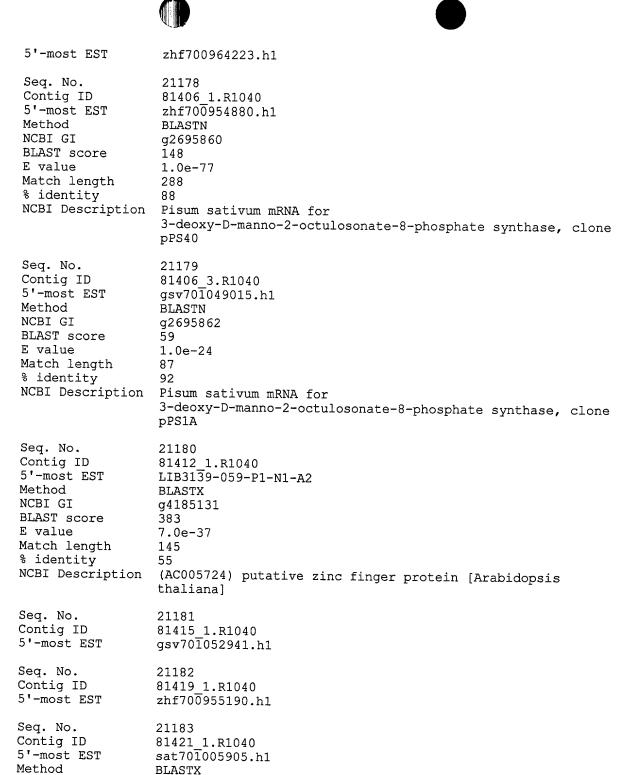
```
NCBI GI
                   g4454567
 BLAST score
                    1027
 E value
                   1.0e-112
 Match length
                   465
 % identity
                   50
                  (AF128407) lipase homolog [Arabidopsis thaliana]
 NCBI Description
 Seq. No.
                   21172
 Contig ID
                   81364 2.R1040
 5'-most EST
                   g5509333
Method
                   BLASTX
NCBI GI
                   g4454567
BLAST score
                   240
E value
                   7.0e-20
Match length
                   140
 % identity
                   52
NCBI Description
                  (AF128407) lipase homolog [Arabidopsis thaliana]
Seq. No.
                   21173
Contig ID
                   81364 3.R1040
5'-most EST
                   bth700844501.h1
Seq. No.
                   21174
Contig ID
                   81364 4.R1040
5'-most EST
                   ncj700981381.hl
Method
                   BLASTX
NCBI GI
                   q4454567
BLAST score
                   143
E value
                   1.0e-08
Match length
                   118
% identity
                   31
NCBI Description
                  (AF128407) lipase homolog [Arabidopsis thaliana]
Seq. No.
                   21175
                   81392 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910020g02a1
Method
                   BLASTX
NCBI GI
                   g2459431
BLAST score
                   326
E value
                   5.0e-30
Match length
                   107
% identity
                   64
NCBI Description (AC002332) unknown protein [Arabidopsis thaliana]
Seq. No.
                   21176
                   81393 1.R1040
Contig ID
5'-most EST
                  LIB3139-053-P1-N1-E1
Method
                  BLASTX
NCBI GI
                  q3935141
BLAST score
                  164
E value
                   2.0e-13
Match length
                  76
% identity
```

Seq. No. 21177

NCBI Description

Contig ID 81398 1.R1040

(AC005106) T25N20.5 [Arabidopsis thaliana]



g2576363 BLAST score 347

E value 1.0e-32 Match length 114 % identity 60

NCBI GI

5'-most EST

Method



```
NCBI Description
                   (U39783) amino acid transport protein [Arabidopsis
                   thaliana]
Seq. No.
                   21184
                   81421 2.R1040
Contig ID
5'-most EST
                   epx701105196.h1
Seq. No.
                   21185
Contig ID
                   81429 1.R1040
5'-most EST
                   LIB3139-054-P1-N1-A1
Seq. No.
                   21186
                   81438 1.R1040
Contig ID
5'-most EST
                   uC-gmropic019h02b1
Method
                   BLASTX
NCBI GI
                   q1362051
BLAST score
                   1339
E value
                   1.0e-148
Match length
                   270
% identity
                   93
NCBI Description
                   protein kinase 3 - soybean >gi_310582 (L19361) protein
                   kinase 3 [Glycine max]
Seq. No.
                   21187
                   81438 3.R1040
Contig ID
5'-most EST
                   seb700651918.h1
Seq. No.
                   21188
Contig ID
                   81445 1.R1040
5'-most EST
                   k1170\overline{1}209441.h1
Seq. No.
                   21189
Contig ID
                   81490 1.R1040
5'-most EST
                   LIB3139-055-P1-N1-A3
Method
                   BLASTX
NCBI GI
                   g4467148
BLAST score
                   263
E value
                   1.0e-22
Match length
                   111
% identity
                   51
NCBI Description (AL035540) putative protein [Arabidopsis thaliana]
Seq. No.
                   21190
Contig ID
                   81494 1.R1040
5'-most EST
                   zhf700954537.hl
Method
                   BLASTX
NCBI GI
                  g3426036
BLAST score
                   259
                   3.0e-22
E value
Match length
                  118
% identity
NCBI Description (AC005168) unknown protein [Arabidopsis thaliana]
Seq. No.
                  21191
Contig ID
                  81494 2.R1040
```

3407

uC-gmflminsoy057d02b1

BLASTX

% identity

77



```
NCBI GI
                    g4309741
 BLAST score
                    261
 E value
                    2.0e-22
 Match length
                    66
 % identity
                    73
                   (AC006439) hypothetical protein [Arabidopsis thaliana]
 NCBI Description
 Seq. No.
                    21192
 Contig ID
                    81519 1.R1040
 5'-most EST
                   uC-gmrominsoy061e03b1
 Seq. No.
                   21193
Contig ID
                   81544 1.R1040
 5'-most EST
                   LIB31\overline{3}9-055-P1-N1-G4
Method
                   BLASTX
NCBI GI
                   g3935187
BLAST score
                   503
E value
                   5.0e-51
Match length
                   145
% identity
                   68
NCBI Description
                   (AC004557) F17L21.30 [Arabidopsis thaliana]
Seq. No.
                   21194
Contig ID
                   81550 1.R1040
5'-most EST
                   zsg701121528.h1
Method
                   BLASTX
NCBI GI
                   g4406759
BLAST score
                   221
E value
                   6.0e-18
Match length
                   82
% identity
                   54
NCBI Description
                   (AC006836) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   21195
Contig ID
                   81553 1.R1040
5'-most EST
                   LIB3139-055-P1-N1-H7
Seq. No.
                   21196
Contig ID
                   81565 1.R1040
5'-most EST
                   fde700876501.h1
Method
                   BLASTX
NCBI GI
                   g3461814
BLAST score
                   603
E value
                   1.0e-62
Match length
                   151
% identity
                   75
NCBI Description
                   (AC004138) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   21197
Contig ID
                   81591 1.R1040
5'-most EST
                  LIB3139-056-P1-N1-F4
Method
                  BLASTX
NCBI GI
                  g4204849
BLAST score
                  341
E value
                  6.0e-32
Match length
                  82
```

```
NCBI Description
                   (U55875) protein kinase [Arabidopsis thaliana]
 Seq. No.
                   21198
 Contig ID
                   81608 1.R1040
 5'-most EST
                   ssr700555405.h1
Method
                   BLASTX
NCBI GI
                   g4455177
BLAST score
                   305
E value
                   2.0e-27
Match length
                   169
 % identity
                   38
NCBI Description
                  (AL035521) putative protein [Arabidopsis thaliana]
Seq. No.
                   21199
Contig ID
                   81616 1.R1040
5'-most EST
                   LIB3139-057-P1-N1-A6
Method
                   BLASTX
NCBI GI
                   g3860249
BLAST score
                   369
E value
                   9.0e-35
Match length
                   162
% identity
                   55
NCBI Description
                   (AC005824) unknown protein [Arabidopsis thaliana]
Seq. No.
                   21200
Contig ID
                   81616 2.R1040
5'-most EST
                   asn701134367.h1
Method
                   BLASTX
NCBI GI
                   g3860249
BLAST score
                   177
E value
                   1.0e-12
Match length
                   79
% identity
                   53
NCBI Description
                  (AC005824) unknown protein [Arabidopsis thaliana]
Seq. No.
                   21201
Contig ID
                   81626 1.R1040
5'-most EST
                   jC-gmro02910065c04a1
Method
                   BLASTX
NCBI GI
                   g4572673
BLAST score
                   487
E value
                   5.0e-49
Match length
                   146
% identity
                   63
                  (AC006954) putative sarcosine oxidase [Arabidopsis
NCBI Description
                  thaliana]
```

Seq. No. 21202

Contig ID 81628\_1.R1040 5'-most EST ncj700986468.h1

Seq. No. 21203

Contig ID 81631\_1.R1040

5'-most EST LIB3139-057-P1-N1-C6

Method BLASTX NCBI GI g4337025 BLAST score 1086

```
E value
                   1.0e-132
Match length
                   382
% identity
                   66
NCBI Description
                   (AF123253) AIM1 protein [Arabidopsis thaliana]
Seq. No.
                   21204
Contig ID
                   81634 1.R1040
5'-most EST
                   LIB3139-057-P1-N1-C9
Method
                   BLASTX
NCBI GI
                   q1652434
BLAST score
                   729
E value
                   3.0e-77
Match length
                   227
% identity
                   63
NCBI Description
                  (D90905) N-acetylglutamate kinase [Synechocystis sp.]
Seq. No.
                   21205
Contig ID
                   81643 1.R1040
5'-most EST
                   kl1701215393.h1
Method
                   BLASTX
NCBI GI
                   q2102691
BLAST score
                   1201
E value
                   1.0e-132
Match length
                   321
% identity
                   72
NCBI Description
                  (U64817) fructokinase [Lycopersicon esculentum]
Seq. No.
                   21206
                   81643 2.R1040
Contig ID
5'-most EST
                   fC-gmst7006513885z1
Method
                  BLASTX
NCBI GI
                   g2102691
BLAST score
                   630
E value
                  1.0e-65
Match length
                  166
% identity
                  72
NCBI Description
                  (U64817) fructokinase [Lycopersicon esculentum]
Seq. No.
                  21207
Contig ID
                  81643 3.R1040
5'-most EST
                  rca700999041.hl
Method
                  BLASTN
NCBI GI
                  g2760170
BLAST score
                  66
E value
                  2.0e-28
Match length
                  146
% identity
```

NCBI Description

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MIO24, complete sequence [Arabidopsis thaliana]

Seq. No. 21208

Contig ID 81643 4.R1040 5'-most EST wvk700684215.hl

Method BLASTN NCBI GI g2760170 BLAST score 53 E value 9.0e-21



Match length 121 % identity 87

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MIO24, complete sequence [Arabidopsis thaliana]

Seq. No. 21209

Contig ID 81644 1.R1040

5'-most EST LIB3139-057-P1-N1-E10

Seq. No. 21210

Contig ID 81658 1.R1040

5'-most EST LIB3139-057-P1-N1-F4

Seq. No. 21211

Contig ID 81666\_1.R1040 5'-most EST smc700748445.h1

Method BLASTX
NCBI GI g4220612
BLAST score 388
E value 2.0e-37
Match length 137
% identity 54

NCBI Description (AB021934) nicotianamine synthase [Arabidopsis thaliana]

Seq. No.

Contig ID 81671\_1.R1040

5'-most EST sat701008591.h1

21212

Method BLASTX
NCBI GI g3860258
BLAST score 185
E value 5.0e-24
Match length 109
% identity 53

NCBI Description (AC005824) unknown protein [Arabidopsis thaliana]

Seq. No. 21213

Contig ID 81673\_1.R1040 5'-most EST zzp700835016.h1

Method BLASTN
NCBI GI g1928873
BLAST score 108
E value 9.0e-54
Match length 232
% identity 87

NCBI Description Medicago sativa MADS-box protein mRNA, partial cds

Seq. No. 21214

Contig ID 81681\_1.R1040

5'-most EST uC-gmrominsoy067d03b1

Seq. No. 21215

Contig ID 81685 1.R1040

5'-most EST LIB3139-059-P1-N1-A4

Seq. No. 21216

Contig ID 81687\_1.R1040 5'-most EST g5058266

Seq. No. 21217

Contig ID 81688\_1.R1040 5'-most EST fua701041312.h1

Method BLASTN
NCBI GI g732912
BLAST score 372
E value 0.0e+00
Match length 654
% identity 89

NCBI Description P.vulgaris mRNA for pectinesterase

Seq. No. 21218

Contig ID 81690\_1.R1040 5'-most EST sat701014573.h1

Method BLASTX
NCBI GI g2961383
BLAST score 387
E value 3.0e-37
Match length 169
% identity 53

NCBI Description (AL022141) putative protein [Arabidopsis thaliana]

Seq. No. 21219

Contig ID 81706 1.R1040

5'-most EST LIB3170-017-Q1-J1-H2

Seq. No. 21220

Contig ID 81715\_1.R1040 5'-most EST trc700562043.h1

Method BLASTX
NCBI GI 9731529
BLAST score 260
E value 4.0e-22
Match length 217
% identity 35

NCBI Description HYPOTHETICAL 92.5 KD PROTEIN IN BEM2-NCB1 INTERGENIC REGION

>gi\_1077719\_pir\_\_S50660 hypothetical protein YER157w yeast (Saccharomyces cerevisiae) >gi 603397 (U18917)

Yer157wp [Saccharomyces cerevisiae]

Seq. No. 21221

Contig ID 81724 1.R1040

5'-most EST uC-gmflminsoy014g08b1

Method BLASTX
NCBI GI g3367519
BLAST score 524
E value 2.0e-53
Match length 171
% identity 65

NCBI Description (AC004392) Contains similarity to gb\_U51898

Ca2+-independent phospholipase A2 from Rattus norvegicus.

[Arabidopsis thaliana]

Seq. No. 21222

Contig ID 81731\_1.R1040

5'-most EST jC-gmro02910074f02a1



Method BLASTX NCBI GI a728905 BLAST score 378 E value 3.0e-36 Match length 169 % identity 49

NCBI Description PROBABLE CALCIUM-TRANSPORTING ATPASE 3 (ENDOPLASMIC

 ${\tt RETICULUM~CA2+-ATPASE)~>} gi\_1078206\_pir\_\_S51995~probable$ ATPase (EC 3.6.1.-) DRS2 - yeast (Saccharomyces cerevisiae) >gi\_171114 (L01795) ATPase [Saccharomyces cerevisiae]

>gi 595560 (U12980) Drs2p: Membrane spanning

Ca-ATPase(P-type), member of the cation transport(E1-E2)

ATPase [Saccharomyces cerevisiae]

Seq. No. 21223

Contig ID 81746 1.R1040 5'-most EST uC-qmropic066b03b1

Method BLASTX NCBI GI g2160189 BLAST score 974 E value 1.0e-105 Match length 351 % identity 11

NCBI Description (AC000132) Similar to A. thaliana receptor-like protein

kinase (gb RLK5 ARATH). ESTs gb ATTS0475, gb ATTS4362 come

from this gene. [Arabidopsis thaliana]

Seq. No. 21224

Contig ID 81752 1.R1040

5'-most EST LIB3139-110-P1-N1-C3

Method BLASTX NCBI GI q3335357 BLAST score 718 5.0e-76 E value Match length 172 70 % identity

NCBI Description (AC003028) putative diphenol oxidase [Arabidopsis thaliana]

Seq. No. 21225

81767 1.R1040 Contig ID

5'-most EST jC-gmf102220102d10a1

Seq. No. 21226

Contig ID 81772 1.R1040 5'-most EST gsv701054226.h1

Method BLASTX NCBI GI q4115377 BLAST score 190 1.0e-14 E value Match length 40 % identity 85

NCBI Description (AC005967) unknown protein [Arabidopsis thaliana]

Seq. No. 21227

Contig ID 81777 1.R1040 5'-most EST uC-gmropic030d02b1



Seq. No. 21228

Contig ID 81780 1.R1040

5'-most EST LIB3139-060-P1-N1-E11

Method BLASTX
NCBI GI g1708899
BLAST score 142
E value 1.0e-08
Match length 34
% identity 74

NCBI Description MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ISOFORM 1

(MAN(9)-ALPHA-MANNOSIDASE) >gi\_2133635\_pir\_\_S60709 alpha

1,2 mannosidase precursor - fruit fly (Drosophila

melanogaster) >gi\_840754\_emb\_CAA57962\_ (X82640) alpha 1,2

mannosidase [Drosophila melanogaster]

Seq. No. 21229

Contig ID 81784\_1.R1040 5'-most EST uaw700664879.h1

Method BLASTX
NCBI GI g3184073
BLAST score 170
E value 5.0e-12
Match length 104
% identity 37

NCBI Description (AL023779) hypothetical protein [Schizosaccharomyces pombe]

Seq. No. 21230

Contig ID 81794\_1.R1040 5'-most EST zhf700956626.h1

Method BLASTX
NCBI GI g2244904
BLAST score 260
E value 2.0e-22
Match length 175
% identity 8

NCBI Description (Z97339) similar to hypothetical protein C02F5.7 - Caenorha

[Arabidopsis thaliana]

Seq. No. 21231

Contig ID 81814\_1.R1040 5'-most EST zhf700959429.h1

Seq. No. 21232

Contig ID 81815 1.R1040

5'-most EST jC-gmst02400060g12a1

Method BLASTX
NCBI GI g3153207
BLAST score 384
E value 6.0e-37
Match length 177
% identity 48

NCBI Description (AF001949) ATHB-12 [Arabidopsis thaliana]

Seq. No. 21233

Contig ID 81818\_1.R1040

5'-most EST LIB3139-061-P1-N1-A8

Method BLASTX



NCBI GI g4138679 BLAST score 371 E value 2.0e-69 Match length 191 % identity 67

NCBI Description (Y09591) amino acid transporter [Vicia faba]

Seq. No. 21234

Contig ID 81827\_2.R1040 5'-most EST ssr700557119.h1

Seq. No. 21235

Contig ID 81830\_1.R1040 5'-most EST V4L-01-Q1-B1-E4

Method BLASTX
NCBI GI g2129550
BLAST score 253
E value 2.0e-24
Match length 109
% identity 66

NCBI Description calcium-dependent protein kinase (EC 2.7.1.-) CDPK6 -

Arabidopsis thaliana >gi\_2129554\_pir\_\_S71901

calcium-dependent protein kinase 6 - Arabidopsis thaliana

>gi 836940 (U20623) calcium-dependent protein kinase

[Arabidopsis thaliana] >gi 836944 (U20625)

calcium-dependent protein kinase [Arabidopsis thaliana] >gi 4454034 emb CAA23031.1 (AL035394) calcium-dependent

protein kinase (CDPK6) [Arabidopsis thaliana]

Seq. No. 21236

Contig ID 81837 1.R1040

5'-most EST LIB3139-061-P1-N1-D4

Seq. No. 21237

Contig ID 81840\_1.R1040 5'-most EST gbt700548062.h1

Seq. No. 21238

Contig ID 81840\_2.R1040 5'-most EST smc700749633.h1

Seq. No. 21239

Contig ID 81849 1.R1040

5'-most EST LIB3139-061-P1-N1-G11

Method BLASTX
NCBI GI g2911040
BLAST score 250
E value 2.0e-21
Match length 91
% identity 56

NCBI Description (AL021961) receptor protein kinase - like protein

[Arabidopsis thaliana]

Seq. No. 21240

Contig ID 81854\_1.R1040

5'-most EST jC-gmle01810023a04d1

Method BLASTX



```
g4220522
NCBI GI
BLAST score
                  253
                  1.0e-21
E value
Match length
                  149
% identity
                  41
                  (AL035356) putative protein [Arabidopsis thaliana]
NCBI Description
                  21241
Seq. No.
                  81862 1.R1040
Contig ID
                  smc700746177.h1
5'-most EST
                  BLASTX
Method
                  q3341679
NCBI GI
                  873
BLAST score
                  1.0e-94
E value
Match length
                  234
% identity
                  76
                  (AC003672) dynamin-like protein phragmoplastin 12
NCBI Description
                   [Arabidopsis thaliana]
                  21242
Seq. No.
                  81877 1.R1040
Contig ID
                  asn70\overline{1}135229.h1
5'-most EST
                  BLASTX
Method
                  g3041652
NCBI GI
                  746
BLAST score
                  4.0e-79
E value
                  210
Match length
                  70
% identity
                  CHALCONE--FLAVONONE ISOMERASE >gi_282910_pir__S24784
NCBI Description
                  chalcone isomerase (EC 5.5.1.6) - kidney bean
                  >gi 20982 emb CAA78763_ (Z15046) chalcone isomerase
                   [Phaseolus vulgaris]
                   21243
Seq. No.
Contig ID
                   81883 1.R1040
5'-most EST
                  LIB3139-062-P1-N1-C12
                   BLASTX
Method
                   a3164222
NCBI GI
                   229
BLAST score
E value
                   6.0e-19
                   66
Match length
% identity
                   (AB008518) RMA1 [Arabidopsis thaliana] >gi_4206205
NCBI Description
                   (AF071527) RMA1 RING zinc finger protein [Arabidopsis
                   thaliana]
Seq. No.
                   21244
Contig ID
                   81887 1.R1040
5'-most EST
                   jC-gmle01810089c12a1
Seq. No.
                   21245
```

Contig ID 81887\_2.R1040 5'-most EST uaw700665060.h1

Method BLASTX
NCBI GI g4049344
BLAST score 155
E value 6.0e-10



Match length 98 % identity 42

NCBI Description (AL034567) putative protein [Arabidopsis thaliana]

Seq. No. 21246

Contig ID 81888\_1.R1040 5'-most EST uC-gmropic071g09b1

Seq. No. 21247

Contig ID 81890\_1.R1040 5'-most EST wrg700787464.h2

Method BLASTX
NCBI GI g4455231
BLAST score 803
E value 2.0e-85
Match length 258
% identity 61

NCBI Description (AL035523) putative protein [Arabidopsis thaliana]

Seq. No. 21248

Contig ID 81899\_1.R1040 5'-most EST uaw700660857.h1

Seq. No. 21249

Contig ID 81912 2.R1040

5'-most EST LIB3139-072-P1-N1-B6

Seq. No. 21250

Contig ID 81912 3.R1040

5'-most EST LIB3170-031-Q1-K1-B9

Seq. No. 21251

Contig ID 81914\_1.R1040 5'-most EST pxt700941411.h1

Seq. No. 21252

Contig ID 81927 1.R1040

5'-most EST jC-gmro02800028f06d1

Seq. No. 21253

Contig ID 81941\_1.R1040 5'-most EST kl1701206775.h1

Seq. No. 21254

Contig ID 81965 1.R1040

5'-most EST uC-gmrominsoy179b07b1

Seq. No. 21255

Contig ID 81965 2.R1040

5'-most EST LIB3139-063-P1-N1-D9

Seq. No. 21256

Contig ID 81973 1.R1040

5'-most EST jC-gmro02910022g08a1

Seq. No. 21257

Contig ID 81973 2.R1040



21258

hrw701061130.hl 5'-most EST

81985 1.R1040 Contig ID 5'-most EST  $epx70\overline{1}106060.h1$ 

Method BLASTX g1742959 NCBI GI BLAST score 631 1.0e-65 E value 174 Match length % identity 75

Seq. No.

(Z71450) CLC-d chloride channel protein [Arabidopsis NCBI Description

thaliana]

Seq. No. 21259

81985 3.R1040 Contig ID

uC-gmflminsoy077d04b1 5'-most EST

BLASTX Method g3319358 NCBI GI BLAST score 264 2.0e-61 E value 168 Match length % identity 83

(AF077407) Arabidopsis thaliana CLC-d chloride channel NCBI Description

protein (GB:Z71450) [Arabidopsis thaliana]

Seq. No. 21260

81988 1.R1040 Contig ID

5'-most EST LIB3139-063-P1-N1-G9

Method BLASTX NCBI GI q2842481 BLAST score 142 7.0e-09 E value Match length 59 % identity 39

NCBI Description (AL021749) extensin-like protein [Arabidopsis thaliana]

Seq. No. 21261

Contig ID 81995 1.R1040

5'-most EST uC-qmrominsoy189e04b1

21262 Seq. No.

82004 1.R1040 Contig ID 5'-most EST rca700996931.hl

21263 Seq. No.

82010 1.R1040 Contig ID

LIB3139-064-P1-N1-C11 5'-most EST

21264 Seq. No.

82028 1.R1040 Contig ID rlr700896503.h1 5'-most EST

BLASTX Method g3913366 NCBI GI BLAST score 704 5.0e-74 E value 306 Match length

```
% identity
                  PUTATIVE RECEPTOR PROTEIN KINASE CRINKLY4 PRECURSOR
NCBI Description
                  >gi 1597723 (U67422) CRINKLY4 precursor [Zea mays]
                  21265
Seq. No.
                  82030 1.R1040
Contig ID
5'-most EST
                  LIB3139-064-P1-N1-E10
Method
                  BLASTN
                  q2264314
NCBI GI
BLAST score
                  37
E value
                  3.0e-11
Match length
                  109
                  83
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MQK4, complete sequence [Arabidopsis thaliana]
                  21266
Seq. No.
                  82040 1.R1040
Contig ID
                  LIB3139-064-P1-N1-E9
5'-most EST
                  BLASTX
Method
                  g4263521
NCBI GI
                  212
BLAST score
                  4.0e-17
E value
Match length
                  97
% identity
                  15
                  (AC004044) putative WD-repeat protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  21267
                  82042 1.R1040
Contig ID
5'-most EST
                  LIB3139-064-P1-N1-F12
                  BLASTX
Method
NCBI GI
                  q4432854
BLAST score
                  194
E value
                  1.0e-14
Match length
                   83
% identity
NCBI Description (AC006300) hypothetical protein [Arabidopsis thaliana]
                   21268
Seq. No.
```

82075 1.R1040 Contig ID uC-gmropic041d12b1 5'-most EST

Method BLASTX NCBI GI q4138265 BLAST score 354 2.0e-33 E value Match length 142 53 % identity

(AJ006228) Avr9 elicitor response protein [Nicotiana NCBI Description

tabacum]

21269 Seq. No.

82075 2.R1040 Contig ID 5'-most EST fua701036978.h1

21270 Seq. No.

82085 1.R1040 Contig ID



LIB3139-065-P1-N1-C2 5'-most EST BLASTX Method g2827773 NCBI GI BLAST score 641 3.0e-82 E value 189 Match length 79 % identity CALCIUM-DEPENDENT PROTEIN KINASE (CDPK) NCBI Description >gi\_1765912\_emb\_CAA39936\_ (X56599) calcium- dependent protein kinase [Daucus carota] 21271 Seq. No. 82091 1.R1040 Contig ID seb700650804.hl 5'-most EST Seq. No. 21272 82107 1.R1040 Contig ID jC-gmst02400077h12a15'-most EST BLASTX Method g4512664 NCBI GI 570 BLAST score 6.0e-59 E value 135 Match length 76 % identity (AC006931) putative ribose phosphate pyrophosphokinase NCBI Description [Arabidopsis thaliana] >gi\_4544471\_gb\_AAD22378.1\_AC006580\_10 (AC006580) putative ribose phosphate pyrophosphokinase [Arabidopsis thaliana] 21273 Seq. No. 82120 1.R1040 Contig ID jC-gmst02400073f10a1 5'-most EST BLASTX Method g556409 NCBI GI BLAST score 385 1.0e-36 E value 185 Match length % identity NCBI Description (L34551) transcriptional activator protein [Oryza sativa] Seq. No. 21274 82122 1.R1040 Contig ID trc700563525.h1 5'-most EST BLASTX Method NCBI GI q4559334 153 BLAST score 7.0e-10 E value 65 Match length % identity NCBI Description (AC007087) unknown protein [Arabidopsis thaliana]

Seq. No. 21275

Contig ID 82160\_1.R1040 5'-most EST zpv700759046.h1

Method BLASTX NCBI GI g2146731 BLAST score 1306



```
E value
                   1.0e-144
                   349
Match length
                   38
% identity
                  FK506-binding protein - Arabidopsis thaliana >gi_1354207
NCBI Description
                   (U49453) rof1 [Arabidopsis thaliana]
                   21276
Seq. No.
Contig ID
                   82160 2.R1040
5'-most EST
                  vwf700678071.h1
                   21277
Seq. No.
                   82172 1.R1040
Contig ID
5'-most EST
                   zhf700952915.h1
Method
                   BLASTX
                   g3063691
NCBI GI
                   211
BLAST score
                   2.0e-21
E value
                   113
Match length
                   47
% identity
                  (AL022537) putative protein [Arabidopsis thaliana]
NCBI Description
                   21278
Seq. No.
                   82178_1.R1040
Contig ID
5'-most EST
                   k1170\overline{1}211876.h1
Method
                   BLASTX
NCBI GI
                   g4455302
                   683
BLAST score
E value
                   6.0e-72
                   208
Match length
% identity
                   62
                  (AL035528) putative protein [Arabidopsis thaliana]
NCBI Description
                   21279
Seq. No.
Contig ID
                   82187 1.R1040
5'-most EST
                   LIB3139-067-P1-N1-A6
                   BLASTX
Method
NCBI GI
                   q3063710
BLAST score
                   151
                   1.0e-09
E value
Match length
                   47
                   53
% identity
                  (AL022537) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   21280
                   82188 1.R1040
Contig ID
5'-most EST
                   uC-gmropic032g10b1
Method
                   BLASTX
NCBI GI
                   g4309760
BLAST score
                   242
E value
                   2.0e-20
                   82
Match length
```

% identity 65

(AC006217) unknown protein [Arabidopsis thaliana] NCBI Description

Seq. No.

21281 82190\_1.R1040 Contig ID 5'-most EST ncj700988157.hl



```
BLASTX
Method
NCBI GI
                  q1171577
                   408
BLAST score
E value
                   6.0e-40
                  115
Match length
                   68
% identity
                  (X95343) hypersensitivity-related gene [Nicotiana tabacum]
NCBI Description
                   21282
Seq. No.
                   82195 1.R1040
Contig ID
                  LIB3139-067-P1-N1-B5
5'-most EST
                  BLASTX
Method
                   g4467126
NCBI GI
                   733
BLAST score
                   4.0e-96
E value
                   275
Match length
                   62
% identity
                  (AL035538) guanine nucleotide-exchange protein-like
NCBI Description
                   [Arabidopsis thaliana]
                   21283
Seq. No.
                   82212 1.R1040
Contig ID
5'-most EST
                   jsh701066941.hl
Seq. No.
                   21284
                   82224 1.R1040
Contig ID
5'-most EST
                   LIB3139-067-P1-N1-F10
                   BLASTX
Method
                   q1491617
NCBI GI
                   457
BLAST score
                   8.0e-49
E value
                   144
Match length
                   71
% identity
NCBI Description (X99952) peroxidase [Arabidopsis thaliana]
                   21285
Seq. No.
                   82229 1.R1040
Contig ID
                   q4396\overline{1}35
5'-most EST
                   BLASTX
Method
NCBI GI
                   q1170601
                   372
BLAST score
                   2.0e-35
E value
                   132
Match length
                   55
% identity
NCBI Description FRUIT PROTEIN PKIWI502 >gi_1085869_pir__S48036 hypothetical
                   protein - kiwi fruit >gi_450237 (L27809) pKIWI502
                   [Actinidia deliciosa]
                   21286
 Seq. No.
                   82240 2.R1040
 Contig ID
                   LIB3139-067-P1-N1-G5
 5'-most EST
                   BLASTX
Method
                   g3237304
 NCBI GI
                   439
 BLAST score
                   3.0e-43
 E value
```

179

49

Match length

% identity



NCBI Description (U91561) pyridoxine 5'-phosphate oxidase [Rattus norvegicus]

Seq. No. 21287

Contig ID 82241\_1.R1040 5'-most EST sat701003281.h1

Method BLASTX
NCBI GI g464806
BLAST score 147
E value 2.0e-09
Match length 139
% identity 33

NCBI Description SIGNAL RECOGNITION PARTICLE 72 KD PROTEIN (SRP72) 
>gi\_423182\_pir\_\_A40692 signal recognition particle 72K 
chain - dog >gi\_297768\_emb\_CAA48014\_ (X67813) signal 
recognition particle,72 kDa subunit [Canis familiaris]

Seq. No. 21288

Contig ID 82242\_1.R1040 5'-most EST zzp700834915.h1

Seq. No. 21289

Contig ID 82252\_1.R1040 5'-most EST dpv701103226.h1

Method BLASTX
NCBI GI g2894534
BLAST score 1086
E value 1.0e-119
Match length 241
% identity 86

NCBI Description (AJ224327) aquaporin [Oryza sativa]

Seq. No. 21290

Contig ID 82259\_1.R1040 5'-most EST crh700850325.h1

Method BLASTX
NCBI GI g3540208
BLAST score 173
E value 5.0e-12
Match length 188
% identity 31

NCBI Description (AC004260) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 21291

Contig ID 82261\_1.R1040

5'-most EST jC-gmro02800025d03a1

Seq. No. 21292

Contig ID 82261\_2.R1040

5'-most EST uC-gmflminsoy115h08b1

Method BLASTX
NCBI GI g4455261
BLAST score 397
E value 2.0e-38
Match length 91
% identity 77

NCBI Description (AL035353) protein kinase-like protein [Arabidopsis



## thaliana]

```
21293
Seq. No.
                  82261 3.R1040
Contig ID
                  kl1701211661.hl
5'-most EST
                  21294
Seq. No.
                  82263 1.R1040
Contig ID
                  zzp700833816.hl
5'-most EST
                  21295
Seq. No.
                  82265_1.R1040
Contig ID
                  zhf700961803.hl
5'-most EST
                  BLASTX
Method
                  g4415912
NCBI GI
                   331
BLAST score
                  1.0e-53
E value
                  185
Match length
                   54
% identity
                  (AC006282) putative protease [Arabidopsis thaliana]
NCBI Description
                   21296
Seq. No.
                   82268_1.R1040
Contig ID
                   uC-gmropic093f10b1
5'-most EST
                   21297
Seq. No.
                   82286 1.R1040
Contig ID
                   LIB3139-068-P1-N1-D7
5'-most EST
                   21298
Seq. No.
                   82291 1.R1040
Contig ID
                   jC-gmro02910020d02a1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g4580390
                   154
BLAST score
E value
                   4.0e-10
Match length
                   37
                   81
% identity
                   (AC007171) putative disease resistance response protein
NCBI Description
                   [Arabidopsis thaliana]
                   21299
Seq. No.
                   82297 1.R1040
Contig ID
                   LIB3139-068-P1-N1-F10
5'-most EST
                   21300
Seq. No.
                   82308 1.R1040
Contig ID
                   LIB3139-068-P1-N1-G5
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3068717
                   728
BLAST score
                   5.0e-77
E value
                   270
Match length
```

21301 Seq. No.

% identity

52

NCBI Description (AF049236) unknown [Arabidopsis thaliana]



Contig ID 82348\_1.R1040

5'-most EST LIB3139-069-P1-N1-D12

Seq. No. 21302

Contig ID 82348\_2.R1040 5'-most EST g4297711

Seq. No. 21303

Contig ID 82357\_1.R1040

5'-most EST LIB3139-069-P1-N1-E11

Seq. No. 21304

Contig ID 82388\_1.R1040 5'-most EST sat701004270.h1

Method BLASTX
NCBI GI g3873621
BLAST score 257
E value 8.0e-22
Match length 225
% identity 25

NCBI Description (Z98262) similar to Ubiquitin family; cDNA EST EMBL:C11990

comes from this gene; cDNA EST EMBL:C08080 comes from this gene; cDNA EST EMBL:C08013 comes from this gene; cDNA EST EMBL:C08074 comes from this gene; cDNA EST EMBL:C090... >gi 3875993 emb CAA95799 (Z71260) similar to Ubiquitin family; cDNA EST EMBL:C11990 comes from this gene; cDNA EST EMBL:C08080 comes from this gene; cDNA EST EMBL:C08074 comes from this

comes from this gene; cDNA EST EMBL: C08074 comes from this

gene; cDNA EST EMBL:C09

Seq. No. 21305

Contig ID 82388\_2.R1040 5'-most EST uC-gmropic108a07b1

Seq. No. 21306

Contig ID 82396\_1.R1040

5'-most EST LIB3139-070-P1-N1-A12

Method BLASTN
NCBI GI g1370284
BLAST score 172
E value 9.0e-92
Match length 316
% identity 89

NCBI Description P.sativum mRNA for glutathione reductase

Seq. No. 21307

Contig ID 82417\_1.R1040

5'-most EST g4291639

Method BLASTX

NCBI GI g2104536

BLAST score 1225

E value 1.0e-135

Match length 273

% identity 82

NCBI Description (AF001308) predicted glycosyl transferase [Arabidopsis

thaliana]



21308 Seq. No.

Contig ID 82419 1.R1040 kl1701205975.h1 5'-most EST

BLASTX Method g555655 NCBI GI 256 BLAST score 1.0e-21 E value Match length 116 54 % identity

NCBI Description (U06712) DNA-binding protein [Nicotiana tabacum]

21309 Seq. No.

82429 1.R1040 Contig ID pxt700944356.h1 5'-most EST

BLASTX Method NCBI GI q4539335 476 BLAST score 9.0e-48 E value 169 Match length % identity 51

NCBI Description (AL035539) putative protein [Arabidopsis thaliana]

21310 Seq. No.

82447 1.R1040 Contig ID 5'-most EST sat701005313.h1

Method BLASTX q4191784 NCBI GI BLAST score 459 E value 5.0e-46 Match length 116 % identity

(AC005917) putative WD-40 repeat protein [Arabidopsis NCBI Description

thaliana]

21311 Seq. No.

Contig ID 82454 1.R1040

5'-most EST LIB3139-070-P1-N1-H1

21312 Seq. No.

82458 1.R1040 Contig ID

jC-qmle01810005d05a1 5'-most EST

Method BLASTX NCBI GI g3914996 BLAST score 1204 1.0e-133 E value Match length 307 % identity 76

NCBI Description

PHOSPHOSERINE AMINOTRANSFERASE PRECURSOR (PSAT) >qi 1665831 dbj BAA13640 (D88541) phosphoserine

aminotransferase [Arabidopsis thaliana]

>qi 2804260 dbj BAA24441 (AB010408) phosphoserine

aminotransferase [Arabidopsis thaliana]

>gi 3367581\_emb\_CAA20033\_ (AL031135) phosphoserine

aminotransferase [Arabidopsis thaliana]

21313 Seq. No.

82462\_1.R1040 Contig ID



```
5'-most EST
                  sat701011892.hl
                  21314
Seq. No.
                  82464 1.R1040
Contig ID
                  LIB3139-071-P1-N1-A11
5'-most EST
                  BLASTX
Method
                  g1777312
NCBI GI
                  245
BLAST score
                  2.0e-20
E value
                  65
Match length
                  71
% identity
                  (D30622) novel serine/threonine protein kinase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  21315
                  82464 2.R1040
Contig ID
                  vwf700678626.hl
5'-most EST
                  21316
Seq. No.
                  82479 1.R1040
Contig ID
                  LIB3139-071-P1-N1-B7
5'-most EST
                  21317
Seq. No.
                  82481 1.R1040
Contig ID
5'-most EST
                  bth700848057.h1
Seq. No.
                  21318
                  82484 1.R1040
Contig ID
                  gsf700698412.h1
5'-most EST
Method
                  BLASTX
                  g3047090
NCBI GI
                   412
BLAST score
                   3.0e-40
E value
Match length
                   96
                  72
% identity
                  (AF058826) T26D22.18 gene product [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   21319
                   82500 1.R1040
Contig ID
                   trc700566494.h1
5'-most EST
                   21320
Seq. No.
                   82501 1.R1040
Contig ID
5'-most EST
                   zzp700835831.h1
Seq. No.
                   21321
                   82501 2.R1040
Contig ID
5'-most EST
                   zsq701119866.h1
Seq. No.
                   21322
```

Contig ID 82502 1.R1040 5'-most EST zhf700960383.h1

Method BLASTX
NCBI GI g3135264
BLAST score 216
E value 2.0e-17
Match length 62

```
% identity
NCBI Description (AC003058) unknown protein [Arabidopsis thaliana]
                  21323
Seq. No.
                  82510 1.R1040
Contig ID
                  LIB3139-071-P1-N1-F4
5'-most EST
                  21324
Seq. No.
                  82511 1.R1040
Contig ID
                  LIB3139-071-P1-N1-F5
5'-most EST
                  21325
Seq. No.
                  82534 1.R1040
Contig ID
                  uC-gmropic099b05b1
5'-most EST
                  BLASTX
Method
                  q3668089
NCBI GI
                  292
BLAST score
                  4.0e-26
E value
                  79
Match length
                  72
% identity
NCBI Description (AC004667) unknown protein [Arabidopsis thaliana]
                   21326
Seq. No.
                   82535 1.R1040
Contig ID
                  uC-gmrominsoy314d07b1
5'-most EST
                  BLASTX
Method
                   g3947735
NCBI GI
                   373
BLAST score
                   1.0e-35
E value
                   148
Match length
                   51
% identity
NCBI Description (AJ009720) NL27 [Solanum tuberosum]
                   21327
Seq. No.
                   82562_1.R1040
Contig ID
                   jC-gmro02910040e07a1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q2280530
BLAST score
                   436
                   4.0e-43
E value
                   107
Match length
                   73
% identity
NCBI Description (AB005889) ATMYB4 [Arabidopsis thaliana]
                   21328
Seq. No.
                   82577 1.R1040
Contig ID
                   LIB3139-072-P1-N1-E9
5'-most EST
                   BLASTX
Method
```

NCBI GI g3451078 266 BLAST score 4.0e-23 E value 169 Match length 38 % identity

(AL031326) putative protein [Arabidopsis thaliana] NCBI Description

Seq. No.

21329

Contig ID

82602\_1.R1040



```
5'-most EST
                  smc700747814.h1
Method
                  BLASTX
NCBI GI
                  q862650
BLAST score
                  326
E value
                  2.0e-30
Match length
                  74
% identity
                  84
NCBI Description
                 (U20193) MADS-box protein AGL12 [Arabidopsis thaliana]
Seq. No.
                  21330
                  82610 1.R1040
Contig ID
5'-most EST
                  jC-gmle01810020f12a1
Method
                  BLASTX
NCBI GI
                  g3043694
BLAST score
                  504
                  1.0e-50
E value
                  246
Match length
% identity
                  43
NCBI Description (AB011157) KIAA0585 protein [Homo sapiens]
Seq. No.
                  21331
Contig ID
                  82612 1.R1040
5'-most EST
                  LIB3139-073-P1-N1-A8
Seq. No.
                  21332
Contig ID
                  82614 1.R1040
5'-most EST
                  wrg700787445.h2
Seq. No.
                  21333
                  82618 1.R1040
Contig ID
5'-most EST
                  jC-gmro02800042h10d1
Seq. No.
                  21334
                  82628 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy115a04b1
Seq. No.
                  21335
Contig ID
                  82635 1.R1040
5'-most EST
                  LIB3139-073-P1-N1-D11
Seq. No.
                  21336
Contig ID
                  82639 1.R1040
                  LIB3139-100-P1-N1-G12
5'-most EST
                  21337
Seq. No.
                  82648 1.R1040
Contig ID
5'-most EST
                  LIB3139-073-P1-N1-E7
Method
                  BLASTX
```

Method BLASTX
NCBI GI g629624
BLAST score 300
E value 4.0e-27
Match length 94
% identity 57

NCBI Description chalcone reductase - alfalfa >gi\_563540\_emb\_CAA57782\_

(X82366) chalcone reductase [Medicago sativa]

Seq. No. 21338



Contig ID 82656\_1.R1040

5'-most EST LIB3139-073-P1-N1-F7

Method BLASTX
NCBI GI g2765244
BLAST score 198
E value 2.0e-15
Match length 58
% identity 60

NCBI Description (Y12807) invertase inhibitor homolog [Arabidopsis thaliana]

Seq. No. 21339

Contig ID 82670 1.R1040

5'-most EST LIB3139-073-P1-N1-H12

Seq. No. 21340

Contig ID 82688 1.R1040

5'-most EST uC-gmrominsoy029h10b1

Method BLASTX
NCBI GI g3912942
BLAST score 181
E value 5.0e-13
Match length 82
% identity 45

NCBI Description (U58033) myotubularin related protein 2 [Homo sapiens]

Seq. No. 21341

Contig ID 82706\_1.R1040 5'-most EST ekl700968267.h1

Method BLASTX
NCBI GI g2388585
BLAST score 720
E value 2.0e-76
Match length 159
% identity 90

NCBI Description (AC000098) Similar to Caenorhabditis unknown protein

T03F1.1 (gb\_U88169). [Arabidopsis thaliana]

Seq. No. 21342

Contig ID 82711\_1.R1040 5'-most EST fua701043082.h1

Method BLASTX
NCBI GI g121631
BLAST score 292
E value 2.0e-26
Match length 81
% identity 69

NCBI Description GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 2 PRECURSOR

>gi 72323 pir KNNT2S glycine-rich protein 2 - wood tobacco

>gi 19743 emb CAA42622 (X60007) nsGRP-2 [Nicotiana

sylvestris]

Seq. No. 21343

Contig ID 82714\_1.R1040

5'-most EST uC-gmrominsoy097b11b1

Method BLASTX NCBI GI g2618686 BLAST score 223



E value 3.0e-18
Match length 105
% identity 50

NCBI Description (AC002510) hypothetical protein [Arabidopsis thaliana]

Seq. No. 21344

Contig ID 82722\_1.R1040

5'-most EST LIB3139-074-P1-N1-F12

Seq. No. 21345

Contig ID 82764\_1.R1040

5'-most EST LIB3139-075-P1-N1-D11

Method BLASTX
NCBI GI g3004550
BLAST score 297
E value 6.0e-27
Match length 70
% identity 87

NCBI Description (AC003673) hypothetical protein [Arabidopsis thaliana]

Seq. No. 21346

Contig ID 82769 1.R1040 5'-most EST bth700849271.h1

Method BLASTX
NCBI GI g2462834
BLAST score 359
E value 1.0e-33
Match length 183
% identity 44

NCBI Description (AF000657) hypothetical protein [Arabidopsis thaliana]

Seq. No. 21347

Contig ID 82774\_1.R1040

5'-most EST LIB3139-075-P1-N1-E2

Method BLASTX
NCBI GI g2804278
BLAST score 1282
E value 1.0e-142
Match length 289
% identity 83

NCBI Description (AB003516) squalene epoxidase [Panax ginseng]

Seq. No.

21348

Contig ID 82776\_1.R1040

5'-most EST LIB31 $\overline{3}$ 9-075-P1-N1-E6

Seq. No.

21349

21350

Contig ID 82797\_1.R1040

5'-most EST LIB3139-075-P1-N1-H7

Seq. No.

Contig ID 82803\_1.R1040

5'-most EST LIB3139-076-P1-N1-A5

Seq. No. 21351

Contig ID 82804 1.R1040 5'-most EST hrw701063282.h1



```
Method
                  BLASTX
NCBI GI
                  g4454048
BLAST score
                  255
E value
                  7.0e-22
                  77
Match length
% identity
                  53
NCBI Description (AL035394) putative protein [Arabidopsis thaliana]
Seq. No.
                  21352
Contig ID
                  82805 1.R1040
5'-most EST
                  LIB3139-076-P1-N1-A7
Method
                  BLASTX
NCBI GI
                  g2735017
BLAST score
                  423
E value
                  9.0e-42
Match length
                  109
% identity
                  71
NCBI Description (U82481) KI domain interacting kinase 1 [Zea mays]
Seq. No.
                  21353
                  82830 1.R1040
Contig ID
5'-most EST
                  sat701015385.hl
Method
                  BLASTX
NCBI GI
                  g3805964
BLAST score
                  1155
                  1.0e-127
E value
Match length
                  285
                  74
% identity
NCBI Description (Y13773) laccase [Populus balsamifera subsp. trichocarpa]
                  21354
Seq. No.
                  82839 1.R1040
Contig ID
5'-most EST
                  LIB3139-076-P1-N1-E7
Method
                  BLASTX
NCBI GI
                  g1685091
BLAST score
                  508
                  9.0e-52
E value
Match length
                  120
% identity
NCBI Description (U45243) diphenol oxidase [Nicotiana tabacum]
Seq. No.
                  21355
                  82849 1.R1040
Contig ID
5'-most EST
                  LIB3139-076-P1-N1-G6
                  21356
Seq. No.
Contig ID
                  82859 1.R1040
5'-most EST
                  jC-gmle01810090e09a1
Seq. No.
                  21357
Contig ID
```

Contig ID 82869\_1.R1040 5'-most EST jsh701069679.h1

Seq. No. 21358

Contig ID 82876 1.R1040

5'-most EST LIB3139-077-P1-N1-C3



Seq. No. 21359

Contig ID 82877 1.R1040

5'-most EST uC-gmrominsoy026h03b1

Method BLASTX
NCBI GI g3335372
BLAST score 842
E value 2.0e-90
Match length 274
% identity 57

NCBI Description (AC003028) putative SRG1 protein [Arabidopsis thaliana]

Seq. No. 21360

Contig ID 82885 1.R1040 5'-most EST sat701009936,h2

Method BLASTX
NCBI GI g4104931
BLAST score 561
E value 3.0e-60
Match length 156
% identity 74

NCBI Description (AF042196) auxin response factor 8 [Arabidopsis thaliana]

Seq. No. 21361

Contig ID 82889\_1.R1040 5'-most EST leu701156446.h1

Seq. No. 21362

Contig ID 82899\_1.R1040

5'-most EST LIB3139-077-P1-N1-E7

Method BLASTX
NCBI GI g114208
BLAST score 426
E value 4.0e-42

Match length 115 % identity 70

NCBI Description PROBABLE GLUTATHIONE S-TRANSFERASE PARA (AUXIN-REGULATED

PROTEIN PARA) (STR246C PROTEIN) >gi\_100374\_pir\_A36225 auxin-regulated protein, protoplast - common tobacco (cv. Xanthi nc) >gi\_170283 (M29274) par peptide [Nicotiana tabacum] >gi 530740 emb CAA56790 (X80829) STR246C

[Nicotiana tabacum]

Seq. No. 21363

Contig ID 82903 1.R1040 5'-most EST zlv700807591.h1

Method BLASTX
NCBI GI g3096922
BLAST score 405
E value 8.0e-39
Match length 187
% identity 51

NCBI Description (AL023094) putative protein [Arabidopsis thaliana]

Seq. No. 21364

Contig ID 82913 1.R1040

5'-most EST LIB3139-077-P1-N1-G1

Method BLASTX



```
g4468812
NCBI GI
BLAST score
                  1135
E value
                  1.0e-124
Match length
                  333
% identity
                  41
NCBI Description (AL035601) putative protein [Arabidopsis thaliana]
Seq. No.
                  82925 1.R1040
Contig ID
                  LIB3139-077-P1-N1-H6
5'-most EST
                  21366
Seq. No.
Contig ID
                  82936 1.R1040
5'-most EST
                  epx701105482.h1
Seq. No.
                  21367
Contig ID
                  82948 1.R1040
5'-most EST
                  fC-gmro700848909y1
Method
                  BLASTX
NCBI GI
                  q4512651
BLAST score
                  920
E value
                  2.0e-99
Match length
                  308
% identity
                  52
NCBI Description (AC007048) putative tyrosine transaminase [Arabidopsis
                  thaliana]
Seq. No.
                  21368
                  82961 1.R1040
Contig ID
                  LIB3139-078-P1-N1-E3
5'-most EST
Seq. No.
                  21369
                  82971 1.R1040
Contig ID
                  LIB3139-078-P1-N1-F3
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4544464
BLAST score
                  222
E value
                  3.0e-18
Match length
                  123
% identity
                  46
NCBI Description (AC006580) putative chloroplast nucleoid DNA binding
                  protein [Arabidopsis thaliana]
Seq. No.
                  21370
Contig ID
                  82974 1.R1040
5'-most EST
                  LIB3139-078-P1-N1-F8
Method
                  BLASTX
NCBI GI
                  g2760325
BLAST score
                  411
```

2.0e-40 E value Match length 119 % identity

NCBI Description (AC002130) F1N21.10 [Arabidopsis thaliana]

Seq. No. 21371

Contig ID 82975 1.R1040 5'-most EST gsv701052070.h1



Seq. No. 21372

Contig ID 82975 2.R1040

5'-most EST jC-gmf102220108c02a1

Seq. No. 21373

Contig ID 82976 1.R1040

5'-most EST jC-gmst02400008h01d1

Seq. No. 21374

Contig ID 82976 2.R1040

5'-most EST uC-gmrominsoy298b04b1

Seq. No. 21375

Contig ID 82977 1.R1040

5'-most EST LIB3139-078-P1-N1-G11

Seq. No. 21376

Contig ID 82983 1.R1040

5'-most EST jC-gmle01810028e09a1

Method BLASTX
NCBI GI g4262148
BLAST score 554
E value 1.0e-56
Match length 151
% identity 70

NCBI Description (AC005275) predicted protein of unknown function

[Arabidopsis thaliana]

Seq. No. 21377

Contig ID 82983 2.R1040

5'-most EST jC-gmle01810080c01a1

Seq. No. 21378

Contig ID 83007 1.R1040

5'-most EST LIB3139-099-P1-N1-H12

Seq. No. 21379

Contig ID 83018\_1.R1040 5'-most EST fde700871926.h1

Method BLASTX
NCBI GI g3335376
BLAST score 342
E value 6.0e-32
Match length 117
% identity 61

NCBI Description (AC003028) putative ammonium transporter [Arabidopsis

thaliana]

Seq. No. 21380

Contig ID 83022 1.R1040

5'-most EST jC-gmro02910031a07a1

Method BLASTX
NCBI GI g3218467
BLAST score 173
E value 3.0e-12
Match length 150



% identity

(AJ006529) putative phosphatase [Gallus gallus] NCBI Description

Seq. No.

21381

Contig ID

83036 1.R1040

5'-most EST

LIB3139-080-P1-N1-A10

Seq. No.

21382

Contig ID 5'-most EST 83043 1.R1040 ssr700555316.h1

Method NCBI GI BLASTX g3128176

BLAST score

348

E value

6.0e-33

Match length % identity

101 67

NCBI Description

(AC004521) unknown protein [Arabidopsis thaliana]

Seq. No.

21383

Contig ID

83049 1.R1040

5'-most EST

jC-gmro02910029b12d1

Method NCBI GI BLASTX g418548

BLAST score

372

E value Match length

2.0e-35 139

% identity

53

NCBI Description

HYPOTHETICAL 15.7 KD PROTEIN IN APHA-UVRA INTERGENIC REGION

(0138) >gi\_396391 (U00006) No definition line found

[Escherichia coli] >gi\_1790491 (AE000479) orf, hypothetical

protein [Escherichia coli]

Seq. No.

21384

Contig ID 5'-most EST 83049 3.R1040 sat701014364.h1

Method

BLASTX

NCBI GI

g3123100

BLAST score

164

E value

6.0e-19

Match length % identity

89 57

NCBI Description

HYPOTHETICAL 15.9 KD PROTEIN C4A8.02C IN CHROMOSOME I

>gi\_4490640\_emb\_CAB11472.1\_ (Z98762) SPAC4A8.02c, unknown, len:142aa, similar eg. to YJBQ ECOLI, P32698, hypothetical 15.7 kd protein, (138aa), fast a scores, opt:403, E():

2.4e-32, (41.0% identity in 134 aa overlap)

[Schizosaccharomyces pombe]

Seq. No.

21385

Contig ID 5'-most EST 83061 1.R1040 sat701003014.h1

Seq. No.

21386

Contig ID

83062 1.R1040

5'-most EST

jC-gmst02400024e06d1

Method

BLASTX

NCBI GI

g499301



BLAST score 252 E value 1.0e-21 Match length 75 % identity 69

NCBI Description (X77116) ABI1 [Arabidopsis thaliana] >gi\_549981 (U12856) abscisic acid insensitive protein [Arabidopsis thaliana] >gi 4538937 emb CAB39673.1 (AL049483) protein phosphatase

ABI1 [Arabidopsis thaliana]

Seq. No. 21387

Contig ID 83067 1.R1040

5'-most EST LIB31 $\overline{3}$ 9-080-P1-N1-D8

Method BLASTX
NCBI GI g2462835
BLAST score 448
E value 1.0e-44
Match length 123
% identity 72

NCBI Description (AF000657) hypothetical protein [Arabidopsis thaliana]

Seq. No. 21388

Contig ID 83078\_1.R1040 5'-most EST taw700657627.h1

Method BLASTX
NCBI GI g3540195
BLAST score 710
E value 3.0e-75
Match length 157
% identity 41

NCBI Description (AC004260) Unknown protein [Arabidopsis thaliana]

Seq. No. 21389

Contig ID 83081\_1.R1040

5'-most EST uC-gmrominsoy315g05b1

Seq. No. 21390

Contig ID 83094 1.R1040 5'-most EST zzp700836032.h1

Method BLASTX
NCBI GI g4220462
BLAST score 1058
E value 1.0e-115
Match length 326
% identity 63

NCBI Description (AC006216) Strong similarity to gb Z50851 HD-zip (athb-8)

gene from Arabidopsis thaliana containing Homeobox PF\_00046

and bZIP PF\_00170 domains. [Arabidopsis thaliana]

Seq. No. 21391

Contig ID 83094\_4.R1040
5'-most EST 94395965
Method BLASTX
NCBI GI 93738325
BLAST score 213
E value 7.0e-17

Match length 98 % identity 39



NCBI Description (AC005170) putative CaMB-channel protein [Arabidopsis thaliana]

Seq. No. 21392

Contig ID 83108\_1.R1040 5'-most EST zzp700835758.h1

Seq. No. 21393

Contig ID 83129\_1.R1040

5'-most EST LIB3139-116-P1-N1-D2

Seq. No. 21394

Contig ID 83141\_1.R1040

5'-most EST LIB3139-081-P1-N1-E5

Seq. No. 21395

Contig ID 83167\_1.R1040 5'-most EST zhf700962595.h1

Seq. No. 21396

Contig ID 83167\_2.R1040

5'-most EST LIB3139-081-P1-N1-H3

Seq. No. 21397

Contig ID 83171 1.R1040 5'-most EST trc700565275.h1

Method BLASTN
NCBI GI g2149379
BLAST score 51
E value 2.0e-19
Match length 220
% identity 84

NCBI Description Arabidopsis thaliana syntaxin homolog mRNA, complete cds

Seq. No. 21398

Contig ID 83175\_1.R1040 5'-most EST uC-gmropic047f09b1

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 1.0e-10
Match length 36
% identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 21399

Contig ID 83184\_1.R1040

5'-most EST  $jC-gm\overline{f}$ 1022220089g09d1

Method BLASTX
NCBI GI g4558673
BLAST score 190
E value 3.0e-14
Match length 68
% identity 44

NCBI Description (AC007063) hypothetical protein [Arabidopsis thaliana]

Seq. No. 21400



```
Contig ID
                  83190 1.R1040
5'-most EST
                  pmv700894941.hl
                  BLASTX
Method
NCBI GI
                  g3128234
BLAST score
                  568
E value
                  3.0e-58
                  179
Match length
                  62
% identity
NCBI Description (AC004077) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  21401
Contig ID
                  83202 1.R1040
5'-most EST
                  ncj700980512.h1
Method
                  BLASTX
NCBI GI
                  q462680
BLAST score
                  181
E value
                  5.0e-13
Match length
                  121
% identity
                  36
                  MYOSIN ID HEAVY CHAIN >gi 422294 pir A47106 myosin heavy
NCBI Description
                  chain ID - slime mold (Dictyostelium discoideum)
                  21402
Seq. No.
Contig ID
                  83207 1.R1040
5'-most EST
                  zhf700954162.h1
Method
                  BLASTX
                  q3033381
NCBI GI
                  273
BLAST score
E value
                  6.0e-24
Match length
                  73
                  70
% identity
                  (AC004238) putative UDP-galactose-4-epimerase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  21403
                  83216 1.R1040
Contig ID
5'-most EST
                  LIB3139-082-P1-N1-F11
                  BLASTX
Method
                  g4455199
NCBI GI
BLAST score
                  224
E value
                  4.0e-18
Match length
                  98
% identity
                   48
                  (AL035440) putative protein [Arabidopsis thaliana]
NCBI Description
                  21404
Seq. No.
Contig ID
                  83220 1.R1040
                  LIB3139-082-P1-N1-F4
5'-most EST
                  BLASTX
Method
NCBI GI
                  g1619321
BLAST score
                  275
                  6.0e-24
E value
Match length
                  167
% identity
                   33
```

21405

Seq. No.

NCBI Description (Y07563) hin1 [Nicotiana tabacum]



Contig.ID 83225\_1.R1040
5'-most EST LIB3139-082-P1-N1-G1
Method BLASTN
NCBI GI 94097879

NCBI GI g4097879
BLAST score 249
E value 1.0e-138
Match length 372
% identity 92

NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein

gene, complete cds

Seq. No. 21406

Contig ID 83230\_1.R1040

5'-most EST LIB3139-082-P1-N1-G8

Seq. No. 21407

Contig ID 83231\_1.R1040 5'-most EST kl1701211143.h1

Method BLASTX
NCBI GI g3355480
BLAST score 691
E value 1.0e-72
Match length 267
% identity 52

NCBI Description (AC004218) Medicago nodulin N21-like protein [Arabidopsis

thaliana]

Seq. No. 21408

Contig ID 83231\_2.R1040 5'-most EST bth700843553.h1

Seq. No. 21409

Contig ID 83232\_1.R1040

5'-most EST LIB3139-082-P1-N1-H1

Seq. No. 21410

Contig ID 83251\_1.R1040

5'-most EST jC-gmf102220079g06a1

Method BLASTX
NCBI GI g3367576
BLAST score 203
E value 6.0e-26
Match length 137
% identity 48

NCBI Description (AL031135) NAM / CUC2 -like protein [Arabidopsis thaliana]

Seq. No. 21411

Contig ID 83251\_3.R1040

5'-most EST LIB3139-083-P1-N1-A7

Method BLASTX
NCBI GI g3367576
BLAST score 129
E value 8.0e-09
Match length 68
% identity 50

NCBI Description (AL031135) NAM / CUC2 -like protein [Arabidopsis thaliana]



```
21412
Seq. No.
                  83251 6.R1040
Contig ID
                  gsv701052589.hl
5'-most EST
                  21413
Seq. No.
                  83289 1.R1040
Contig ID
                  LIB3139-083-P1-N1-E8
5'-most EST
                  21414
Seq. No.
                  83292 1.R1040
Contig ID
                  uaw700665771.hl
5'-most EST
                  BLASTX
Method
                  g2465923
NCBI GI
                  317
BLAST score
                   6.0e-29
E value
                   123
Match length
                   50
% identity
                  (AF024648) receptor-like serine/threonine kinase
NCBI Description
                   [Arabidopsis thaliana]
                   21415
Seq. No.
                   83292 2.R1040
Contig ID
                   uC-gmflminsoy063c05b1
5'-most EST
                   BLASTX
Method
                   g2465923
NCBI GI
                   151
BLAST score
                   7.0e-10
E value
                   48
Match length
                   56
% identity
                   (AF024648) receptor-like serine/threonine kinase
NCBI Description
                   [Arabidopsis thaliana]
                   21416
Seq. No.
Contig ID
                   83299 1.R1040
                   zhf700954460.h1
5'-most EST
                   BLASTX
Method
                   q3250693
NCBI GI
                   231
BLAST score
                   3.0e-19
E value
Match length
                   74
% identity
NCBI Description (AL024486) lectin like protein [Arabidopsis thaliana]
                   21417
Seq. No.
                   83304 1.R1040
Contig ID
                   jC-gmro02910069e05a1
 5'-most EST
                   BLASTX
Method
                   g4559346
NCBI GI
                   283
 BLAST score
                   3.0e-25
 E value
                   115
```

Match length 45 % identity

NCBI Description (AC006585) early nodulin 16 [Arabidopsis thaliana]

21418 Seq. No.

83328 1.R1040 Contig ID

LIB3139-084-P1-N1-B5 5'-most EST



```
Method
                  BLASTX
NCBI GI
                  g282873
                  325
BLAST score
                  4.0e-30
E value
                  146
Match length
                  49
% identity
                  transforming protein (myb) homolog - Arabidopsis thaliana
NCBI Description
                  >gi 217859 dbj BAA01730 (D10936) ATMYB1 protein
                  [Arabidopsis thaliana]
Seq. No.
                  21419
```

Contig ID 83332 1.R1040 5'-most EST LIB3139-084-P1-N1-B9

21420

83336 1.R1040 Contig ID 5'-most EST fde700874040.hl Method BLASTX NCBI GI q3450842 405 BLAST score 1.0e-39 E value

Match length 175 55 % identity

Seq. No.

NCBI Description (AF080436) mitogen activated protein kinase kinase [Oryza

sativa]

21421 Seq. No. Contig ID 83341 1.R1040

5'-most EST gsv701044755.h1 Method BLASTX

NCBI GI g2252828 BLAST score 402 E value 3.0e-39 Match length 112 % identity

NCBI Description (AF013293) No definition line found [Arabidopsis thaliana]

Seq. No. 21422

Contig ID 83380 1.R1040 5'-most EST g4313789 Method BLASTX NCBI GI g1171577 BLAST score 903 E value 2.0e-97 Match length 321 53 % identity

NCBI Description (X95343) hypersensitivity-related gene [Nicotiana tabacum]

Seq. No. 21423

83385 1.R1040 Contig ID leu701153480.h1 5'-most EST

Seg. No. 21424

83469 1.R1040 Contig ID

5'-most EST uC-gmrominsoy300f08b1

Method BLASTX NCBI GI g2827555



BLAST score 695 E value 4.0e-73 Match length 221 % identity 32

NCBI Description (AL021635) Translation factor EF-1 alpha - like protein

[Arabidopsis thaliana]

Seq. No. 21425

Contig ID 83487\_1.R1040 5'-most EST xzm700763810.h1

Method BLASTX
NCBI GI g2626753
BLAST score 1352
E value 1.0e-150
Match length 368
% identity 73

NCBI Description (AB008782) sulfate transporter [Arabidopsis thaliana]

Seq. No. 21426

Contig ID 83495\_1.R1040 5'-most EST dpv701100716.h1

Method BLASTX
NCBI GI g3702331
BLAST score 511
E value 8.0e-52
Match length 183
% identity 58

NCBI Description (AC005397) hypothetical protein [Arabidopsis thaliana]

Seq. No. 21427

Contig ID 83497\_1.R1040

5'-most EST LIB3139-086-P1-N1-D7

Method BLASTX
NCBI GI g3929339
BLAST score 393
E value 5.0e-38
Match length 135
% identity 55

NCBI Description BYSTIN >gi 1160619 (L36720) bystin [Homo sapiens]

Seq. No. 21428

Contig ID 83517\_1.R1040

5'-most EST LIB3139-086-P1-N1-G4

Method BLASTX
NCBI GI g3550077
BLAST score 174
E value 2.0e-12
Match length 82
% identity 34

NCBI Description (AF071184) formin binding protein 21 [Mus musculus]

Seq. No. 21429

Contig ID 83538 1.R1040

5'-most EST LIB3139-087-P1-N1-B1

Method BLASTX NCBI GI g3885341 BLAST score 137



E value 5.0e-16 Match length 106 % identity 47

NCBI Description (AC005623) unknown protein [Arabidopsis thaliana]

Seq. No. 21430

Contig ID 83565\_1.R1040 5'-most EST epx701107514.h1

Method BLASTX
NCBI GI g2191187
BLAST score 263
E value 6.0e-23
Match length 93
% identity 55

NCBI Description (AF007271) contains similarity to a DNAJ-like domain

[Arabidopsis thaliana]

Seq. No. 21431

Contig ID 83569\_1.R1040 5'-most EST zzp700834605.h1

Method BLASTX
NCBI GI g3395440
BLAST score 326
E value 4.0e-30
Match length 182
% identity 37

NCBI Description (AC004683) hypothetical protein [Arabidopsis thaliana]

Seq. No. 21432

Contig ID 83572 1.R1040 5'-most EST trc700563308.h1

Method BLASTX
NCBI GI g1769901
BLAST score 413
E value 3.0e-40
Match length 106
% identity 75

NCBI Description (X95737) proline transporter 1 [Arabidopsis thaliana]

>gi 2088642 (AF002109) proline transporter 1 [Arabidopsis

thaliana]

Seq. No. 21433

Contig ID 83577\_1.R1040

5'-most EST LIB3139-087-P1-N1-F5

Method BLASTX
NCBI GI g3080420
BLAST score 1111
E value 1.0e-122
Match length 328
% identity 66

NCBI Description (AL022604) putative sugar transporter protein [Arabidopsis

thaliana]

Seq. No. 21434

Contig ID 83578 1.R1040

5'-most EST uC-gmrominsoy262e02b1

Method BLASTX



NCBI GI g3785995 BLAST score 1046 E value 1.0e-114 Match length 214 % identity 91

NCBI Description (AC005499) unknown protein [Arabidopsis thaliana]

Seq. No.

21435 83586 2.R1040 ary700764370.h1

Contig ID 5'-most EST

21436

Seq. No. Contig ID

83596 1.R1040

5'-most EST

uC-gmflminsoy024b06b1

Method BLASTX
NCBI GI g3643608
BLAST score 559
E value 3.0e-57
Match length 202
% identity 65

NCBI Description (AC005395) hypothetical protein [Arabidopsis thaliana]

Seq. No.

21437

Contig ID 5'-most EST

83596\_2.R1040 wvk700685816.h1

Method BLASTX
NCBI GI g3643608
BLAST score 190
E value 1.0e-14
Match length 87
% identity 46

NCBI Description (AC005395) hypothetical protein [Arabidopsis thaliana]

Seg. No.

21438

Contig ID 5'-most EST 83598\_1.R1040 gsv701052415.h1

Seq. No.

21439

Contig ID

83607 1.R1040

5'-most EST

LIB3139-088-P1-N1-A8

Seq. No.

21440

Contig ID

83619 1.R1040

5'-most EST

LIB3139-088-P1-N1-C11

Method

BLASTX

NCBI GI

g4432860

BLAST score

426

E value

420

Match length

1.0e-41

% dantitu

136 18

% identity

NCBI Description (AC006300) putative glucose-induced repressor protein

[Arabidopsis thaliana]

Seq. No.

21441

Contig ID

83624 1.R1040

5'-most EST

LIB3139-088-P1-N1-C5

Method

BLASTX



```
q3600061
NCBI GI
BLAST score
                  376
E value
                  1.0e-35
Match length
                  223
                  42
% identity
                  (AF080120) contains similarity to DNA binding proteins
NCBI Description
                  [Arabidopsis thaliana]
                  21442
Seq. No.
                  83624 3.R1040
Contig ID
5'-most EST
                  zzp700835928.h1
Seq. No.
                  21443
                  83637 1.R1040
Contig ID
5'-most EST
                  uC-gmflminsoy062g01b1
Method
                  BLASTX
NCBI GI
                  g2980770
BLAST score
                  469
                  9.0e-47
E value
                  121
Match length
% identity
                  71
                 (AL022198) putative protein kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  21444
                  83637 2.R1040
Contig ID
                  uC-gmropic073d05b1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g1777312
BLAST score
                  303
                  2.0e-27
E value
                  82
Match length
                  68
% identity
                  (D30622) novel serine/threonine protein kinase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  21445
Contig ID
                  83639 1.R1040
                  LIB3139-088-P1-N1-E4
5'-most EST
Method
                  BLASTX
NCBI GI
                  g4324965
```

BLAST score 183 4.0e-14 E value 155 Match length % identity 37

NCBI Description (AF114753) polytropic murine leukamia virus receptor SYG1

[Mus musculus]

Seq. No. 21446

83640 1.R1040 Contig ID

LIB3139-088-P1-N1-E5 5'-most EST

BLASTX Method NCBI GI g2213588 BLAST score 378 2.0e-36 E value Match length 115 % identity

NCBI Description (AC000348) T7N9.8 [Arabidopsis thaliana]

```
21447
Seq. No.
Contig ID
                  83644 1.R1040
                  sat701008719.hl
5'-most EST
Method
                  BLASTX
NCBI GI
                  q2104536
BLAST score
                  583
E value
                  3.0e-60
Match length
                  186
% identity
                  60
                  (AF001308) predicted glycosyl transferase [Arabidopsis
NCBI Description
                  21448
Seq. No.
Contig ID
                  83649 1.R1040
                  LIB3139-088-P1-N1-F7
5'-most EST
                  BLASTX
Method
NCBI GI
                  g3152613
BLAST score
                  225
                  3.0e-18
E value
Match length
                  90
                  58
% identity
                  (AC004482) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  21449
Contig ID
                  83666 1.R1040
5'-most EST
                  LIB3139-089-P1-N1-A12
Method
                  BLASTX
                  g3451071
NCBI GI
BLAST score
                  447
                  2.0e-44
E value
Match length
                  92
% identity
                  98
                   (AL031326) beta adaptin - like protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  21450
Contig ID
                  83681 1.R1040
                  zhf700965292.h1
5'-most EST
                  21451
Seq. No.
                  83685 1.R1040
Contig ID
5'-most EST
                  hrw701062252.h1
                  21452
Seq. No.
Contig ID
                  83688 1.R1040
5'-most EST
                  seb700649129.hl
Method
                  BLASTX
NCBI GI
                  q2262159
BLAST score
                  630
```

E value 1.0e-65 164 Match length % identity 66

(AC002329) predicted protein similar to S.pombe protein NCBI Description

C5H10.03 [Arabidopsis thaliana]

Seq. No. 21453

```
83688 2.R1040
Contig ID
5'-most EST
                  dpv701102739.hl
Method
                  BLASTX
NCBI GI
                  g2262159
BLAST score
                  146
                  2.0e-09
E value
Match length
                  28
% identity
                  (AC002329) predicted protein similar to S.pombe protein
NCBI Description
                  C5H10.03 [Arabidopsis thaliana]
Seq. No.
                  21454
Contig ID
                  83719 1.R1040
5'-most EST
                  6HC-01-Q1-B1-F9
Method
                  BLASTN
NCBI GI
                  g2564044
BLAST score
                  39
                  2.0e-12
E value
Match length
                  119
% identity
                  89
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K19P17, complete sequence [Arabidopsis thaliana]
Seq. No.
                  21455
                  83721 1.R1040
Contig ID
5'-most EST
                  jC-gmf102220097a03a1
Seq. No.
                  21456
                  83725 1.R1040
Contig ID
                  LIB3139-089-P1-N1-G6
5'-most EST
                  BLASTX
Method
NCBI GI
                  g3021409
BLAST score
                  183
                  2.0e-13
E value
Match length
                  98
% identity
                  36
                  (Y12781) transducin (beta) like 1 protein [Homo sapiens]
NCBI Description
Seq. No.
                  21457
                  83735 1.R1040
Contig ID
5'-most EST
                  pmv700890447.h1
Method
                  BLASTX
NCBI GI
                  g2129473
BLAST score
                  208
E value
                   3.0e-16
Match length
                  127
% identity
                  40
                  arabinogalactan-like protein - loblolly pine >gi_607774
NCBI Description
                   (U09556) arabinogalactan-like protein [Pinus taeda]
Seq. No.
                  21458
```

Contig ID 83741\_1.R1040

5'-most EST jC-gmst02400072d12a1

Seq. No. 21459

Contig ID 83746\_1.R1040 5'-most EST ncj700985757.h1



```
Seq. No.
                  21460
                  83748 1.R1040
Contig ID
5'-most EST
                  epx701107740.hl
Seq. No.
                  21461
                  83771 1.R1040
Contig ID
5'-most EST
                  LIB3139-090-P1-N1-F5
Method
                  BLASTX
NCBI GI
                  q2739279
BLAST score
                  703
E value
                  5.0e-74
                  272
Match length
% identity
                  53
NCBI Description (AJ223177) short chain alcohol dehydrogenase [Nicotiana
                  tabacum] >gi 2791348 emb CAA11154 (AJ223178) short chain
                  alcohol dehydrogenase [Nicotiana tabacum]
Seg. No.
                  21462
Contig ID
                  83786 1.R1040
5'-most EST
                  ssr700560814.hl
                  21463
Seq. No.
                  83794 1.R1040
Contig ID
5'-most EST
                  LIB3139-091-P1-N1-A9
Seq. No.
                  21464
                  83795 1.R1040
Contig ID
                  LIB3139-091-P1-N1-B1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q3033375
BLAST score
                  253
E value
                  8.0e-22
Match length
                  98
% identity
                  50
NCBI Description (AC004238) putative berberine bridge enzyme [Arabidopsis
                  thaliana]
                  21465
Seq. No.
Contig ID
                  83796 1.R1040
5'-most EST
                  LIB3139-091-P1-N1-B10
Method
                  BLASTX
NCBI GI
                  g2244785
BLAST score
                  512
E value
                  8.0e-52
                  133
Match length
% identity
NCBI Description (Z97335) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  21466
Contig ID
                  83801 1.R1040
```

Contig ID 83801\_1.R1040 5'-most EST dpv701102901.h1

Seq. No. 21467

Contig ID 83804 1.R1040

5'-most EST jC-gmro02910041008d1



Seq. No. 21468

Contig ID 83805\_1.R1040 5'-most EST pcp700990392.h1

Method BLASTX
NCBI GI g4235641
BLAST score 175
E value 8.0e-13
Match length 72
% identity 51

NCBI Description (AF119040) NLOD [Lycopersicon esculentum]

Seq. No. 21469

Contig ID 83822\_1.R1040 5'-most EST jsh701064214.h1

Method BLASTX
NCBI GI g3820531
BLAST score 442
E value 1.0e-43
Match length 146
% identity 55

NCBI Description (AF072736) beta-glucosidase [Pinus contorta]

Seq. No. 21470

Contig ID 83825\_1.R1040 5'-most EST rlr700900892.h1

Seq. No. 21471

Contig ID 83837\_1.R1040 5'-most EST g4295443

Seq. No. 21472

Contig ID 83844\_1.R1040 5'-most EST rlr700896026.h1

Seq. No. 21473

Contig ID 83852 1.R1040

5'-most EST LIB3139-091-P1-N1-H2

Seq. No. 21474

Contig ID 83856 1.R1040

5'-most EST jC-gmf102220101e07a1

Method BLASTX
NCBI GI g1352440
BLAST score 572
E value 6.0e-59
Match length 141
% identity 71

NCBI Description EUKARYOTIC TRANSLATION INITIATION FACTOR 4E (EIF-4E)

(EIF4E) (MRNA CAP-BINDING PROTEIN) (EIF-4F 25 KD SUBUNIT) (EIF-4F P26 SUBUNIT) >qi 1002915 (U34597) p26 [Oryza

satival

Seq. No. 21475

Contig ID 83857\_1.R1040

5'-most EST LIB3139-091-P1-N1-H8

Method BLASTX NCBI GI q2789660



BLAST score 571 E value 4.0e-59 125 Match length 86 % identity

(AF040102) p105 [Arabidopsis thaliana] NCBI Description

Seq. No. Contig ID 21476

83862 1.R1040 5'-most EST

awf700838262.h1

BLASTX Method NCBI GI q4454470 BLAST score 623 E value 6.0e-65 Match length 194 % identity

NCBI Description (AC006234) putative sugar transporter [Arabidopsis

thaliana]

Seq. No.

21477

Contig ID 5'-most EST 83866 1.R1040 hyd700727341.h1

Seq. No.

21478

Contig ID

83877 1.R1040

5'-most EST

LIB3139-092-P1-N1-G8

Seq. No.

21479

Contig ID 5'-most EST 83877 2.R1040 pmv700890865.hl

Method BLASTX NCBI GI g2342730 BLAST score 102

E value 1.0e-11 Match length 49 % identity

NCBI Description (AC002341) hypothetical protein [Arabidopsis thaliana]

Seq. No.

21480

Contig ID

83885 1.R1040

5'-most EST

LIB3139-092-P1-N1-D12

Method BLASTX NCBI GI q3876805 BLAST score 153 E value 8.0e-10 Match length 103 37 % identity

(Z81532) similar to Zinc finger, C3HC4 type (RING finger), NCBI Description

Zinc finger, CCHC class; cDNA EST EMBL: D76268 comes from this gene; cDNA EST EMBL: D68142 comes from this gene; cDNA

EST EMBL:C13529 comes from this gene; cDNA EST yk208

Seq. No. 21481

83894 1.R1040 Contig ID

5'-most EST fC-gmle7000740910a1

BLASTX Method NCBI GI q2944385 BLAST score 567



E value 3.0e-58 Match length 235 % identity 46

NCBI Description (AF048691) calcium dependent protein kinase [Oryza sativa]

Seq. No. 21482

83896 1.R1040 Contig ID uC-gmronoir028g02b1 5'-most EST

Method BLASTX NCBI GI q4510346 BLAST score 404 E value 3.0e-39 Match length 150 57 % identity

NCBI Description (AC006921) hypothetical protein [Arabidopsis thaliana]

Seq. No. 21483

Contig ID 83904 1.R1040

5'-most EST uC-gmrominsoy300a12b1

Seq. No. 21484

Contig ID 83904 2.R1040 5'-most EST fua701037025.h1

Seq. No. 21485

83912 1.R1040 Contig ID 5'-most EST ssr700560802.hl

Method BLASTX NCBI GI q3913437 BLAST score 257 4.0e-22 E value Match length 65 75 % identity

PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA NCBI Description

HELICASE >gi\_1402875\_emb\_CAA66825\_ (X98130) RNA helicase [Arabidopsis thaliana] >gi\_1495271\_emb\_CAA66613\_ (X97970)

RNA helicase [Arabidopsis thaliana]

21486 Seq. No.

Contig ID 83916 1.R1040 5'-most EST sat701003882.hl

21487 Seq. No.

83930 1.R1040 Contig ID 5'-most EST pcp700993631.h1

Seq. No. 21488

83940 1.R1040 Contig ID

LIB3139-093-P1-N1-B3 5'-most EST

BLASTX Method NCBI GI g2738996 BLAST score 413 E value 4.0e-40 Match length 156

% identity 59

NCBI Description (AF022457) CYP97B2p [Glycine max]



Seq. No. 21489

Contig ID 83947\_1.R1040

5'-most EST LIB3139-093-P1-N1-C10

Method BLASTX
NCBI GI 94097880
BLAST score 154
E value 2.0e-18
Match length 128
% identity 52

NCBI Description (U70866) polyprotein [Bean pod mottle virus]

Seq. No. 21490

Contig ID 83954\_1.R1040 5'-most EST 2zp700833125.h1 Method BLASTX

Method BLASTX
NCBI GI 94104933
BLAST score 259
E value 4.0e-22
Match length 104
% identity 50

NCBI Description (AF042346) putative phenylalanyl-tRNA synthetase

beta-subunit; PheHB [Homo sapiens]

Seq. No. 21491

Contig ID 83954\_2.R1040 5'-most EST uaw700666337.h1

Seq. No. 21492

Contig ID 83955 1.R1040

5'-most EST LIB3139-093-P1-N1-D11

Method BLASTX
NCBI GI g2651310
BLAST score 314
E value 6.0e-29
Match length 137
% identity 54

NCBI Description (AC002336) putative PTR2-B peptide transporter [Arabidopsis

thaliana]

Seq. No. 21493

Contig ID 83960 1.R1040

5'-most EST uC-gmrominsoy213f05b1

Method BLASTX
NCBI GI g3023637
BLAST score 162
E value 6.0e-11
Match length 79
% identity 44

NCBI Description PROBABLE ATP-DEPENDENT RNA HELICASE HRH1 (DEAH BOX PROTEIN

8) >gi\_1362899\_pir\_\_ A56236 probable RNA helicase 1 - human >gi\_807817\_dbj\_BAA09078\_ (D50487) RNA helicase (HRH1) [Homo

sapiens]

Seq. No. 21494

Contig ID 83961\_1.R1040 5'-most EST trc700563354.h1

Method BLASTX

% identity NCBI Description

21501

Seq. No.



```
NCBI GI
                  g1777312
BLAST score
                  998
E value
                  1.0e-108
Match length
                  364
% identity
                  54
                  (D30622) novel serine/threonine protein kinase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  21495
Contig ID
                  83971 1.R1040
                  zhf700952245.h1
5'-most EST
Seq. No.
                  21496
                  83974 1.R1040
Contig ID
                  LIB3139-093-P1-N1-F9
5'-most EST
                  BLASTX
Method
NCBI GI
                  g2129698
BLAST score
                  468
E value
                  6.0e-47
Match length
                  100
% identity
                  86
                  protein kinase ATN1 (EC 2.7.1.-) - Arabidopsis thaliana
NCBI Description
                  >gi_1054633_emb_CAA63387_ (X92728) protein kinase
                   [Arabidopsis thaliana]
Seq. No.
                  21497
                  83979 1.R1040
Contig ID
5'-most EST
                  djj700605986.h2
Seq. No.
                  21498
                  83980 1.R1040
Contig ID
5'-most EST
                  rlr700898219.h1
                  21499
Seq. No.
                  84014 1.R1040
Contig ID
5'-most EST
                  bth700845130.h1
Method
                  BLASTX
NCBI GI
                  g2746086
BLAST score
                  200
                  2.0e-15
E value
Match length
                  71
% identity
                   54
NCBI Description
                  (AF025292) putative high-affinity potassium transporter
                   [Hordeum vulgare]
Seq. No.
                  21500
                  84016 1.R1040
Contig ID
5'-most EST
                  LIB3139-094-P1-N1-B9
Method
                  BLASTX
NCBI GI
                  g4455312
BLAST score
                  173
E value
                  4.0e-12
Match length
                  117
```

3454

(AL035528) DnaJ-like protein [Arabidopsis thaliana]



Contig ID 84019 1.R1040 5'-most EST q5057887 Method BLASTX NCBI GI g2129648 BLAST score 335 4.0e-31 E value 74 Match length % identity 81

NCBI Description MYB-related protein 33,3K - Arabidopsis thaliana

>gi\_1263095\_emb\_CAA90809\_ (Z54136) MYB-related protein

[Arabidopsis thaliana]

Seq. No. 21502

Contig ID 84040 1.R1040

5'-most EST LIB3139-094-P1-N1-F10

Method BLASTX
NCBI GI g3600057
BLAST score 285
E value 2.0e-25
Match length 154
% identity 38

NCBI Description (AF080120) similar to several Arabidopsis thaliana disease

resistance proteins [Arabidopsis thaliana]

Seq. No. 21503

Contig ID 84040 2.R1040

5'-most EST fC-gmro7000748726f1

Method BLASTX
NCBI GI g3600057
BLAST score 157
E value 3.0e-10
Match length 152
% identity 34

NCBI Description (AF080120) similar to several Arabidopsis thaliana disease

resistance proteins [Arabidopsis thaliana]

Seq. No. 21504

Contig ID 84055\_1.R1040 5'-most EST trc700565064.h1

Method BLASTX
NCBI GI g3355480
BLAST score 181
E value 4.0e-13
Match length 146
% identity 32

NCBI Description (AC004218) Medicago nodulin N21-like protein [Arabidopsis

thaliana]

Seq. No. 21505

84094 1.R1040 Contig ID 5'-most EST g5666681 Method BLASTX NCBI GI g3451071 BLAST score 969 E value 1.0e-105 Match length 209 % identity 94



NCBI Description (AL031326) beta adaptin - like protein [Arabidopsis thaliana]

Seq. No. 21506

Contig ID 84094\_2.R1040

5'-most EST LIB3139-095-P1-N1-D2

Method BLASTX
NCBI GI g3451071
BLAST score 407
E value 2.0e-83
Match length 241
% identity 73

NCBI Description (AL031326) beta adaptin - like protein [Arabidopsis

thaliana]

Seq. No. 21507

Contig ID 84106\_1.R1040 5'-most EST zzp700834228.h1

Seq. No. 21508

Contig ID 84114\_1.R1040 5'-most EST rlr700895496.h1

Method BLASTX
NCBI GI g3269292
BLAST score 269
E value 2.0e-23
Match length 70
% identity 66

NCBI Description (AL030978) putative protein [Arabidopsis thaliana]

Seq. No. 21509

Contig ID 84115\_1.R1040 5'-most EST vzy700755951.h1

Method BLASTN
NCBI GI g2264312
BLAST score 38
E value 1.0e-11
Match length 46
% identity 96

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MOK16, complete sequence [Arabidopsis thaliana]

Seq. No. 21510

Contig ID 84119 1.R1040

5'-most EST jC-gmle01810009h04a1

Method BLASTX
NCBI GI g3172023
BLAST score 133
E value 8.0e-10
Match length 59
% identity 63

NCBI Description (AB005804) aldehyde oxidase [Arabidopsis thaliana]

Seq. No. 21511

Contig ID 84132\_1.R1040

5'-most EST LIB3139-096-P1-N1-A8

Method BLASTX



NCBI GI g2827552
BLAST score 238
E value 8.0e-20
Match length 125
% identity 42
NCBI Description (AL021635) predicted protein

NCBI Description (AL021635) predicted protein [Arabidopsis thaliana]

Seq. No. 21512

Contig ID 84142\_1.R1040 5'-most EST gsv701045707.h1

Method BLASTX
NCBI GI g3287695
BLAST score 845
E value 6.0e-91
Match length 207
% identity 77

NCBI Description (AC003979) Similar to hypothetical protein C34B7.2

gb 1729503 from C. elegans cosmid gb Z83220. [Arabidopsis

thaliana]

Seq. No. 21513

Contig ID 84145 1.R1040

5'-most EST LIB3139-096-P1-N1-C11

Method BLASTX
NCBI GI g2464872
BLAST score 168
E value 1.0e-11
Match length 130
% identity 37

NCBI Description (Z99707) hypothetical protein [Arabidopsis thaliana]

Seq. No. 21514

Contig ID 84149 1.R1040 5'-most EST uC-gmropic010b12b1

Method BLASTX
NCBI GI g2102679
BLAST score 413
E value 5.0e-40
Match length 249
% identity 40

NCBI Description (U07424) putative tRNA synthetase-like protein [Homo

sapiens] >gi\_4104935\_gb\_AAD02221\_ (AF042347) putative
phenylalanyl-tRNA synthetase alpha-subunit; PheHA [Homo

sapiens]

Seq. No. 21515

Contig ID 84151\_1.R1040

5'-most EST uC-gmrominsoy194c10b1

Seq. No. 21516

Contig ID 84152 1.R1040

5'-most EST uC-gmflminsoy057e02b1

Method BLASTX
NCBI GI g2262105
BLAST score 852
E value 1.0e-91
Match length 251



% identity 63
NCBI Description (AC002343) unknown protein [Arabidopsis thaliana]

Seq. No. 21517

Contig ID 84161\_1.R1040 5'-most EST wvk700685496.h1

Seq. No. 21518

Contig ID 84177\_1.R1040 5'-most EST pcp700995578.h1

Method BLASTX
NCBI GI g1685005
BLAST score 348
E value 5.0e-33
Match length 94
% identity 65

NCBI Description (U32644) immediate-early salicylate-induced glucosyltransferase [Nicotiana tabacum]

Seq. No. 21519

Contig ID 84201 1.R1040

5'-most EST LIB3139-097-P1-N1-A10

Method BLASTX
NCBI GI g3402758
BLAST score 312
E value 2.0e-28
Match length 118
% identity 56

NCBI Description (AL031187) serine/threonine kinase - like protein

[Arabidopsis thaliana]

Seq. No. 21520

Contig ID 84217\_1.R1040 5'-most EST hrw701062875.h1

Method BLASTX
NCBI GI g4454479
BLAST score 251
E value 3.0e-21
Match length 74
% identity 70

NCBI Description (AC006234) putative riboflavin synthase alpha chain

[Arabidopsis thaliana]

Seq. No. 21521

Contig ID 84226\_1.R1040

5'-most EST LIB3139-097-P1-N1-D1

Method BLASTX
NCBI GI g2191187
BLAST score 257
E value 3.0e-22
Match length 113
% identity 46

NCBI Description (AF007271) contains similarity to a DNAJ-like domain

[Arabidopsis thaliana]

Seq. No. 21522

Contig ID 84257\_1.R1040

3458

```
5'-most EST
                  LIB3139-114-P1-N1-F10
Method
                  BLASTX
                  g3451078
NCBI GI
BLAST score
                  346
                  1.0e-32
E value
                  154
Match length
                  51
% identity
NCBI Description (AL031326) putative protein [Arabidopsis thaliana]
Seq. No.
                  21523
                  84279 1.R1040
Contig ID
                  LIB3139-098-P1-N1-A7
5'-most EST
Method
                  BLASTN
NCBI GI
                  g210811
BLAST score
                  116
E value
                  2.0e-58
Match length
                  329
% identity
                  88
NCBI Description Bean pod mottle virus coat protein gene, complete cds,
                  complete middle component (M) RNA
                  21524
Seq. No.
                  84296 1.R1040
Contig ID
5'-most EST
                  LIB3139-098-P1-N1-C12
Method
                  BLASTX
                  q3831469
NCBI GI
BLAST score
                  379
E value
                  1.0e-36
Match length
                  111
                  59
% identity
NCBI Description (AC005700) hypothetical protein [Arabidopsis thaliana]
                  21525
Seq. No.
                  84297 1.R1040
Contig ID
5'-most EST
                  LIB3139-098-P1-N1-C2
Method
                  BLASTX
NCBI GI
                  g2213602
BLAST score
                  284
E value
                  2.0e-25
                  117
Match length
                  47
% identity
NCBI Description (ACO00348) T7N9.22 [Arabidopsis thaliana]
Seq. No.
                  21526
                  84312 1.R1040
Contig ID
5'-most EST
                  sat701003805.h1
Seq. No.
                  21527
                  84317 1.R1040
Contig ID
5'-most EST
                  uaw700661804.hl
                  BLASTX
Method
NCBI GI
                  q4559329
BLAST score
                  245
E value
                  7.0e-28
Match length
                  158
                  51
% identity
```

NCBI Description (AC007087) putative protein kinase MAP3K [Arabidopsis



## thaliana]

Seq. No. 21528
Contig ID 84320\_1.R1040
5'-most EST uC-gmrominsoy284c11b1

Seq. No. 21529
Contig ID 84332\_1.R1040
5'-most EST LIB3139-098-P1-N1-G5
Method BLASTX
NCBI GI 92160177

Method BLASTX
NCBI GI g2160177
BLAST score 580
E value 6.0e-60
Match length 165
% identity 66

NCBI Description (AC000132) EST gb\_R64758 comes from this gene. [Arabidopsis

thaliana]

Seq. No. 21530

Contig ID 84365\_1.R1040 5'-most EST zzp700836033.h1

Method BLASTX
NCBI GI g4580395
BLAST score 470
E value 4.0e-47
Match length 147
% identity 65

NCBI Description (AC007171) putative kinesin-related protein [Arabidopsis

thaliana]

Seq. No. 21531

Contig ID 84367\_1.R1040

5'-most EST LIB3139-099-P1-N1-D10

Method BLASTX
NCBI GI g3877855
BLAST score 264
E value 4.0e-23
Match length 119
% identity 44

NCBI Description (Z34801) cDNA EST yk336d5.5 comes from this gene; cDNA EST

yk332a10.5 comes from this gene; cDNA EST yk452d3.5 comes from this gene; cDNA EST yk449e12.5 comes from this gene; cDNA EST yk472b11.5 comes from this gene; cDNA EST E

Seq. No. 21532

Contig ID 84382 1.R1040

5'-most EST LIB3139-099-P1-N1-F3

Seq. No. 21533

Contig ID 84386\_1.R1040

5'-most EST uC-gmflminsoy018h04b1

Method BLASTX
NCBI GI g4056506
BLAST score 553
E value 1.0e-70
Match length 206
% identity 67

% identity

NCBI Description

52



```
NCBI Description (AC005896) nodulin-like protein [Arabidopsis thaliana]
                  21534
Seq. No.
Contig ID
                  84405 1.R1040
5'-most EST
                  LIB3139-100-P1-N1-A2
Seq. No.
                  21535
Contig ID
                  84422 1.R1040
5'-most EST
                  fC-gmst700888668r7
                  BLASTN
Method
NCBI GI
                  g1142618
BLAST score
                  111
                  2.0e-55
E value
                  273
Match length
% identity
                  88
NCBI Description Phaseolus vulgaris phaseolin G-box binding protein PG1
                  (PG1) mRNA, complete cds
                  21536
Seq. No.
Contig ID
                  84428_1.R1040
5'-most EST
                  LIB3139-100-P1-N1-C9
Method
                  BLASTX
NCBI GI
                  q4454460
BLAST score
                  396
                  2.0e-38
E value
                  102
Match length
                  75
% identity
NCBI Description (AC006234) unknown protein [Arabidopsis thaliana]
Seq. No.
                  21537
Contig ID
                  84429 1.R1040
5'-most EST
                  LIB3139-100-P1-N1-D1
Method
                  BLASTX
NCBI GI
                  g3785977
BLAST score
                  780
E value
                  4.0e-83
Match length
                  189
% identity
NCBI Description (AC005560) putative growth regulator protein [Arabidopsis
                  thaliana]
                  21538
Seq. No.
                  84431 1.R1040
Contig ID
5'-most EST
                  smc700746451.hl
Seq. No.
                  21539
Contig ID
                  84443 1.R1040
5'-most EST
                  zhf700959612.h1
Method
                  BLASTX
                  g2194124
NCBI GI
BLAST score
                  330
E value
                  1.0e-38
Match length
                  161
```

(gb\_U63725). [Arabidopsis thaliana]

(AC002062) Similar to Glycine metalloendoproteinase



Seq. No. 21540

Contig ID 84445\_1.R1040 5'-most EST gsv701052519.h1

Seq. No. 21541

Contig ID 84447\_1.R1040

5'-most EST LIB3139-100-P1-N1-E9

Method BLASTX
NCBI GI g465975
BLAST score 434
E value 7.0e-43
Match length 137
% identity 61

NCBI Description PUTATIVE ATP-DEPENDENT RNA HELICASE T26G10.1 IN CHROMOSOME

III >gi\_482102\_pir\_\_S40731 ATP-dependent RNA helicase

homolog T26G10.1 - Caenorhabditis elegans

>gi 3880293 emb CAA82362 (Z29115) similar to RNA helicases, deleted exon 1397-1495 which introduced stop codon at 3' splice; 5' splice looks v. good; ?possible alternate final exon.; cDNA EST yk368a4.3 comes from this

gene; cDNA EST yk368a4.5 comes fr

Seq. No. 21542

Contig ID 84447\_2.R1040 5'-most EST crh700856067.h1

Seq. No. 21543

Contig ID 84462\_1.R1040

5'-most EST LIB3139-100-P1-N1-G8

Seq. No. 21544

Contig ID 84525\_1.R1040

5'-most EST LIB3139-101-P1-N1-G6

Method BLASTX
NCBI GI g728905
BLAST score 415
E value 1.0e-41
Match length 229
% identity 45

NCBI Description PROBABLE CALCIUM-TRANSPORTING ATPASE 3 (ENDOPLASMIC

RETICULUM CA2+-ATPASE) >gi\_1078206\_pir\_\_S51995 probable ATPase (EC 3.6.1.-) DRS2 - yeast (Saccharomyces cerevisiae)

>gi\_171114 (L01795) ATPase [Saccharomyces cerevisiae]

>gi\_595560 (U12980) Drs2p: Membrane spanning

Ca-ATPase(P-type), member of the cation transport(E1-E2)

ATPase [Saccharomyces cerevisiae]

Seq. No. 21545

Contig ID 84527\_1.R1040 5'-most EST trc700567759.h1 Method BLASTX

Method BLASTX
NCBI GI g3184098
BLAST score 198
E value 4.0e-15
Match length 107
% identity 44

NCBI Description (AL023777) coenzyme a synthetase [Schizosaccharomyces



## pombe]

```
21546
Seq. No.
Contig ID
                  84530 1.R1040
5'-most EST
                  kl1701213664.hl
Seq. No.
                  21547
Contig ID
                  84531 1.R1040
5'-most EST
                  LIB3139-101-P1-N1-H4
                  21548
Seq. No.
                  84545 1.R1040
Contig ID
```

5'-most EST g5058373

Method BLASTX

NCBI GI g3242708

BLAST score 349

E value 1.0e-32

Match length 170

% identity 42

NCBI Description (AC003040) putative serine/threonine protein kinase [Arabidopsis thaliana]

 Seq. No.
 21549

 Contig ID
 84555\_1.R1040

 5'-most EST
 fC-gmst700651436a1

Method BLASTX
NCBI GI g3327275
BLAST score 709
E value 9.0e-75
Match length 222
% identity 64

NCBI Description (AB016002) PKn3 [Ipomoea nil]

Seq. No. 21550

Contig ID 84568\_1.R1040

5'-most EST LIB3139-102-P1-N1-E1

Seq. No. 21551

Contig ID 84576\_1.R1040 5'-most EST sat701014173.h1

Method BLASTX
NCBI GI g3746064
BLAST score 174
E value 2.0e-12
Match length 52
% identity 58

NCBI Description (AC005311) unknown protein [Arabidopsis thaliana]

Seq. No. 21552

Contig ID 84599 1.R1040

5'-most EST LIB3139-102-P1-N1-H10

Seq. No. 21553

Contig ID 84602 1.R1040

5'-most EST jC-gmle01810023f02a1

Seq. No. 21554



```
84602 2.R1040
Contig ID
5'-most EST
                  pmv700892446.h1
                  21555
Seq. No.
Contig ID
                  84606 1.R1040
5'-most EST
                  LIB3139-103-P1-N1-A11
Method
                  BLASTX
NCBI GI
                  g4455191
                  224
BLAST score
                  3.0e-18
E value
Match length
                  152
% identity
NCBI Description (AL035440) putative protein [Arabidopsis thaliana]
Seq. No.
                  21556
                  84611 1.R1040
Contig ID
5'-most EST
                  jC-gmst02400043c01a1
Method
                  BLASTX
NCBI GI
                  g3746060
BLAST score
                  300
E value
                  6.0e-27
Match length
                  123
% identity
NCBI Description (AC005311) unknown protein [Arabidopsis thaliana]
Seq. No.
                  21557
Contig ID
                  84611 2.R1040
5'-most EST
                  pmv700891819.h1
Method
                  BLASTX
                  g3746060
NCBI GI
BLAST score
                  329
                  2.0e-30
E value
Match length
                  61
% identity
                  95
NCBI Description (AC005311) unknown protein [Arabidopsis thaliana]
Seq. No.
                  21558
Contig ID
                  84613 1.R1040
5'-most EST
                  LIB3139-103-P1-N1-B2
                  21559
Seq. No.
Contig ID
                  84619 1.R1040
5'-most EST
                  smc700747393.h1
Method
                  BLASTX
NCBI GI
                  g2213586
BLAST score
                  386
E value
                  6.0e-37
                  192
Match length
% identity
                  43
NCBI Description (AC000348) T7N9.6 [Arabidopsis thaliana]
```

Seq. No. 21560

Contig ID 84620 1.R1040 5'-most FST LIB3139-103-P1

5'-most EST LIB3139-103-P1-N1-C1

Method BLASTX NCBI GI g419789 BLAST score 750



E value 2.0e-82 Match length 213 % identity 70

NCBI Description hypothetical protein - potato

Seq. No. 21561

Contig ID 84620 2.R1040 5'-most EST vzy700754929.h1

Seq. No. 21562

Contig ID 84624 1.R1040

5'-most EST LIB3139-103-P1-N1-C3

Method BLASTX
NCBI GI g2459436
BLAST score 528
E value 4.0e-54
Match length 122
% identity 80

NCBI Description (AC002332) unknown protein [Arabidopsis thaliana]

Seq. No. 21563

Contig ID 84628\_1.R1040 5'-most EST jsh701070489.h1

Method BLASTX
NCBI GI g4262226
BLAST score 504
E value 6.0e-51
Match length 140
% identity 70

NCBI Description (AC006200) putative protein kinase [Arabidopsis thaliana]

Seq. No. 21564

Contig ID 84634\_1.R1040 5'-most EST zsg701125470.h1

Method BLASTX
NCBI GI g3548802
BLAST score 277
E value 3.0e-30
Match length 141
% identity 55

NCBI Description (AC005313) axi 1-like protein [Arabidopsis thaliana]

>gi\_4335769\_gb\_AAD17446\_ (AC006284) putative axi1 protein

[Nicotiana tabacum] [Arabidopsis thaliana]

Seq. No. 21565

Contig ID 84638\_1.R1040 5'-most EST pmv700891822.h1

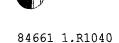
Seq. No. 21566

Contig ID 84647 1.R1040 5'-most EST zhf700963643.h1

Seq. No. 21567

Contig ID 84654\_1.R1040 5'-most EST zpv700758757.h1

Seq. No. 21568



hrw701060110.h1

Seq. No. 21569

Contig ID 5'-most EST

Contig ID 84671 2.R1040 5'-most EST trc700565557.h1

Seq. No. 21570

Contig ID 84672 1.R1040

5'-most EST LIB3139-104-P1-N1-A4

Seq. No. 21571

Contig ID 84678 1.R1040

5'-most EST LIB3139-104-P1-N1-B1

Method BLASTX
NCBI GI g3080412
BLAST score 217
E value 1.0e-17
Match length 107
% identity 39

NCBI Description (AL022604) putative protein [Arabídopsis thaliana]

Seq. No. 21572

Contig ID 84689 1.R1040

5'-most EST LIB3139-104-P1-N1-C12

Method BLASTX
NCBI GI g3600031
BLAST score 386
E value 3.0e-37
Match length 91
% identity 80

NCBI Description (AF080119) similar to 2,4-dihydroxyhept-2-ene-1,7-dioic

acid aldolases [Arabidopsis thaliana]

Seq. No. 21573

Contig ID 84696\_1.R1040 5'-most EST hyd700730038.h1

Method BLASTX
NCBI GI g3142303
BLAST score 802
E value 9.0e-86
Match length 192
% identity 80

NCBI Description (AC002411) Strong similarity to MRP-like ABC transporter

gb\_U92650 from A. thaliana and canalicular multi-drug resistance protein gb\_L49379 from Rattus norvegicus.

[Arabidopsis thaliana]

Seq. No. 21574

Contig ID 84702\_1.R1040 5'-most EST uxk700668193.h1

Seq. No. 21575

Contig ID 84711\_1.R1040 5'-most EST zhf700960679.h1

Method BLASTX NCBI GI g3075398



```
BLAST score
                   543
                   1.0e-55
E value
Match length
                  150
% identity
                   67
                  (AC004484) unknown protein [Arabidopsis thaliana]
NCBI Description
                  21576
Seq. No.
                  84711 2.R1040
Contig ID
5'-most EST
                  jex700904331.h1
Seq. No.
                  21577
                  84720 1.R1040
Contig ID
                  uaw700666970.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g2392771
BLAST score
                   232
E value
                   3.0e-19
Match length
                  74
% identity
NCBI Description
                  (AC002534) putative kinesin-like protein [Arabidopsis
                  thaliana]
                  21578
Seq. No.
                   84725 1.R1040
Contig ID
5'-most EST
                  LIB3139-104-P1-N1-G5
Method
                  BLASTX
                   q2853083
NCBI GI
BLAST score
                  159
E value
                   2.0e-10
Match length
                   67
% identity
                   54
NCBI Description
                  (AL021768) putative protein [Arabidopsis thaliana]
Seq. No.
                   21579
Contig ID
                   84727 1.R1040
5'-most EST
                   gsv701053894.hl
Method
                   BLASTX
NCBI GI
                   g2911042
BLAST score
                   466
E value
                   2.0e-46
Match length
                   103
                   86
% identity
NCBI Description
                   (AL021961) Phosphoglycerate dehydrogenase - like protein
                   [Arabidopsis thaliana]
Seq. No.
                   21580
Contig ID
                   84730 1.R1040
5'-most EST
                   zhf700964346.h1
                  BLASTX
Method
NCBI GI
                   g2244990
BLAST score
                   374
E value
                   1.0e-41
Match length
                  139
% identity
                   68
                  (Z97340) similarity to LIM homeobox protein -
NCBI Description
```

Caenorhabditis [Arabidopsis thaliana]



Seq. No. 21581

Contig ID 84733\_1.R1040 5'-most EST pxt700944738.h1

Method BLASTX
NCBI GI 94559331
BLAST score 675
E value 1.0e-70
Match length 131
% identity 91

NCBI Description (AC007087) unknown protein [Arabidopsis thaliana]

Seq. No. 21582

Contig ID 84733\_2.R1040 5'-most EST zzp700833729.h1

Method BLASTX
NCBI GI g4559331
BLAST score 680
E value 2.0e-71
Match length 147
% identity 86

NCBI Description (AC007087) unknown protein [Arabidopsis thaliana]

Seq. No. 21583

Contig ID 84742 1.R1040

5'-most EST LIB3139-105-P1-N1-B11

Method BLASTX
NCBI GI g416758
BLAST score 527
E value 1.0e-53
Match length 160
% identity 62

NCBI Description SERINE CARBOXYPEPTIDASE PRECURSOR >gi\_166674 (M81130)

carboxypeptidase Y-like protein [Arabidopsis thaliana]
>gi\_445120\_prf \_1908426A carboxypeptidase Y [Arabidopsis

thaliana]

Seq. No. 21584

Contig ID 84760\_1.R1040 5'-most EST zsg701117457.h1

Method BLASTX
NCBI GI g4455335
BLAST score 1009
E value 1.0e-110
Match length 276
% identity 28

NCBI Description (AL035525) putative protein [Arabidopsis thaliana]

Seq. No. 21585

Contig ID 84765 1.R1040 5'-most EST hyd700729344.h1

Method BLASTX
NCBI GI g1709358
BLAST score 201
E value 4.0e-21
Match length 132
% identity 39

NCBI Description NUCLEOSIDE-TRIPHOSPHATASE (NUCLEOSIDE TRIPHOSPHATE



PHOSPHOHYDROLASE) (NTPASE) >gi\_629638\_pir\_\_S48859 nucleoside triphosphatase - garden pea >gi\_2129890\_pir\_\_S65147 nucleoside triphosphatase precursor, chromatin-associated - garden pea >gi\_563612\_emb\_CAA83655\_ (Z32743) nucleoside triphosphatase [Pisum\_sativum] >gi\_4519173\_dbj\_BAA75506.1\_ (AB022319) nucleoside triphosphatase (NTPase) [Pisum\_sativum]

```
Seq. No.
                  21586
Contig ID
                  84794 1.R1040
5'-most EST
                  LIB3139-105-P1-N1-H8
                  BLASTX
Method
NCBI GI
                  q2244818
BLAST score
                  164
                  4.0e-11
E value
Match length
                  47
% identity
NCBI Description (Z97336) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  21587
Contig ID
                  84799 1.R1040
5'-most EST
                  jC-qmst02400039h08a1
```

Seq. No. 21588

Contig ID 84802 1.R1040 5'-most EST dpv701098949.h1 Method BLASTX

NCBI GI g2944180 BLAST score 586 E value 1.0e-60 Match length 152 % identity 73

NCBI Description (AF007779) trehalose-6-phosphate phosphatase [Arabidopsis

thaliana]

Seq. No. 21589

Contig ID 84803 1.R1040

5'-most EST LIB3139-106-P1-N1-A7

Seq. No. 21590

Contig ID 84807 1.R1040

5'-most EST jC-gmro02910074e12a1

Method BLASTX
NCBI GI g4522012
BLAST score 444
E value 1.0e-81
Match length 232
% identity 68

NCBI Description (AC007069) hypothetical protein [Arabidopsis thaliana]

Seq. No. 21591

Contig ID 84817\_1.R1040 5'-most EST bth700849182.h1

Method BLASTX NCBI GI g399505 BLAST score 196 E value 8.0e-15

NCBI Description

sativa]



159

```
Match length
                    35
  % identity
 NCBI Description
                    DIMETHYLANILINE MONOOXYGENASE (N-OXIDE FORMING) 1 (FETAL
                    HEPATIC FLAVIN-CONTAINING MONOOXYGENASE 1) (FMO 1)
                    (DIMETHYLANILINE OXIDASE 1) >gi_105847_pir__A40876
                    dimethylaniline monooxygenase (N-oxide-forming) (EC
                    1.14.13.8), hepatic 1 - human >gi 182671 (M64082)
                    flavin-containing monooxygenase [Homo sapiens]
                    >gi 4503755 ref NP 002012.1 pFMO1 flavin containing
                    monooxygenase
                    21592
  Seq. No.
                    84841 1.R1040
 Contig ID
                    LIB3139-106-P1-N1-F2
  5'-most EST
                    BLASTX
 Method
 NCBI GI
                    q1871184
 BLAST score
                    160
 E value
                    7.0e-11
 Match length
                    112
  % identity
                    31
 NCBI Description (U90439) unknown protein [Arabidopsis thaliana]
 Seq. No.
                    21593
 Contig ID
                    84857 1.R1040
  5'-most EST
                    LIB3139-106-P1-N1-H2
 Method
                    BLASTX
                    q3421378
 NCBI GI
 BLAST score
                    876
 E value
                    2.0e-94
 Match length
                    234
  % identity
                    71
 NCBI Description (AF080249) kinesin-like heavy chain [Arabidopsis thaliana]
                    21594
 Seq. No.
                    84864 1.R1040
  Contig ID
  5'-most EST
                    LIB3139-107-P1-N1-A10
  Method
                    BLASTX
 NCBI GI
                    q2501326
  BLAST score
                    509
 E value
                    9.0e-52
 Match length
                    118
                    76
  % identity
 NCBI Description PYRUVATE DECARBOXYLASE >gi 2160688 (U73194) pyruvate
                    decarboxylase [Emericella nidulans]
  Seq. No.
                    21595
  Contig ID
                    84909 1.R1040
                    hrw701061973.h1
  5'-most EST
                    BLASTX
 Method
 NCBI GI
                    q1843462
 BLAST score
                    309
 E value
                    5.0e-28
 Match length
                    201
  % identity
```

(L10211) isoliquiritiqenin 2'-O-methyltransferase [Medicago



Seq. No. 21596

Contig ID 84910\_1.R1040 5'-most EST asn701134263.h1

Method BLASTX
NCBI GI g3885327
BLAST score 403
E value 3.0e-39
Match length 107
% identity 73

NCBI Description (AC005623) hypothetical protein [Arabidopsis thaliana]

Seq. No. 21597

Contig ID 84922\_1.R1040

5'-most EST LIB3139-107-P1-N1-G9

Method BLASTN
NCBI GI g210811
BLAST score 148
E value 1.0e-77
Match length 364
% identity 85

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 21598

Contig ID 84932 1.R1040 5'-most EST pxt700943263.h1

Seq. No. 21599

Contig ID 84941\_1.R1040 5'-most EST seb700653626.h1

Method BLASTX
NCBI GI g4006886
BLAST score 223
E value 7.0e-18
Match length 164
% identity 38

NCBI Description (Z99708) putative protein [Arabidopsis thaliana]

Seq. No. 21600

Contig ID 84959\_1.R1040 5'-most EST hrw701062283.h1

Seq. No. 21601

Contig ID 84968 1.R1040

5'-most EST LIB3139-109-P1-N1-E5

Seq. No. 21602

Contig ID 84979 1.R1040

5'-most EST jC-gmf102220106h11a1

Seq. No. 21603

Contig ID 84987 1.R1040

5'-most EST LIB3139-109-P1-N1-G9

Seq. No. 21604

Contig ID 85009 1.R1040 5'-most EST vwf700673566.h1



Method BLASTX
NCBI GI g3892204
BLAST score 505
E value 5.0e-82
Match length 201
% identity 74

NCBI Description (AF078105) site-1 protease of sterol regulatory element

binding proteins [Cricetulus griseus]

Seq. No. 21605

Contig ID 85014 1.R1040

5'-most EST jC-qmst02400046h01a1

Method BLASTX
NCBI GI g2244865
BLAST score 385
E value 4.0e-37
Match length 133
% identity 61

NCBI Description (Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No. 21606

Contig ID 85020\_1.R1040 5'-most EST ncj700977338.h1

Method BLASTX
NCBI GI g121418
BLAST score 155
E value 3.0e-10
Match length 66
% identity 50

NCBI Description GLYCEROPHOSPHORYL DIESTER PHOSPHODIESTERASE PERIPLASMIC

PRECURSOR (GLYCEROPHOSPHODIESTER PHOSPHODIESTERASE)

>gi\_95906\_pir\_\_S15945 glycerophosphodiester

phosphodiesterase (EC 3.1.4.46) precursor, periplasmic -

Escherichia coli >gi\_41581\_emb\_CAA40223\_ (X56907)

glycerophosphocholine phosphodiesterase [Escherichia coli]

>gi\_1788572 (AE000314) glycerophosphodiester

phosphodiesterase, periplasmic [Escherichia coli]

>gi\_1799586\_dbj\_BAA16058\_ (D90855) glycerophosphodiester phosphodiesterase (EC 3.1.4.46) precursor, periplasmic

[Escherichia coli] >gi 227847 prf 1712315A

glycerophosphoryl diester esterase [Escherichia coli]

Seq. No. 21607

Contig ID 85061\_1.R1040 5'-most EST seb700648986.h1

Method BLASTX
NCBI GI g2760322
BLAST score 730
E value 3.0e-77
Match length 211
% identity 67

NCBI Description (AC002130) F1N21.7 [Arabidopsis thaliana]

Seq. No. 21608

Contig ID 85061 2.R1040 5'-most EST trc700561810.h1

Method BLASTX



NCBI GI q2760322 367 BLAST score E value 6.0e-35 143 Match length 54 % identity

NCBI Description (AC002130) F1N21.7 [Arabidopsis thaliana]

21609 Seq. No.

Contig ID 85069 1,R1040 5'-most EST g4313966 Method BLASTX NCBI GI g2244979 BLAST score 221 6.0e-18 E value Match length 64 % identity 67

(Z97340) similarity to enoyl-CoA hydratase [Arabidopsis NCBI Description

thaliana]

21610 Seq. No.

85081 1.R1040 Contig ID

5'-most EST LIB3139-111-P1-N1-D12

Seq. No. 21611

Contig ID 85085 1.R1040

5'-most EST LIB3139-111-P1-N1-B9

Method BLASTX NCBI GI g1184075 BLAST score 277 E value 2.0e-24 Match length 172 3

% identity NCBI Description

(U42444) Cf-2.1 [Lycopersicon pimpinellifolium]

>gi 1587673 prf 2207203A Cf-2 gene [Lycopersicon

esculentum

21612 Seq. No.

85091 1.R1040 Contig ID 5'-most EST sat701006116.hl

21613 Seq. No.

85098 1.R1040 Contig ID

5'-most EST LIB3139-111-P1-N1-D8

Method BLASTX NCBI GI q2642154 BLAST score 169 E value 7.0e-12 Match length 107 % identity 44

NCBI Description (AC003000) unknown protein [Arabidopsis thaliana]

>gi 3790595 (AF079186) RING-H2 finger protein RHC2a

[Arabidopsis thaliana]

21614 Seq. No.

Contig ID 85102 1.R1040

5'-most EST uC-gmflminsoy074h09b1

5'-most EST

Method



```
21615
Seq. No.
Contig ID
                  85104 1.R1040
5'-most EST
                  LIB3139-111-P1-N1-E7
                  21616
Seq. No.
                  85108 1.R1040
Contig ID
5'-most EST
                  crh700855335.hl
Seq. No.
                  21617
                  85109 1.R1040
Contig ID
5'-most EST
                  LIB3139-111-P1-N1-F3
Method
                  BLASTX
NCBI GI
                  g2583128
BLAST score
                  423
                  1.0e-60
E value
Match length
                  172
% identity
                  72
NCBI Description (AC002387) hypothetical protein [Arabidopsis thaliana]
                  21618
Seq. No.
                  85149 1.R1040
Contig ID
5'-most EST
                  LIB3139-112-P1-N1-E10
                  BLASTN
Method
                  g3128166
NCBI GI
BLAST score
                  36
                  1.0e-10
E value
Match length
                  44
                  95
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC F4I1 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  21619
                  85157 1.R1040
Contig ID
                  LIB3139-112-P1-N1-F12
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2213594
BLAST score
                  229
E value
                  7.0e-19
Match length
                  120
% identity
                  38
NCBI Description (AC000348) T7N9.14 [Arabidopsis thaliana]
Seq. No.
                  21620
Contig ID
                  85184 1.R1040
5'-most EST
                  uC-gmrominsoy074d04b1
Method
                  BLASTX
NCBI GI
                  g2827623
BLAST score
                  281
E value
                  5.0e-25
Match length
                  60
% identity
NCBI Description (AL021636) putative protein [Arabidopsis thaliana]
Seq. No.
                  21621
                  85192_1.R1040
Contig ID
```

3474

jC-gmst02400029c08a1

BLASTX



NCBI GI g3831456 BLAST score 600 E value 5.0e-62 Match length 230 % identity 55

NCBI Description (AC005700) putative ion channel protein [Arabidopsis

thaliana]

Seq. No. 21622

Contig ID 85211\_1.R1040 5'-most EST uC-gmropic109h11b1

Method BLASTX
NCBI GI g3249105
BLAST score 335
E value 4.0e-31
Match length 105
% identity 58

NCBI Description (AC003114) Contains similarity to protein phosphatase 2C

(ABI1) gb\_X78886 from A. thaliana. [Arabidopsis thaliana]

Seq. No. 21623

Contig ID 85219\_1.R1040 5'-most EST zzp700835044.h1

Seq. No. 21624

Contig ID 85234\_1.R1040 5'-most EST taw700658908.h1

Method BLASTX
NCBI GI g2760322
BLAST score 249
E value 2.0e-21
Match length 106
% identity 55

NCBI Description (AC002130) F1N21.7 [Arabidopsis thaliana]

Seq. No. 21625

Contig ID 85237\_1.R1040

5'-most EST LIB3170-074-Q1-K1-B5

Method BLASTX
NCBI GI g3273196
BLAST score 246
E value 6.0e-21
Match length 87
% identity 64

NCBI Description (AB010915) responce regulator1 [Arabidopsis thaliana]

>gi\_3323583 (AF057282) two-component response regulator homolog [Arabidopsis thaliana] >gi\_3953597\_dbj\_BAA34726\_ (AB008487) response regulator 4 [Arabidopsis thaliana]

Seq. No. 21626

Contig ID 85244 1.R1040

5'-most EST jC-gmle01810058f12a1

Method BLASTX
NCBI GI g4056431
BLAST score 573
E value 3.0e-59
Match length 158

Contig ID

21632

85312 2.R1040



```
% identity
NCBI Description
                  (AC005990) Similar to gb AJ002532 endo-polygalacturonase
                  from Arabidopsis thaliana and is a member of the
                  polygalacturonase family PF 00295. [Arabidopsis thaliana]
Seq. No.
                  21627
                  85259 1.R1040
Contig ID
5'-most EST
                  LIB3170-077-Q1-J1-B10
Seq. No.
                  21628
Contig ID
                  85303 1.R1040
5'-most EST
                  LIB3139-115-P1-N1-B6
Method
                  BLASTN
NCBI GI
                  g2924653
BLAST score
                  43
E value
                  6.0e-15
                  51
Match length
                  96
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:
                  MDA7, complete sequence [Arabidopsis thaliana]
Seq. No.
                  21629
Contig ID
                  85303 2.R1040
5'-most EST
                  ncj700981223.h1
Method
                  BLASTN
                  g2924653
NCBI GI
BLAST score
                  43
E value
                  5.0e-15
Match length
                  51
                  96
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:
                  MDA7, complete sequence [Arabidopsis thaliana]
Seq. No.
                  21630
Contig ID
                  85311 1.R1040
5'-most EST
                  jC-qmst02400026d05a1
                  BLASTN
Method
NCBI GI
                  g4138678
BLAST score
                  142
E value
                  8.0e-74
                  350
Match length
                  85
% identity
NCBI Description V.faba mRNA for amino acid transporter
                  21631
Seq. No.
Contig ID
                  85312 1.R1040
5'-most EST
                  LIB3139-115-P1-N1-D6
Method
                  BLASTX
NCBI GI
                  g1542941
BLAST score
                  781
                  3.0e-83
E value
Match length
                  218
% identity
NCBI Description
                  (X78116) Acetoacetyl-coenzyme A thiolase [Raphanus sativus]
```

3476



```
fC-gmro700870186f3
5'-most EST
Method
                   BLASTX
NCBI GI
                   q1542941
BLAST score
                   360
                   2.0e-34
E value
Match length
                   85
                   84
% identity
NCBI Description (X78116) Acetoacetyl-coenzyme A thiolase [Raphanus sativus]
                   21633
Seq. No.
Contig ID
                   85312 3.R1040
                   zhf700955857.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q1749576
BLAST score
                   172
E value
                   2.0e-12
Match length
                   74
% identity
                   51
                  (D89184) similar to Saccharomyces cerevisiae acetyl-CoA
NCBI Description
                   acetyltransferase, SWISS-PROT Accession Number P41338
                   [Schizosaccharomyces pombe]
Seq. No.
                   21634
Contig ID
                   85316 1.R1040
5'-most EST
                   LIB3139-115-P1-N1-E6
Method
                   BLASTX
NCBI GI
                   q2623295
BLAST score
                   141
E value
                   3.0e-17
Match length
                   83
                   59
% identity
NCBI Description
                  (AC002409) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   21635
                   85317 1.R1040
Contig ID
5'-most EST
                   jC-qmst02400020q04a1
Method
                   BLASTX
NCBI GI
                   g3024135
BLAST score
                   394
E value
                   4.0e-38
Match length
                   166
                   50
% identity
NCBI Description
                  PUTATIVE SEPTUM SITE-DETERMINING PROTEIN MIND
                   >gi_2224467_dbj_BAA57951_ (AB001684) cell division
inhibitor MinD [Chlorella vulgaris]
Seq. No.
                   21636
Contig ID
                   85335 1.R1040
5'-most EST
                   LIB3139-115-P1-N1-H5
Method
                   BLASTX
NCBI GI
                   q2766452
```

Method BLASTX
NCBI GI g2766452
BLAST score 113
E value 5.0e-09
Match length 64
% identity 55

NCBI Description (AF029858) cytochrome P450 CYP71E1 [Sorghum bicolor]



```
21637
Seq. No.
                   85342 1.R1040
Contig ID
5'-most EST
                   fC-gmle700789055a4
                   BLASTX
Method
                   g1871192
NCBI GI
BLAST score
                   507
E value
                   7.0e-51
Match length
                   220
% identity
NCBI Description
                  (U90439) Cys3His zinc finger protein isolog [Arabidopsis
                   thaliana]
                   21638
Seq. No.
Contig ID
                   85362 1.R1040
5'-most EST
                   eep700866913.hl
Method
                   BLASTX
NCBI GI
                   g3421384
BLAST score
                   870
E value
                   8.0e-94
Match length
                   217
                   74
% identity
NCBI Description (AF081067) IAA-Ala hydrolase; IAA-amino acid hydrolase
                   [Arabidopsis thaliana]
                   21639
Seq. No.
                   85380 1.R1040
Contig ID
5'-most EST
                  pmv700891184.h1
Method
                   BLASTX
NCBI GI
                   g1706956
BLAST score
                   2231
E value
                   0.0e+00
                   467
Match length
% identity
                   90
NCBI Description (U58283) cellulose synthase [Gossypium hirsutum]
Seq. No.
                   21640
Contig ID
                   85380 2.R1040
5'-most EST
                   jC-gmst02400077a08a1
Method
                   BLASTX
                   g1706956
NCBI GI
BLAST score
                   362
                   5.0e-53
E value
Match length
                   135
% identity
NCBI Description (U58283) cellulose synthase [Gossypium hirsutum]
                  21641
Seq. No.
                   85395 1.R1040
Contig ID
5'-most EST
                  uC-gmropic030f08b1
Method
                  BLASTX
NCBI GI
                  g1350512
BLAST score
                  148
E value
                  2.0e-09
Match length
                  106
% identity
                   30
```

NCBI Description (L47671) embryo-abundant protein [Picea glauca]



```
21642
Seq. No.
Contig ID
                  85419 1.R1040
                  LIB3139-117-P1-N1-C2
5'-most EST
Method
                  BLASTX
NCBI GI
                  q2911075
BLAST score
                  307
E value
                  6.0e-28
Match length
                  103
% identity
                  57
NCBI Description (AL021960) putative protein [Arabidopsis thaliana]
Seq. No.
                  21643
                  85431 1.R1040
Contig ID
                  uC-gmropic107g04b1
5'-most EST
Method
                  BLASTN
NCBI GI
                  g1321626
BLAST score
                  155
E value
                  2.0e-81
Match length
                  525
% identity
                  84
```

NCBI Description Cucurbita sp. mRNA for thylakoid-bound ascorbate

peroxidase, complete cds

21644 Seq. No. Contig ID 85431 2.R1040 5'-most EST LIB3139-117-P1-N1-E11 BLASTX Method NCBI GI q1321627 BLAST score 715 E value 9.0e-76

Match length 163 % identity 86

NCBI Description (D83656) thylakoid-bound ascorbate peroxidase [Cucurbita

sp.]

Seq. No. 21645

85433 1.R1040 Contig ID 5'-most EST uC-gmropic104f10b1

Seq. No. 21646

Contig ID 85433 4.R1040

jC-gmf102220090a11a1 5'-most EST

Seq. No. 21647

85434 1.R1040 Contig ID 5'-most EST fC-gmro7000746614f1

Seq. No. 21648

Contig ID 85463 1.R1040

5'-most EST LIB3139-118-P1-N1-A10

Seq. No. 21649

85464 1.R1040 Contig ID

5'-most EST LIB3139-118-P1-N1-A12

BLASTX Method NCBI GI q3413886 BLAST score 183



E value 2.0e-13 Match length 126 % identity 34

NCBI Description (AB007931) KIAA0462 protein [Homo sapiens]

Seq. No. 21650

Contig ID 85469\_1.R1040 5'-most EST uC-gmronoir053g02b1

Method BLASTX
NCBI GI g1360141
BLAST score 176
E value 1.0e-12
Match length 119
% identity 34

NCBI Description (X97980) protein kinase [Solanum berthaultii]

Seq. No. 21651

Contig ID 85482\_1.R1040 5'-most EST eep700869385.h1 Method BLASTX

NCBI GI g4455153
BLAST score 332
E value 1.0e-30
Match length 139
% identity 50

NCBI Description (AL022198) putative protein [Arabidopsis thaliana]

Seq. No. 21652

Contig ID 85484 1.R1040

5'-most EST LIB3139-118-P1-N1-C6

Method BLASTN
NCBI GI g3510343
BLAST score 35
E value 4.0e-10
Match length 43
% identity 95

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MJC20, complete sequence [Arabidopsis thaliana]

Seq. No. 21653

Contig ID 85485\_1.R1040 5'-most EST zzp700833901.h1

Method BLASTX
NCBI GI g3355480
BLAST score 184
E value 2.0e-13
Match length 74
% identity 46

NCBI Description (AC004218) Medicago nodulin N21-like protein [Arabidopsis

thaliana]

Seq. No. 21654

Contig ID 85492\_1.R1040

5'-most EST LIB3139-118-P1-N1-D8

Seq. No. 21655

Contig ID 85493 1.R1040



```
5'-most EST
                  LIB3139-118-P1-N1-D9
Method
                  BLASTX
NCBI GI
                  a3399767
BLAST score
                  261
                  1.0e-22
E value
Match length
                  114
% identity
                  41
NCBI Description
                 (U76298) uclacyanin I [Arabidopsis thaliana] >qi 3831466
                  (AC005700) uclacyanin I [Arabidopsis thaliana]
                  21656
Seq. No.
Contig ID
                  85560 1.R1040
5'-most EST
                  q4284159
Method
                  BLASTX
NCBI GI
                  g3193296
BLAST score
                  285
                  2.0e-25
E value
Match length
                  107
% identity
                  57
NCBI Description (AF069298) similar to pectinesterase [Arabidopsis thaliana]
                  21657
Seq. No.
                  85562 1.R1040
Contig ID
5'-most EST
                  k1170\overline{1}212445.h1
Method
                  BLASTX
                  q3152587
NCBI GI
BLAST score
                  833
E value
                  2.0e-89
Match length
                  261
                  45
% identity
NCBI Description (AC002986) Similar to CREB-binding protein homolog
                  gb_U88570 from D. melanogaster and contains similarity to
                  callus-associated protein gb U01961 from Nicotiana tabacum.
                  EST gb W43427 comes from this gene. [Arabidopsis thaliana]
                  21658
Seq. No.
                  85590 1.R1040
Contig ID
5'-most EST
                  bth700846743.h1
Method
                  BLASTX
NCBI GI
                  q2842490
BLAST score
                  257
E value
                  5.0e-22
Match length
                  112
% identity
                  59
NCBI Description (AL021749) heat-shock protein [Arabidopsis thaliana]
Seq. No.
                  21659
                  85608 1.R1040
Contig ID
5'-most EST
                  uC-gmflminsoy098f03b1
Method
                  BLASTX
NCBI GI
                  g1170621
BLAST score
                  368
```

E value 4.0e-35 99

Match length % identity 70

NCBI Description KINESIN-LIKE PROTEIN C >gi 1084342 pir S48020 kinesin-related protein katC - Arabidopsis thaliana



>gi\_1438844\_dbj\_BAA04674\_ (D21138) heavy chain polypeptide
of kinesin-like protein [Arabidopsis thaliana]

Seq. No. 21660
Contig ID 85621\_1.R1040
5'-most EST LIB3139-120-P1-N1-C3
Seq. No. 21661

Seq. No. Contig ID 85641 1.R1040 5'-most EST q5752<del>5</del>31 Method BLASTX NCBI GI q3482974 BLAST score 269 E value 3.0e-23 105 Match length 52 % identity

NCBI Description (AL031369) ATP-dependent Clp proteinase-like protein

[Arabidopsis thaliana]

Seq. No. 21662

Contig ID 85664\_1.R1040 5'-most EST bth700848892.h1

Seq. No. 21663

Contig ID 85671\_1.R1040

5'-most EST uC-gmrominsoy048a10b1

Seq. No. 21664

Contig ID 85678 1.R1040

5'-most EST LIB3139-121-P1-N1-C10

Method BLASTX
NCBI GI g1168782
BLAST score 218
E value 2.0e-17
Match length 67
% identity 44

NCBI Description CALCIUM-BINDING PROTEIN CAST >gi\_169481 (L02830)

calcium-binding protein [Solanum tuberosum]

Seq. No. 21665

Contig ID 85683\_1.R1040 5'-most EST zhf700960813.h1

Method BLASTX
NCBI GI g2497542
BLAST score 1673
E value 0.0e+00
Match length 527
% identity 76

NCBI Description PYRUVATE KINASE, CHLOROPLAST ISOZYME G PRECURSOR

>gi\_629696\_pir\_\_S44287 pyruvate kinase, plastid - common
tobacco >gi\_482938\_emb\_CAA82223\_ (Z28374) Pyruvate kinase;

plastid isozyme [Nicotiana tabacum]

Seq. No. 21666

Contig ID 85711\_1.R1040 5'-most EST jex700903565.h1

Method BLASTX

3482



```
NCBI GI
                  g2661412
BLAST score
                  216
E value
                  1.0e-33
Match length
                  162
                  59
% identity
NCBI Description (AJ000728) MAP kinase kinase [Lycopersicon esculentum]
                  21667
Seq. No.
Contig ID
                  85717_1.R1040
                  uC-gmflminsoy037a03b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g4262186
BLAST score
                  799
                  1.0e-85
E value
                  196
Match length
                  79
% identity
NCBI Description (AC005508) Highly similar to cullin 3 [Arabidopsis
                  thaliana]
                  21668
Seq. No.
Contig ID
                  85718 1.R1040
5'-most EST
                  uC-gmrominsoy070g12b1
Method
                  BLASTX
                  g1402886
NCBI GI
                  924
BLAST score
E value
                  1.0e-100
Match length
                  236
% identity
                  74
NCBI Description (X98130) unknown [Arabidopsis thaliana]
                  21669
Seq. No.
Contig ID
                  85745 1.R1040
5'-most EST
                  LIB3139-122-P1-N1-B4
Method
                  BLASTX
NCBI GI
                  g2642158
BLAST score
                  249
E value
                  4.0e-21
Match length
                  51
% identity
                  86
NCBI Description (AC003000) hypothetical protein [Arabidopsis thaliana]
                  21670
Seq. No.
                  85745 2.R1040
Contig ID
5'-most EST
                  jex700905378.hl
Seq. No.
                  21671
Contig ID
                  85749 1.R1040
5'-most EST
                  gsv701056504.hl
Method
                  BLASTX
NCBI GI
                  q3068704
BLAST score
                  639
E value
                  5.0e-67
Match length
                  137
% identity
NCBI Description (AF049236) unknown [Arabidopsis thaliana]
```

21672

Seq. No.

Contig ID

5'-most EST

21680

85821 1.R1040

 $asn70\overline{1}138644.h1$ 

4.00 A4 (12)



```
Contig ID
                  85758 1.R1040
                  kl1701213348.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q3122313
BLAST score
                  234
                  2.0e-19
E value
Match length
                  89
                  54
% identity
NCBI Description LEC14B HOMOLOG >gi_2351587 (U82760) LEC14B homolog [Prunus
                  armeniaca]
                  21673
Seq. No.
                  85772 1.R1040
Contig ID
5'-most EST
                  LIB3139-122-P1-N1-E9
                  BLASTX
Method
NCBI GI
                  g2281115
BLAST score
                  693
E value
                  9.0e-73
Match length
                  336
% identity
                   65
NCBI Description (AC002330) putative cullin-like 1 protein [Arabidopsis
                  thaliana]
Seq. No.
                  21674
Contig ID
                  85783 1.R1040
5'-most EST
                  leu701151060.h1
Seq. No.
                   21675
                  85786 1.R1040
Contig ID
5'-most EST
                  g5058118
Seq. No.
                  21676
                  85787 1.R1040
Contig ID
                  LIB3170-050-Q1-J1-A4
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2980806
BLAST score
                  199
E value
                  2.0e-15
Match length
                  59
% identity
                  58
NCBI Description (AL022197) putative protein [Arabidopsis thaliana]
Seq. No.
                  21677
                  85803 1.R1040
Contig ID
5'-most EST
                  LIB3167-023-P4-K4-H2
Seq. No.
                  21678
                   85817 1.R1040
Contig ID
5'-most EST
                  hyd700728723.h1
Seq. No.
                   21679
Contig ID
                  85817 2.R1040
5'-most EST
                  g4405<del>6</del>96
```



```
Method BLASTX
NCBI GI g4539418
BLAST score 406
E value 1.0e-39
Match length 125
% identity 68
```

NCBI Description (AL049171) caffeoyl-CoA O-methyltransferase-like protein

[Arabidopsis thaliana]

Seq. No. 21681

Contig ID 85824 1.R1040 5'-most EST hrw701057807.h1

Seq. No. 21682

Contig ID 85824 2.R1040 5'-most EST kll701215417.h1

Seq. No. 21683

Contig ID 85894\_1.R1040

5'-most EST LIB3167-002-Q1-K1-E6

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 9.0e-11
Match length 36
% identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 21684

Contig ID 85915\_1.R1040 5'-most EST pxt700942694.h1

Method BLASTX
NCBI GI g2129473
BLAST score 214
E value 3.0e-17
Match length 77
% identity 53

NCBI Description arabinogalactan-like protein - loblolly pine >gi\_607774

(U09556) arabinogalactan-like protein [Pinus taeda]

Seq. No. 21685

Contig ID 85951\_1.R1040 5'-most EST uC-gmropic074f03b1

Method BLASTX
NCBI GI g3193287
BLAST score 325
E value 5.0e-30
Match length 80
% identity 66

NCBI Description (AF069298) Arabidopsis predicted protein of unknown

function T10P11.19 (GB:AC002330) [Arabidopsis thaliana]

Seq. No. 21686

Contig ID 85953 1.R1040

5'-most EST LIB3167-004-P1-K1-C7

Seq. No. 21687



Contig ID 85991\_1.R1040

5'-most EST uC-gmflminsoy028e02b1

Method BLASTX
NCBI GI g2244929
BLAST score 254
E value 1.0e-21
Match length 164
% identity 38

NCBI Description (297339) unnamed protein product [Arabidopsis thaliana]

Seq. No. 21688

Contig ID 86002\_1.R1040
5'-most EST 94397455
Method BLASTX
NCBI GI 94567310
BLAST score 262
E value 2.0e-22
Match length 62
% identity 81

NCBI Description (AC005956) unknown protein [Arabidopsis thaliana]

Seq. No. 21689

Contig ID 86018 1.R1040

5'-most EST LIB3167-010-P1-K1-B9

Seq. No. 21690

Contig ID 86026 1.R1040

5'-most EST uC-gmflminsoy089c05b1

Method BLASTX
NCBI GI g4510426
BLAST score 824
E value 3.0e-88
Match length 325
% identity 54

NCBI Description (AC006929) hypothetical protein [Arabidopsis thaliana]

Seq. No. 21691

Contig ID 86046\_1.R1040

5'-most EST jC-gmle01810013e07d1

Seq. No. 21692

Contig ID 86065\_1.R1040 5'-most EST kmv700742883.h1

Seq. No. 21693

Contig ID 86067 1.R1040

5'-most EST LIB3167-010-P1-K1-H4

Seq. No. 21694

Contig ID 86097\_1.R1040 5'-most EST kmv700738073.h1

Seq. No. 21695

Contig ID 86124 1.R1040

5'-most EST LIB3167-017-P1-K1-A3

Seq. No. 21696



Contig ID 86148\_1.R1040 5'-most EST sat701004377.h1

Method BLASTX
NCBI GI g3831447
BLAST score 146
E value 8.0e-09
Match length 112
% identity 34

NCBI Description (AC005819) putative extensin [Arabidopsis thaliana] >gi\_4415943\_gb\_AAD20173\_ (AC006418) putative extensin

[Arabidopsis thaliana]

Seq. No. 21697

Contig ID 86159 1.R1040

5'-most EST jC-gmfl02220061a09d1

Seq. No. 21698

Contig ID 86180 1.R1040

5'-most EST jC-gmro02910005f03a1

Seq. No. 21699

Contig ID 86206 1.R1040

5'-most EST LIB3167-019-P1-K1-B7

Method BLASTX
NCBI GI g1168646
BLAST score 331
E value 1.0e-30
Match length 179
% identity 36

NCBI Description GTP-BINDING PROTEIN ERA HOMOLOG (BEX PROTEIN) >gi\_606745

(U18532) Bex [Bacillus subtilis] >gi\_1303826\_dbj\_BAA12482 (D84432) YqfH [Bacillus subtilis] >gi\_2634961\_emb\_CAB14458\_

(Z99116) GTP-binding protein [Bacillus subtilis]

>gi\_2634975\_emb\_CAB14471\_ (Z99117) GTP-binding protein

[Bacillus subtilis]

Seq. No. 21700

Contig ID 86224 1.R1040

5'-most EST jC-gmle01810018e12a2

Seq. No. 21701

Contig ID 86224\_2.R1040

5'-most EST LIB3167-019-P1-K1-F1

Seq. No. 21702

Contig ID 86255\_1.R1040

5'-most EST LIB3167-027-P1-K1-B8

Method BLASTX
NCBI GI g4469021
BLAST score 635
E value 3.0e-66
Match length 160
% identity 77

NCBI Description (AL035602) hypothetical protein [Arabidopsis thaliana]

Seq. No. 21703

Contig ID 86260 1.R1040

Match length

% identity

131

40



```
5'-most EST
                  LIB3167-027-P1-K1-C2
                  21704
Seq. No.
Contig ID
                  86268 1.R1040
5'-most EST
                  asn701138159.hl
Method
                  BLASTX
NCBI GI
                  q4220524
BLAST score
                  192
E value
                  2.0e-14
Match length
                  106
% identity
                  51
NCBI Description (AL035356) putative protein [Arabidopsis thaliana]
Seq. No.
                  86273 1.R1040
Contig ID
5'-most EST
                  g5606747
Seq. No.
                  21706
                  86287 1.R1040
Contig ID
5'-most EST
                  LIB3167-027-P1-K1-F11
Seq. No.
                  21707
Contig ID
                  86291 1.R1040
5'-most EST
                  leu701149474.hl
Method
                  BLASTN
NCBI GI
                  g2224728
BLAST score
                  105
                  7.0e-52
E value
Match length
                  271
% identity
                  87
NCBI Description Vigna radiata mRNA for Aux22c, complete cds
Seq. No.
                  21708
Contig ID
                  86314 1.R1040
                  LIB3167-029-P1-K1-A4
5'-most EST
Seq. No.
                  21709
Contig ID
                  86328 1.R1040
5'-most EST
                  LIB3167-029-P1-K1-B4
                  21710
Seq. No.
Contig ID
                  86335 1.R1040
5'-most EST
                  LIB3167-029-P1-K1-C11
                  21711
Seq. No.
                  86339 1.R1040
Contig ID
5'-most EST
                  LIB3167-029-P1-K1-C5
Seq. No.
                  21712
Contig ID
                  86355 1.R1040
5'-most EST
                  LIB3167-029-P1-K1-E1
Method
                  BLASTX
                  g3912926
NCBI GI
BLAST score
                  160
E value
                  2.0e-10
```

NCBI Description (AF001308) drought-induced-19-like 1 [Arabidopsis thaliana]

Seq. No. 21713

Contig ID 86369\_1.R1040 5'-most EST eep700863812.h1

Seq. No. 21714

Contig ID 86381 1.R1040

5'-most EST LIB3167-029-P1-K1-G4

Seq. No. 21715

Contig ID 86384 1.R1040

5'-most EST g5509008

Seq. No. 21716

Contig ID 86412 1.R1040

5'-most EST LIB3167-031-P1-K1-B6

Method BLASTX
NCBI GI g4204315
BLAST score 357
E value 7.0e-34
Match length 105
% identity 61

NCBI Description (AC003027) Unknown protein [Arabidopsis thaliana]

Seq. No. 21717

Contig ID 86415\_1.R1040

5'-most EST LIB3167-031-P1-K1-C1

Method BLASTN
NCBI GI g3413169
BLAST score 37
E value 2.0e-11
Match length 61
% identity 90

NCBI Description Cicer arietinum mRNA for 40S ribosomal protein S6, partial

Seq. No. 21718

Contig ID 86426\_1.R1040

5'-most EST LIB3167-031-P1-K1-C9

Seq. No. 21719

Contig ID 86431 1.R1040

5'-most EST LIB3167-031-P1-K1-D2

Seq. No. 21720

Contig ID 86453\_1.R1040

5'-most EST jC-gmst02400036d10a1

Seq. No. 21721

Contig ID 86458 1.R1040

5'-most EST jC-gmst02400025e07a1

Method BLASTX
NCBI GI g3152582
BLAST score 268
E value 2.0e-23
Match length 140
% identity 43



NCBI Description (AC002986) YUP8H12R.20 [Arabidopsis thaliana]

Seq. No. 21722

Contig ID 86467\_1.R1040 5'-most EST zhf700954552.h1

Method BLASTX
NCBI GI g2655008
BLAST score 319
E value 3.0e-29
Match length 123
% identity 51

NCBI Description (AF017144) (1-4)-beta-mannan endohydrolase [Lycopersicon

esculentum]

Seq. No. 21723

Contig ID 86481 1.R1040 5'-most EST leu701154685.h1

Method BLASTX
NCBI GI g4467130
BLAST score 526
E value 1.0e-101
Match length 248
% identity 77

NCBI Description (AL035538) glycosyltransferase like protein [Arabidopsis

thaliana]

Seq. No. 21724

Contig ID 86485 1.R1040 5'-most EST epx701105561.h1

Method BLASTX
NCBI GI g4508069
BLAST score 231
E value 6.0e-19
Match length 148
% identity 38

NCBI Description (AC005882) 12246 [Arabidopsis thaliana]

Seq. No. 21725

Contig ID 86497\_1.R1040 5'-most EST vzy700751850.h1

Method BLASTX
NCBI GI g2132018
BLAST score 214
E value 5.0e-17
Match length 105
% identity 46

NCBI Description hypothetical protein YOL135c - yeast (Saccharomyces

cerevisiae) >gi\_1420026\_emb\_CAA99156\_ (Z74877) ORF YOL135c

[Saccharomyces cerevisiae] >gi 1628440 emb CAA64734\_

(X95465) ORF [Saccharomyces cerevisiae]

Seq. No. 21726

Contig ID 86501 1.R1040 5'-most EST ssr700559764.h1

Method BLASTX NCBI GI g4490706 BLAST score 582



E value 4.0e-60 Match length 182 67

% identity NCBI Description (AL035680) putative protein [Arabidopsis thaliana]

21727 Seq. No.

86511 1.R1040 Contig ID 5'-most EST kl1701208626.hl

21728 Seq. No.

86531 1.R1040 Contig ID

5'-most EST LIB3167-038-P1-K1-H10

Seq. No. 21729

86574 1.R1040 Contig ID

5'-most EST LIB3170-039-Q1-K2-E11

Method BLASTX NCBI GI g3063439 BLAST score 448 E value 4.0e-44 119 Match length 76 % identity

NCBI Description (AC003981) F22013.1 [Arabidopsis thaliana]

Seq. No. 21730

86582 2.R1040 Contig ID 5'-most EST uaw700660977.hl

21731 Seq. No.

86582 3.R1040 Contig ID 5'-most EST wrg700786643.hl

21732 Seq. No.

86587 1.R1040 Contig ID 5'-most EST zhf700951882.h1

21733 Seq. No.

86605 1.R1040 Contig ID 5'-most EST g5666932 Method BLASTX g1362056 NCBI GI BLAST score 268 2.0e-23 E value

Match length 92 55 % identity

NCBI Description trypsin inhibitor precursor (clone ATI21) - alfalfa

>gi\_509374\_emb\_CAA56254\_ (X79880) serine proteinase
inhibitor [Medicago sativa]

21734 Seq. No.

Contig ID 86613 1.R1040 5'-most EST epx701106478.hl

BLASTX Method NCBI GI q3006152 BLAST score 156 E value 3.0e-10 Match length 108



% identity 37
NCBI Description (AL022299) hypothetical protein [Schizosaccharomyces pombe]

Seq. No. 21735

Contig ID 86613 2.R1040 5'-most EST epx701109254.h1

Seq. No. 21736

Contig ID 86614 1.R1040

5'-most EST LIB3167-049-P1-K1-D6

Method BLASTX
NCBI GI g2129516
BLAST score 382
E value 1.0e-36
Match length 154
% identity 48

NCBI Description 1-aminocyclopropane-1-carboxylate oxidase homolog (clone

2A6) - Arabidopsis thaliana >gi\_599622\_emb\_CAA58151\_

(X83096) 2A6 [Arabidopsis thaliana] >gi 2809261 (AC002560)

F21B7.30 [Arabidopsis thaliana]

Seq. No. 21737

Contig ID 86627 1.R1040

5'-most EST LIB3167-049-P1-K1-F1

Seq. No. 21738

Contig ID 86638\_1.R1040 5'-most EST awf700837485.h1

Seq. No. 21739

Contig ID 86652 1.R1040 5'-most EST gsv70\overline{1}047912.h1

Seq. No. 21740

Contig ID 86662 1.R1040 5'-most EST jsh701066581.h1

Method BLASTX
NCBI GI g1708462
BLAST score 542
E value 2.0e-55
Match length 140
% identity 70

NCBI Description IAA-AMINO ACID HYDROLASE HOMOLOG 2 PRECURSOR >gi\_902791

(U23796) ILL2 [Arabidopsis thaliana]

Seq. No. 21741

Contig ID 86695 1.R1040

5'-most EST LIB3167-050-P1-K1-D8

Seq. No. 21742

Contig ID 86698\_1.R1040 5'-most EST 2hf700951984.h1

Method BLASTX
NCBI GI g2497486
BLAST score 268
E value 2.0e-23
Match length 64



% identity 81
NCBI Description URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP
KINASE) >gi\_2121275 (AF000147) UMP/CMP kinase [Arabidopsis
thaliana]

Seq. No. 21743

Contig ID 86699 1.R1040

5'-most EST jC-gmro02910021f11a1

Method BLASTX
NCBI GI g4105798
BLAST score 263
E value 9.0e-23
Match length 138
% identity 41

NCBI Description (AF049930) PGP237-11 [Petunia x hybrida]

Seq. No. 21744

Contig ID 86702\_1.R1040 5'-most EST wvk700683119.h1

Seq. No. 21745

Contig ID 86705\_1.R1040

5'-most EST jC-gmro02800031h11a1

Seq. No. 21746

Contig ID 86712\_1.R1040

5'-most EST LIB3167-050-P1-K1-F5

Seq. No. 21747

Contig ID 86720\_1.R1040 5'-most EST dpv701100978.h1

Method BLASTX
NCBI GI g1039318
BLAST score 208
E value 1.0e-16
Match length 70
% identity 56

NCBI Description (Z30093) basic transcription factor 2, 35 kD subunit [Homo

sapiens] >gi\_4504199\_ref\_NP\_001507.1\_pGTF2H3\_ general
transcription factor IIH, polypeptide 3 (34kD subunit)

Seq. No. 21748

Contig ID 86721 1.R1040

5'-most EST LIB3167-050-P1-K1-G4

Seq. No. 21749

Contig ID 86727\_1.R1040 5'-most EST kl1701214673.h1

Method BLASTX
NCBI GI g1084397
BLAST score 360
E value 3.0e-34
Match length 133
% identity 58

NCBI Description P541 protein - Pepper >gi\_840729\_emb\_CAA54961\_ (X78030) putative chromoplastic oxydo-reductase [Capsicum annuum]



Contig ID 86827\_1.R1040 5'-most EST zsg701118635.h1

Seq. No. 21751

Contig ID 86864\_1.R1040 5'-most EST jsh701065633.h1

Method BLASTX
NCBI GI g2459435
BLAST score 451
E value 6.0e-45
Match length 135
% identity 65

NCBI Description (AC002332) putative serine carboxypeptidase [Arabidopsis

thaliana]

Seq. No. 21752

Contig ID 86868 1.R1040

5'-most EST LIB3167-077-P1-K2-F5

Seq. No. 21753

Contig ID 86871 1.R1040

5'-most EST jC-gmro02910062e11a1

Method BLASTX
NCBI GI g3335378
BLAST score 513
E value 6.0e-57
Match length 162

% identity 65

NCBI Description (AC003028) Myb-related transcription activator [Arabidopsis

thaliana]

Seq. No. 21754

Contig ID 86873\_1.R1040 5'-most EST txt700734516.h1

Seq. No. 21755

Contig ID 86950\_1.R1040 5'-most EST kl1701212701.h1

Method BLASTX
NCBI GI g1730910
BLAST score 176
E value 1.0e-12
Match length 136
% identity 40

NCBI Description HYPOTHETICAL 23.1 KD PROTEIN IN BSAA-ILVD INTERGENIC REGION

>gi\_1256633 (L77246) putative [Bacillus subtilis]

>gi 2634609 emb CAB14107 (Z99115) similar to hypothetical

proteins [Bacillus subtilis]

Seq. No. 21756

Contig ID 86951\_1.R1040

5'-most EST LIB3167-078-P1-K2-A8

Method BLASTX
NCBI GI g2827282
BLAST score 189
E value 6.0e-14



Match length 111 % identity 37

NCBI Description (AF040701) TATA binding protein associated factor [Homo

sapiens]

Seq. No. 21757

Contig ID 86957\_1.R1040 5'-most EST uC-gmropic097d12b1

Seq. No. 21758

Contig ID 86978\_1.R1040

5'-most EST LIB3167-078-P1-K2-D7

Method BLASTX
NCBI GI g4455198
BLAST score 440
E value 3.0e-43
Match length 177
% identity 56

NCBI Description (AL035440) putative protein [Arabidopsis thaliana]

Seq. No. 21759

Contig ID 86980\_1.R1040 5'-most EST zhf700956702.h1

Method BLASTX
NCBI GI g3250695
BLAST score 172
E value 4.0e-12
Match length 65
% identity 54

NCBI Description (AL024486) putative protein [Arabidopsis thaliana]

Seq. No. 21760

Contig ID 86980 2.R1040

5'-most EST jC-qmro02910039c04a1

Seq. No. 21761

Contig ID 86995\_1.R1040

5'-most EST LIB3170-017-Q1-J1-B9

Method BLASTX
NCBI GI 94455365
BLAST score 282
E value 4.0e-25
Match length 59
% identity 80

NCBI Description (AL035524) putative protein [Arabidopsis thaliana]

Seq. No. 21762

Contig ID 86997 1.R1040

5'-most EST LIB3167-078-P1-K2-F8

Seq. No. 21763

Contig ID 87033\_1.R1040

5'-most EST LIB3170-001-Q1-J1-A3

Method BLASTX
NCBI GI g4006827
BLAST score 233
E value 8.0e-23



Match length 92 % identity 65

NCBI Description (AC005970) subtilisin-like protease [Arabidopsis thaliana]

Seq. No. 21764

Contig ID 87035\_1.R1040

5'-most EST LIB3170-001-Q1-J1-A8

Method BLASTX
NCBI GI g3915194
BLAST score 183
E value 3.0e-13
Match length 120
% identity 38

NCBI Description HYPOTHETICAL TRANSTHYRETIN-LIKE PROTEIN R09H10.3 IN

CHROMOSOME IV >gi\_3879090\_emb\_CAB00872\_ (Z77134) Similarity

to Sheep transthyretin precursor (SW:TTHY\_SHEEP)

[Caenorhabditis elegans]

Seq. No. 21765

Contig ID 87036\_1.R1040

5'-most EST jC-gmle01810063f02d1

Method BLASTX
NCBI GI g3335374
BLAST score 353
E value 2.0e-33
Match length 78
% identity 82

NCBI Description (AC003028) glutaredoxin-like protein [Arabidopsis thaliana]

Seq. No. 21766

Contig ID 87049\_1.R1040

5'-most EST LIB3170-001-Q1-J1-D3

Method BLASTX
NCBI GI g3831471
BLAST score 552
E value 2.0e-56
Match length 160
% identity 60

NCBI Description (AC005700) hypothetical protein [Arabidopsis thaliana]

Seq. No. 21767

Contig ID 87101\_1.R1040

5'-most EST LIB3170-001-Q1-K1-E11

Seq. No. 21768

Contig ID 87132\_1.R1040

5'-most EST LIB3170-002-Q1-J1-A8

Seq. No. 21769

Contig ID 87150\_2.R1040 5'-most EST fC-gmse700839380b1

Method BLASTX
NCBI GI g4006829
BLAST score 470
E value 7.0e-67
Match length 212
% identity 62



```
NCBI Description (AC005970) putative protein kinase [Arabidopsis thaliana]
Seq. No.
                  21770
Contig ID
                  87150 3.R1040
                  LIB3170-037-Q1-J1-F1
5'-most EST
                  21771
Seq. No.
                  87219 1.R1040
Contig ID
                  LIB3170-003-Q1-J1-A12
5'-most EST
Method
                  BLASTX
                  g2342683
NCBI GI
BLAST score
                  721
                  2.0e-76
E value
                  144
Match length
                  88
% identity
                  (ACO00106) Contains similarity to Bos beta-mannosidase
NCBI Description
                   (gb_U46067). [Arabidopsis thaliana]
                  21772
Seq. No.
                  87225 1.R1040
Contig ID
5'-most EST
                  zsg701118819.h1
Method
                  BLASTX
                  g3769673
NCBI GI
BLAST score
                   503
                  8.0e-51
E value
Match length
                  115
                  76
% identity
                  (AF095285) Tic20 [Pisum sativum]
NCBI Description
                   21773
Seq. No.
                   87229 1.R1040
Contig ID
                   LIB3170-003-Q1-J1-B4
5'-most EST
                   BLASTX
Method
                   g2769642
NCBI GI
BLAST score
                   223
                   4.0e-18
E value
                   60
Match length
                   67
% identity
                   (Z97215) nine-cis-epoxycarotenoid dioxygenase [Lycopersicon
NCBI Description
                   esculentum]
                   21774
Seq. No.
                   87243 1.R1040
Contig ID
                   jC-gmle01810064c12d1
5'-most EST
                   21775
Seq. No.
                   87244 1.R1040
Contig ID
5'-most EST
                   LIB3170-006-Q1-J1-D11
                   21776
Seq. No.
                   87257 1.R1040
```

Contig ID

LIB3170-003-Q1-K1-G12 5'-most EST

21777 Seq. No.

87264 1.R1040 Contig ID

LIB3170-003-Q1-J1-H7 5'-most EST



```
21778
Seq. No.
Contig ID
                  87266 1.R1040
5'-most EST
                  LIB3170-042-Q1-J1-H9
Seq. No.
                  21779
                  87352 1.R1040
Contig ID
                   jC-gmf102220073a03d1
5'-most EST
                  BLASTX
Method
                  g2760839
NCBI GI
BLAST score
                  174
                   2.0e-12
E value
Match length
                  83
% identity
                  (AC003105) putative receptor kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   21780
                   87358 1.R1040
Contig ID
5'-most EST
                   fua701036931.h1
                  BLASTX
Method
                   g1209756
NCBI GI
BLAST score
                   179
                   6.0e-13
E value
Match length
                   48
% identity
                   71
                  (U43629) integral membrane protein [Beta vulgaris]
NCBI Description
                   21781
Seq. No.
                   87367 1.R1040
Contig ID
                  LIB3170-004-Q1-J1-F3
5'-most EST
Seq. No.
                   21782
                   87376 1.R1040
Contig ID
                   LIB3170-004-Q1-K1-H6
5'-most EST
Seq. No.
                   21783
                   87449 1.R1040
Contig ID
5'-most EST
                   LIB3170-012-Q1-J1-B4
                   21784
Seq. No.
Contig ID
                   87464 1.R1040
                   LIB3170-005-Q1-J1-E10
5'-most EST
Seq. No.
                   21785
Contig ID
                   87465 1.R1040
5'-most EST
                   LIB3170-005-Q1-J1-E2
Method
                   BLASTX
                   g2583135
NCBI GI
BLAST score
                   150
E value
                   1.0e-09
                   50
Match length
```

% identity 64

(AC002387) hypothetical protein [Arabidopsis thaliana] NCBI Description

>gi\_3822216 (AF074948) FIL [Arabidopsis thaliana]

>gi\_4322477\_gb\_AAD16053 (AF087015) abnormal floral organs

protein [Arabidopsis thaliana]

Seq. No. 21786



Contig ID 87478\_1.R1040

5'-most EST LIB31 $\overline{7}$ 0-005-Q1-J1-F5

Method BLASTX
NCBI GI g1352439
BLAST score 279
E value 8.0e-25
Match length 73
% identity 70

NCBI Description EUKARYOTIC TRANSLATION INITIATION FACTOR 5 (EIF-5)

>gi 1008881 (L47221) eukaryotic initiation factor 5

[Phaseolus vulgaris]

Seq. No. 21787

Contig ID 87492 1.R1040

5'-most EST LIB3170-005-Q1-J1-H8

Seq. No. 21788

Contig ID 87501 1.R1040

5'-most EST LIB3170-005-Q1-K1-B4

Seq. No. 21789

Contig ID 87520 1.R1040

5'-most EST uC-gmflminsoy042a04b1

Seq. No. 21790

Contig ID 87520\_2.R1040 5'-most EST gsv701049687.h1

Seq. No. 21791

Contig ID 87598 1.R1040

5'-most EST LIB3170-006-Q1-J1-H6

Seq. No. 21792

Contig ID 87620\_1.R1040

5'-most EST LIB3170-006-Q1-K1-E4

Method BLASTX
NCBI GI g2062167
BLAST score 444
E value 5.0e-44
Match length 133
% identity 65

NCBI Description (AC001645) Proline-rich protein APG isolog [Arabidopsis

thaliana]

Seq. No. 21793

Contig ID 87644 1.R1040

5'-most EST LIB3170-007-Q1-J1-A4

Seq. No. 21794

Contig ID 87662\_1.R1040

5'-most EST LIB3170-007-Q1-K1-D5

Seq. No. 21795

Contig ID 87706 1.R1040

5'-most EST LIB3170-007-Q1-K1-D12

Method BLASTN NCBI GI g3641869



BLAST score E value 4.0e-26 Match length 98 91 % identity

NCBI Description Cicer arietinum epicotyl EST, clone Can133

Seq. No. 21796

Contig ID 87744 1.R1040

5'-most EST LIB3170-009-Q1-J1-E10

Method BLASTN NCBI GI g498788 BLAST score 97 4.0e-47 E value Match length 197 % identity 87

NCBI Description S.tuberosum (Desiree) cycl II mRNA. for cytochrome c1

Seq. No. 21797

Contig ID 87754 1.R1040

5'-most EST LIB3170-009-Q2-K1-A4

Seq. No. 21798

Contig ID 87785 1.R1040 5'-most EST  $leu70\overline{1}147452.h1$ 

Seq. No. 21799

Contig ID 87918 1.R1040

5'-most EST LIB3170-010-Q1-J1-B4

Method BLASTX NCBI GI q4467130 BLAST score 158 2.0e-10 E value Match length 40 % identity 75

NCBI Description (AL035538) glycosyltransferase like protein [Arabidopsis

thaliana]

Seq. No. 21800

Contig ID 87940 1.R1040

5'-most EST LIB3170-010-Q1-J1-F12

Seq. No. 21801

Contig ID 88008 1.R1040

5'-most EST LIB3170-011-Q1-J1-A5

Seq. No. 21802

Contig ID 88040 1.R1040 5'-most EST g5057504 Method BLASTX NCBI GI g3063450 BLAST score 501 E value 2.0e-50 Match length 133

% identity 69

NCBI Description (AC003981) F22013.12 [Arabidopsis thaliana]

Seq. No. 21803

Contig ID 5'-most EST

21813

88237 1.R1040

jC-gmf102220131a10a1



```
Contig ID
                  88051 1.R1040
5'-most EST
                  LIB3170-011-Q1-J1-H7
Method
                  BLASTX
NCBI GI
                  g4249418
BLAST score
                  235
                  2.0e-19
E value
Match length
                  74
% identity
                  19
NCBI Description (AC006072) putative zinc-finger protein (C-x8-C-x5-C-x3-H
                  type domains), 5' partial [Arabidopsis thaliana]
Seq. No.
                  21804
                  88052 1.R1040
Contig ID
5'-most EST
                  jC-gmst02400049h04d1
Seq. No.
                  21805
                  88110 1.R1040
Contig ID
5'-most EST
                  LIB3170-012-Q1-J1-A6
Seq. No.
                  21806
Contig ID
                  88118 1.R1040
5'-most EST
                  LIB3170-012-Q1-J1-B8
Seq. No.
                  21807
Contig ID
                  88128 1.R1040
5'-most EST
                  LIB3170-012-Q1-J1-D2
                  21808
Seq. No.
Contig ID
                  88131 1.R1040
5'-most EST
                  fC-gmle700556983b1
Seq. No.
                  21809
Contig ID
                  88153 1.R1040
5'-most EST
                  LIB3170-012-Q1-J1-H6
Seq. No.
                  21810
Contig ID
                  88162 1.R1040
5'-most EST
                  trc700563819.h1
Seq. No.
                  21811
Contig ID
                  88217 1.R1040
5'-most EST
                  jsh701070009.h2
Seq. No.
                  21812
                  88233 1.R1040
Contig ID
5'-most EST
                  LIB3170-013-Q1-J1-E3
Method
                  BLASTX
NCBI GI
                  g3415117
BLAST score
                  327
E value
                  5.0e-31
Match length
                  70
% identity
                  47
NCBI Description (AF081203) villin 3 [Arabidopsis thaliana]
```



```
Seq. No.
                  21814
Contig ID
                  88247 1.R1040
5'-most EST
                  LIB3170-026-Q1-J1-H9
Method
                  BLASTX
NCBI GI
                  g629561
BLAST score
                  377
E value
                  4.0e-36
Match length
                  115
% identity
                  58
NCBI Description SRG1 protein - Arabidopsis thaliana
                  >gi 479047 emb CAA55654 (X79052) SRG1 [Arabidopsis
                  thaliana]
Seq. No.
                  21815
Contig ID
                  88248 1.R1040
                  LIB3170-013-Q1-J1-G12
5'-most EST
```

Contig ID 88255 1.R1040

5'-most EST LIB3170-013-Q1-J1-H10

Method BLASTX NCBI GI g3122254 BLAST score 189 E value 2.0e-14 Match length 48 % identity 73

NCBI Description EUKARYOTIC TRANSLATION INITIATION FACTOR 6 (EIF-6)

>gi 2642164 (AC003000) hypothetical protein [Arabidopsis

thaliana]

Seq. No. 21817

Contig ID 88305 1.R1040

5'-most EST LIB3170-013-Q1-K1-G12

Method BLASTX NCBI GI g3037045 170 BLAST score E value 1.0e-11 192 Match length 26 % identity

NCBI Description (AF052621) hypothetical protein COX4AL [Mus musculus]

Seq. No. 21818

Contiq ID 88327 1.R1040 5'-most EST jsh701065732.h1

21819 Seq. No.

88344 1.R1040 Contig ID

5'-most EST LIB3170-014-Q1-J1-E6

Method BLASTN NCBI GI g2315210 BLAST score 34 E value 4.0e-10 Match length 70 % identity 87

NCBI Description Lycopersicon esculentum mRNA for proteasome, alpha subunit



```
21820
Seq. No.
                  88348 1.R1040
Contig ID
                  LIB3170-014-Q1-K1-F11
5'-most EST
Seq. No.
                  21821
                  88355 1.R1040
Contig ID
                  LIB3170-014-Q1-K1-G3
5'-most EST
                  BLASTX
Method
                  q3548808
NCBI GI
BLAST score
                  485
                  7.0e-49
E value
Match length
                  104
% identity
NCBI Description (AC005313) unknown protein [Arabidopsis thaliana]
                   21822
Seq. No.
                   88366 1.R1040
Contig ID
                   LIB3170-014-Q1-K1-A5
5'-most EST
                   BLASTX
Method
                   q4559327
NCBI GI
                   283
BLAST score
                   4.0e-25
E value
                   141
Match length
% identity
                   45
NCBI Description (AC007087) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   21823
                   88376 1.R1040
Contig ID
                   jC-gmle01810047a12d1
5'-most EST
                   21824
Seq. No.
                   88428 1.R1040
Contig ID
                   LIB3170-015-Q1-J1-C2
5'-most EST
                   21825
Seq. No.
                   88437 1.R1040
Contig ID
                   LIB3170-015-Q1-J1-D5
5'-most EST
                   21826
Seq. No.
                   88450 1.R1040
Contig ID
                   \verb|jC-gm\overline{l}e01810094h02d1|
5'-most EST
                   BLASTX
Method
                   q2894611
NCBI GI
                   164
BLAST score
                   3.0e-11
E value
                   154
Match length
 % identity
NCBI Description (AL021889) putative protein [Arabidopsis thaliana]
                   21827
```

Seq. No. Contig ID

88454 1.R1040 LIB3170-015-Q1-K1-H2 5'-most EST

21828 Seq. No.

88459 1.R1040 Contig ID

jC-gmf102220104d03d1 5'-most EST



21829

```
Seq. No.
Contig ID
                  88513 1.R1040
5'-most EST
                  LIB3170-086-Q1-J1-D1
                  21830
Seq. No.
                  88515 1.R1040
Contig ID
5'-most EST
                  jC-qmf102220077h07d1
Method
                  BLASTX
                  g557084
NCBI GI
BLAST score
                  158
E value
                  3.0e-10
Match length
                  115
                  5
% identity
NCBI Description (L35601) ankyrin [Drosophila melanogaster]
                  >gi 1092123 prf 2022340A ankyrin [Drosophila melanogaster]
Seq. No.
                  21831
Contig ID
                  88515 2.R1040
5'-most EST
                  LIB3170-016-Q1-J1-A6
Seq. No.
                  21832
Contig ID
                  88520 1.R1040
                  LIB3170-016-Q1-J1-B3
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3540181
BLAST score
                  402
                  4.0e-39
E value
                  136
Match length
                   57
% identity
NCBI Description (AC004122) Unknown protein [Arabidopsis thaliana]
                  21833
Seq. No.
                   88522 1.R1040
Contig ID
                  LIB3170-016-Q1-J1-B5
5'-most EST
Seq. No.
                  21834
Contig ID
                  88543 1.R1040
                  LIB3170-016-Q1-J1-E9
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3264759
BLAST score
                   437
E value
                   4.0e-43
Match length
                  109
                  79
% identity
NCBI Description (AF071889) 40S ribosomal protein S8 [Prunus armeniaca]
                   21835
Seq. No.
                   88561 1.R1040
Contig ID
5'-most EST
                  uaw700664307.hl
                   21836
Seq. No.
                   88669 1.R1040
Contig ID
5'-most EST
                  LIB3170-017-Q1-K1-E2
```

21837

88676 1.R1040

uC-gmrominsoy106e12b1

Seq. No.

Contig ID 5'-most EST



Contig ID 88679 1.R1040

5'-most EST LIB3170-017-Q1-K1-F2

Method BLASTX
NCBI GI g3738315
BLAST score 359
E value 5.0e-34
Match length 102
% identity 70

NCBI Description (AC005170) unknown protein [Arabidopsis thaliana]

Seq. No. 21839

Contig ID 88709 1.R1040

5'-most EST jC-gmle01810048f11d1

Method BLASTX
NCBI GI g2119045
BLAST score 463
E value 5.0e-46
Match length 129
% identity 71

NCBI Description small nuclear ribonucleoprotein U1A - potato

>gi\_1050840\_emb\_CAA90282\_ (Z49990) U1snRNP-specific

protein, U1A [Solanum tuberosum]

Seq. No. 21840

Contig ID 88727\_1.R1040

5'-most EST LIB3170-018-Q1-J1-D4

Method BLASTX
NCBI GI g3738298
BLAST score 465
E value 3.0e-46
Match length 165
% identity 55

NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]

>gi 4249394 (AC006072) unknown protein [Arabidopsis

thaliana]

Seq. No. 21841

Contig ID 88795 1.R1040

5'-most EST jC-gmro02910005d07d1

Seq. No. 21842

Contig ID 88825\_1.R1040

5'-most EST LIB3170-019-Q1-J1-H7

Seq. No. 21843

Contig ID 88872 1.R1040

5'-most EST LIB3170-020-Q1-J1-A11

Method BLASTX
NCBI GI g266410
BLAST score 605
E value 1.0e-62
Match length 184
% identity 72

NCBI Description CDC2+/CDC28-RELATED PROTEIN KINASE R2 >gi\_82507\_pir\_\_S13934

protein kinase (EC 2.7.1.37) chain cdc2/cdc28 homolog -



rice >gi\_20194\_emb\_CAA41172\_ (X58194) cdc2+/CDC28-related
protein kinase [Oryza sativa]

Seq. No. 21844

Contig ID 88872 2.R1040

5'-most FST iC-om[e01810054

5'-most EST jC-gmle01810054h09d1

Seq. No. 21845

Contig ID 88876 1.R1040

5'-most EST LIB3170-020-Q1-K1-B11

Seq. No. 21846

Contig ID 88904\_1.R1040

5'-most EST LIB3170-020-Q1-J1-G1

Seq. No. 21847

Contig ID 88909 1.R1040

5'-most EST LIB3170-020-Q1-J1-G5

Method BLASTX
NCBI GI 94490741
BLAST score 244
E value 1.0e-20
Match length 117
% identity 46

NCBI Description (AL035708) hypothetical protein [Arabidopsis thaliana]

Seq. No.

Contig ID 88913 1.R1040

5'-most EST jC-gmf102220068c02d1

21848

Seq. No. 21849

Contig ID 88987 1.R1040

5'-most EST LIB3170-030-Q1-J1-A9

Seq. No. 21850

Contig ID 88994\_1.R1040

5'-most EST jC-gmro02910073f04d1

Seq. No. 21851

Contig ID 88996 1.R1040

5'-most EST jC-gmf102220130f06d1

Seq. No. 21852

Contig ID 89001 1.R1040

5'-most EST LIB3170-021-Q1-J1-D1

Seq. No. 21853

Contig ID 89017\_1.R1040

5'-most EST jC-gmro02800024a01d1

Seq. No. 21854

Contig ID 89030 1.R1040

5'-most EST LIB3170-021-Q1-J1-G10

Seq. No. 21855

Contig ID 89031\_1.R1040

5'-most EST LIB3170-021-Q1-J1-G2



89032 1.R1040 Contig ID

5'-most EST jC-gmro02910005f05d1

Seq. No. 21857

Contig ID 89041 1.R1040

LIB3170-021-Q1-J1-H2 5'-most EST

Seq. No. 21858

Contig ID 89044 1.R1040

5'-most EST LIB3170-021-Q1-J1-H6

Seq. No. 21859

Contig ID 89117 1.R1040

5'-most EST LIB3170-024-Q1-K1-G3

Method BLASTX NCBI GI g1246823 BLAST score 148 2.0e-09 E value Match length 102

32 % identity

(X89865) unknown [Phoenix dactylifera] NCBI Description

Seq. No.

21860

89128 1.R1040 Contig ID

5'-most EST LIB3170-021-Q1-K1-H3

Method BLASTX NCBI GI q2129677 BLAST score 183 1.0e-13 E value Match length 57 % identity 65

probablel N-acetyltransferase hookless 1 - Arabidopsis NCBI Description

thaliana >gi 1277090 (U50399) putative N-acetyltransferase

hookless1 [Arabidopsis thaliana] >gi\_1277092 (U50400) putative N-acetyltransferase hookless1 [Arabidopsis thaliana] >gi 4468983 emb CAB38297 (AL035605) probable N-acetyltransferase hookless 1 [Arabidopsis thaliana]

21861 Seq. No.

89136 1.R1040 Contig ID

5'-most EST jC-gmro02910008g02d1

21862 Seq. No.

Contig ID 89144 1.R1040

5'-most EST jC-qmst02400062f06d1

21863 Seq. No.

Contig ID 89146 1.R1040

5'-most EST LIB3170-022-Q1-J1-B2

Method BLASTX g3269287 NCBI GI BLAST score 207 2.0e-16 E value 42 Match length % identity 83



```
NCBI Description (AL030978) GH3 like protein [Arabidopsis thaliana]
```

Contig ID 89147 1.R1040

5'-most EST jC-gmle01810024b11d1

Method BLASTX
NCBI GI g3096920
BLAST score 345
E value 2.0e-32

Match length 71 % identity 85

NCBI Description (AL023094) putative ketoacyl-CoA synthase [Arabidopsis

thaliana]

Seq. No. 21865

Contig ID 89149\_1.R1040

5'-most EST LIB3170-023-Q1-J1-F3

Seq. No. 21866

Contig ID 89151\_1.R1040

5'-most EST LIB3170-022-Q1-J1-C1

Seq. No. 21867

Contig ID 89182 1.R1040

5'-most EST jC-gmro02910074d07d1

Seq. No. 21868

Contig ID 89194\_1.R1040 5'-most EST zzp700835224.h1

Method BLASTX
NCBI GI g4490727
BLAST score 191
E value 2.0e-14
Match length 64
% identity 56

NCBI Description (AL035709) putative protein [Arabidopsis thaliana]

Seq. No. 21869

Contig ID 89198 1.R1040

5'-most EST jC-gmro02910034d08d1

Method BLASTX
NCBI GI g22490
BLAST score 193
E value 3.0e-14
Match length 134
% identity 33

NCBI Description (X01380) ORF1 [Zea mays]

Seq. No. 21870

Contig ID 89203\_1.R1040

5'-most EST LIB3170-022-Q1-J1-G9

Seq. No. 21871

Contig ID 89204\_1.R1040 5'-most EST g5509859

Method BLASTX NCBI GI g4165183

3508



BLAST score 381 E value 2.0e-40 Match length 195 % identity 51

NCBI Description (AJ132349) SAP1 protein [Antirrhinum majus]

Seq. No. 21872

89267 1.R1040 Contig ID ncj700979969.h1 5'-most EST

Method BLASTX NCBI GI g3395427 BLAST score 201 2.0e-15 E value 48 Match length % identity

NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]

Seq. No. 21873

Contig ID 89267 2.R1040 5'-most EST uC-qmropic068a09b1

Seq. No. 21874

Contig ID 89299 1.R1040

5'-most EST LIB3170-023-Q1-J1-A1

Seq. No. 21875

Contig ID 89303 1.R1040

5'-most EST LIB3170-023-Q1-J1-A2

Method BLASTX NCBI GI g3953461 BLAST score 193 E value 1.0e-14

Match length 87 44 % identity

NCBI Description (AC002328) F20N2.6 [Arabidopsis thaliana]

21876 Seq. No.

Contig ID 89304 1.R1040

5'-most EST LIB3170-023-Q1-J1-A4

Seq. No. 21877

89305 1.R1040 Contig ID

5'-most EST LIB3170-076-Q1-J1-G3

BLASTX Method NCBI GI g4580461 BLAST score 220 E value 9.0e-18 Match length 64 % identity

NCBI Description (AC006081) unknown protein [Arabidopsis thaliana]

Seq. No. 21878

89307 1.R1040 Contig ID 6HC-02-Q1-E1-H5 5'-most EST

Seq. No. 21879

Contig ID 89311 1.R1040



5'-most EST LIB3170-034-Q1-J1-E2

Method BLASTX
NCBI GI g3549683
BLAST score 295
E value 1.0e-26
Match length 118
% identity 53

NCBI Description (AL031394) beta-xylan endohydrolase -like protein

[Arabidopsis thaliana]

Seq. No. 21880

Contig ID 89311 2.R1040

5'-most EST LIB3170-023-Q1-J1-B12

Method BLASTX
NCBI GI g3549683
BLAST score 207
E value 2.0e-16
Match length 97
% identity 47

NCBI Description (AL031394) beta-xylan endohydrolase -like protein

[Arabidopsis thaliana]

Seq. No. 21881

Contig ID 89320 1.R1040

5'-most EST jC-gmle01810048a09d1

Seq. No. 21882

Contig ID 89332\_1.R1040

5'-most EST LIB3170-023-Q1-J1-D12

Method BLASTX
NCBI GI 94432835
BLAST score 207
E value 3.0e-16
Match length 62

% identity 58

NCBI Description (AC006283) unknown protein [Arabidopsis thaliana]

Seq. No. 21883

Contig ID 89332\_2.R1040

5'-most EST LIB3170-038-Q1-J1-A3

Seq. No. 21884

Contig ID 89338 1.R1040

5'-most EST LIB3170-023-Q1-J1-D7

Seq. No. 21885

Contig ID 89344 1.R1040

5'-most EST LIB3170-023-Q1-J1-E2

Seq. No. 21886

Contig ID 89373 1.R1040

5'-most EST LIB3170-028-Q1-J1-F6

Seq. No. 21887

Contig ID 89374 1.R1040

5'-most EST LIB3170-023-Q1-J1-H1

Method BLASTN



NCBI GI g1778373 BLAST score 56 E value 1.0e-22 Match length 194 % identity 82

NCBI Description Pisum sativum glycine-rich RNA-binding protein PsGRBP mRNA,

complete cds

Seq. No. 21888

Contig ID 89480 2.R1040

5'-most EST jC-gmle01810049c08d1

Method BLASTX
NCBI GI g1076634
BLAST score 276
E value 3.0e-24
Match length 93
% identity 58

NCBI Description protein-serine/threonine kinase NPK15 - common tobacco

>gi 505146 dbj BAA06538 (D31737) protein-serine/threonine

kinase [Nicotiana tabacum]

Seq. No. 21889

Contig ID 89484 1.R1040

5'-most EST LIB3170-024-Q1-J1-B12

Seq. No. 21890

Contig ID 89488 1.R1040

5'-most EST jC-gmro02910069g11d1

Seq. No. 21891

Contig ID 89503 1.R1040

5'-most EST LIB3170-024-Q1-J1-D2

Method BLASTX
NCBI GI g3420054
BLAST score 146
E value 3.0e-09
Match length 86
% identity 41

NCBI Description (AC004680) unknown protein [Arabidopsis thaliana]

Seq. No. 21892

Contig ID 89506\_1.R1040

5'-most EST LIB3170-024-Q1-J1-D6

Seq. No. 21893

Contig ID 89509 1.R1040

5'-most EST LIB3170-024-Q1-J1-D9

Seq. No. 21894

Contig ID 89515\_1.R1040

5'-most EST LIB3170-024-Q1-J1-E5

Seq. No. 21895

Contig ID 89535\_1.R1040 5'-most EST zhf700956117.h1

Seq. No. 21896

NCBI Description



```
Contig ID
                   89535 2.R1040
5'-most EST
                  jC-gmro02910015a10d1
Seq. No.
Contig ID
                  89542 1.R1040
5'-most EST
                  jC-gmst02400014g06d1
Seq. No.
                  21898
Contig ID
                  89630 1.R1040
                  LIB3170-024-Q1-K1-H5
5'-most EST
                  21899
Seq. No.
                  89637 1.R1040
Contig ID
5'-most EST
                  LIB3170-025-Q1-J1-A4
                  21900
Seq. No.
Contig ID
                  89649 1.R1040
5'-most EST
                  LIB3170-025-Q1-J1-B5
Seq. No.
                  21901
Contig ID
                  89656 1.R1040
5'-most EST
                  LIB3170-025-Q1-J1-C11
Method
                  BLASTN
NCBI GI
                   g2760316
BLAST score
                   40
E value
                   6.0e-13
Match length
                   84
% identity
                  87
NCBI Description
                  The sequence of BAC F1N21 from Arabidopsis thaliana
                  chromosome 1, complete sequence [Arabidopsis thaliana]
Seq. No.
                  21902
Contig ID
                   89663 1.R1040
5'-most EST
                  LIB3170-025-Q1-J1-C7
Seq. No.
                   21903
                   89702 1.R1040
Contig ID
                  LIB3170-025-Q1-J1-G3
5'-most EST
Method
                  BLASTX
NCBI GI
                   g3643603
BLAST score
                   298
E value
                  1.0e-26
                   89
Match length
                   62
% identity
NCBI Description
                  (AC005395) unknown protein [Arabidopsis thaliana]
Seq. No.
                   21904
Contig ID
                   89704 1.R1040
5'-most EST
                   LIB3170-025-Q1-J1-G5
Method
                  BLASTX
NCBI GI
                   g3913517
BLAST score
                   376
E value
                   6.0e-40
Match length
                  133
% identity
                   62
```

(3'(2'),5-BISPHOSPHONUCLEOSIDE 3'(2')-PHOSPHOHYDROLASE)

3'(2'),5'-BISPHOSPHATE NUCLEOTIDASE



(DPNPASE) >gi\_1109672 (U33283) 3'(2'),5-diphosphonucleoside 3'(2') phosphohydrolase [Oryza sativa]

>gi\_1586671\_prf\_\_2204308A diphosphonucleoside phosphohydrolase [Oryza sativa]

21905 Seq. No.

89751 1.R1040 Contig ID ssr700554217.h1 5'-most EST

21906 Seq. No.

89815 1.R1040 Contig ID 5'-most EST g4306359

Method BLASTX g4322940 NCBI GI BLAST score 162 E value 7.0e-21 Match length 104

% identity (AF096299) DNA-binding protein 2 [Nicotiana tabacum] NCBI Description

Seq. No.

21907 Contig ID 89817 1.R1040

5'-most EST LIB3170-026-Q1-J1-B6

30

Method BLASTX NCBI GI g2739369 BLAST score 655 E value 1.0e-68 Match length 168

% identity 69

(AC002505) putative pectinesterase [Arabidopsis thaliana] NCBI Description

21908 Seq. No.

Contig ID 89826 1.R1040 5'-most EST k11701206120.h1

Seq. No. 21909

Contig ID 89835 1.R1040

jC-gmst02400049d08d1 5'-most EST

Method BLASTX g4191796 NCBI GI BLAST score 836 1.0e-89 E value 269 Match length 59 % identity

(AC005917) putative senescence-associated protein 5 NCBI Description

[Arabidopsis thaliana]

21910 Seq. No.

89838 1.R1040 Contig ID

5'-most EST LIB3170-026-Q1-J1-E12

Method BLASTX NCBI GI g4469011 BLAST score 453 E value 4.0e-45 Match length 111 77 % identity

NCBI Description (AL035602) carbohydrate kinase-like protein [Arabidopsis



## thaliana]

Seq. No. Contig ID 21911

89850 1.R1040

5'-most EST

LIB3170-026-Q1-J1-F5

Seq. No.

21912

Contig ID 5'-most EST 89854\_1.R1040 jC-gmro02910026g11a1

Method NCBI GI BLASTX

BLAST score

q1175978 222

E value

8.0e-18

Match length % identity

159 38

NCBI Description

HYPOTHETICAL 39.9 KD PROTEIN IN MPR1-GCN20 INTERGENIC

REGION >gi\_1084732\_pir\_\_S56262 hypothetical protein YFR007w - yeast (Saccharomyces cerevisiae) >gi 836762 dbj BAA09246

(D50617) YFR007W [Saccharomyces cerevisiae]

Seq. No.

Contig ID

21913

89871 1.R1040

5'-most EST

jC-gmro02910007g07d1

Method NCBI GI BLASTX q2880055

BLAST score

893

E value

3.0e-96

Match length

315

% identity

NCBI Description

(AC002340) hypothetical protein [Arabidopsis thaliana]

Seq. No.

21914

Contig ID

89873 1.R1040

5'-most EST

LIB3170-026-Q1-J1-H6

Seq. No.

21915

Contig ID

89873 2.R1040

5'-most EST

jC-gmle01810054h10d1

Seq. No.

21916

Contig ID

89947 1.R1040

5'-most EST

LIB3170-026-Q1-K1-G4

Seq. No.

21917

Contig ID 5'-most EST

89965 1.R1040 awf700837568.h1

Method

BLASTX

NCBI GI

g2992543

BLAST score

185

E value

7.0e-14

Match length

47

% identity

66

NCBI Description

(AF021797) peroxisomal receptor for PTS2-containing

proteins Pex7p [Pichia pastoris]

Seq. No.

21918

Contig ID

89982 1.R1040



5'-most EST hrw701062589.h1

Method BLASTX
NCBI GI g2842490
BLAST score 185
E value 1.0e-13
Match length 66
% identity 53

NCBI Description (AL021749) heat-shock protein [Arabidopsis thaliana]

Seq. No. 21919

89992 1.R1040 Contig ID 5'-most EST g4283822 BLASTX Method NCBI GI g4432840 BLAST score 312 E value 2.0e-28 Match length 148 % identity 45

NCBI Description (AC006283) unknown protein [Arabidopsis thaliana]

Seq. No. 21920

Contig ID 90008 1.R1040

5'-most EST LIB3170-028-Q1-K1-F1

Seq. No. 21921

Contig ID 90039 1.R1040

5'-most EST LIB3170-028-Q1-J1-A11

Method BLASTX

NCBI GI g3763918 BLAST score 210 E value 1.0e-16 Match length 49

% identity 86

NCBI Description (AC004450) putative isopropylmalate dehydratase

[Arabidopsis thaliana]

Seq. No. 21922

Contig ID 90039 2.R1040

5'-most EST jC-gmst02400005e01d1

Seq. No. 21923

Contig ID 90058\_1.R1040

5'-most EST jC-gmro02800038e12a1

Seq. No. 21924

Contig ID 90093 1.R1040

5'-most EST LIB3170-028-Q1-J1-H3

Seq. No. 21925

Contig ID 90199\_1.R1040

5'-most EST LIB3170-029-Q1-J1-B5

Method BLASTX
NCBI GI g4539460
BLAST score 193
E value 1.0e-14
Match length 120
% identity 4



NCBI Description (AL049500) putative protein [Arabidopsis thaliana]

Seq. No.

21926

Contig ID

90206 1.R1040

5'-most EST

LIB3170-029-Q1-J1-C3

Seq. No.

21927

Contig ID 5'-most EST

90218\_1.R1040 LIB3170-032-Q1-J1-G11

Method NCBI GI BLASTX

BLAST score

q4103342

E value

314 7.0e-29

Match length

82

% identity

78

NCBI Description

(AF022377) agamous-like putative transcription factor

[Cucumis sativus]

Seq. No.

21928

Contig ID

90224 1.R1040

5'-most EST

jC-gmf102220094h01a1

Seq. No.

21929

Contig ID

90225 1.R1040

5'-most EST

LIB3170-029-Q1-J1-E12

Method NCBI GI BLASTX

g3063709

BLAST score

223

E value

3.0e-18 50

Match length

76

% identity NCBI Description

(AL022537) putative protein [Arabidopsis thaliana]

Seq. No.

21930

Contig ID

90227 1.R1040

5'-most EST

jC-gmro02910060f02a1

Seq. No.

21931

Contig ID

90239 1.R1040

5'-most EST

LIB3170-029-Q1-J1-F9

Seq. No.

21932

Contig ID

90277 1.R1040

5'-most EST

leu701152979.h1

Seq. No.

21933

Contig ID

90283 1.R1040

5'-most EST

uaw700664736.hl

Seq. No.

21934

Contig ID

90308 1.R1040

5'-most EST

LIB3170-029-Q1-K1-E9

Seq. No.

21935

Contig ID

90326 1.R1040

5'-most EST

LIB3170-029-Q1-K1-G8



```
Seq. No.
                  21936
Contig ID
                  90353 1.R1040
5'-most EST
                  LIB3170-030-Q1-J1-B2
                  21937
Seq. No.
                  90364 1.R1040
Contig ID
5'-most EST
                  LIB3170-044-Q1-J1-D10
Seq. No.
                  21938
                  90382 1.R1040
Contig ID
                  jC-gmf102220073c01a1
5'-most EST
                  BLASTX
Method
                  g2618689
NCBI GI
BLAST score
                  212
E value
                  7.0e-17
Match length
                  99
% identity
                  45
NCBI Description
                  (AC002510) unknown protein [Arabidopsis thaliana]
                  21939
Seq. No.
Contig ID
                  90385 1.R1040
5'-most EST
                  jC-qmle01810043h12d1
Method
                  BLASTN
                  g2104678
NCBI GI
BLAST score
                  168
                  3.0e-89
E value
Match length
                  431
% identity
                  88
NCBI Description V.faba mRNA for transcription factor containing HMG-box
                  21940
Seq. No.
Contig ID
                   90387_1.R1040
5'-most EST
                  LIB3170-030-Q1-J1-E4
Method
                  BLASTX
NCBI GI
                  g2781363
BLAST score
                  158
                   4.0e-12
E value
Match length
                  56
% identity
                   64
                  (AC003113) F2401.19 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  21941
Contig ID
                  90395 1.R1040
                   jC-gmle01810015g04d1
5'-most EST
                  BLASTX
Method
```

NCBI GI q1663724 BLAST score 224 E value 4.0e-18 Match length 67 61 % identity

(U50846) 4-coumarate:coenzyme A ligase [Nicotiana tabacum] NCBI Description

21942 Seq. No.

Contig ID 90399 1.R1040

5'-most EST LIB3170-030-Q1-J1-F6

Seq. No. 21943



```
90401 1.R1040
Contig ID
                  LIB3170-030-Q1-J1-F9
5'-most EST
Seq. No.
                  21944
                   90506 1.R1040
Contig ID
5'-most EST
                  LIB3170-038-Q1-J1-F3
Method
                  BLASTX
NCBI GI
                  q3077640
BLAST score
                  267
E value
                   2.0e-23
Match length
                  71
% identity
                  72
                  (AJ223151) O-methyltransferase [Prunus dulcis]
NCBI Description
Seq. No.
                  21945
                   90506 2.R1040
Contig ID
5'-most EST
                  LIB3170-031-Q1-J1-A3
Seq. No.
                  21946
                  90506 3.R1040
Contig ID
5'-most EST
                  asn701137419.hl
                   21947
Seq. No.
Contig ID
                   90517 1.R1040
5'-most EST
                  LIB3170-031-Q1-J1-C10
Method
                  BLASTX
NCBI GI
                  g2062154
BLAST score
                  179
E value
                   6.0e-13
Match length
                  76
% identity
                   55
                  (AC001645) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   21948
Seq. No.
Contig ID
                   90523 1.R1040
5'-most EST
                  LIB3170-031-Q1-J1-C7
Method
                  BLASTX
NCBI GI
                   q2959767
BLAST score
                   481
                   4.0e-48
E value
Match length
                   155
% identity
                   63
                   (AJ002584) AtMRP4 [Arabidopsis thaliana] >gi 3738292
NCBI Description
                   (AC005309) glutathione-conjugate transporter AtMRP4
                   [Arabidopsis thaliana]
Seq. No.
                   21949
                   90535 1.R1040
Contig ID
5'-most EST
                   jC-qmst02400031e01d1
```

Method BLASTX NCBI GI g927025 BLAST score 212 9.0e-17 E value Match length 61 66 % identity

(L44134) SPF1-like DNA-binding protein [Cucumis sativus] NCBI Description



Seq. No. 21950

Contig ID 90535\_2.R1040

5'-most EST jC-gmro02910030c09d1

Seq. No. 21951

Contig ID 90539 2.R1040

5'-most EST LIB3170-031-Q1-J1-E3

Seq. No. 21952

Contig ID 90548 1.R1040

Method BLASTX
NCBI GI g2618701
BLAST score 355
E value 2.0e-33
Match length 122
% identity 60

NCBI Description (AC002510) hypothetical protein [Arabidopsis thaliana]

Seq. No. 21953

Contig ID 90551\_1.R1040 5'-most EST q4313413

Seq. No. 21954

Contig ID 90567 1.R1040

5'-most EST  $jC-gm\overline{f}102220103b03d1$ 

Method BLASTX
NCBI GI g3193286
BLAST score 331
E value 8.0e-31
Match length 84
% identity 71

NCBI Description (AF069298) T14P8.22 gene product [Arabidopsis thaliana]

Seq. No. 21955

Contig ID 90591 1.R1040

5'-most EST jC-gmst02400023f10a1

Seq. No. 21956

Contig ID 90640 1.R1040

5'-most EST jC-gmle01810040c09d1

Seq. No. 21957

Contig ID 90646\_1.R1040

5'-most EST LIB3170-032-Q1-J1-B11

Seq. No. 21958

Contig ID 90656 1.R1040

5'-most EST LIB3170-032-Q1-J1-B9

Seq. No. 21959

Contig ID 90673\_1.R1040

5'-most EST jC-gmle01810084e09d1

Seq. No. 21960

Contig ID 90677 1.R1040 5'-most EST txt700734586.h1



Method BLASTX NCBI GI g2982243 BLAST score 218 1.0e-17 E value Match length 46 85 % identity

(AF051204) hypothetical protein [Picea mariana] NCBI Description

Seq. No. Contig ID 5'-most EST 21961 90686 1.R1040 awf700839504.h1

Seq. No.

21962

Contig ID

90686 2.R1040

5'-most EST

LIB3170-032-Q1-J1-E6

BLASTN Method NCBI GI g2062705 BLAST score 39 E value 3.0e-12 39

Match length 39 % identity

NCBI Description Human butyrophilin (BTF5) mRNA, complete cds

Seq. No.

Contig ID

90695 1.R1040

5'-most EST

LIB3170-032-Q1-J1-F5

Seq. No.

21964

Contig ID

90698 1.R1040

5'-most EST

LIB3170-032-Q1-J1-F8

BLASTN Method g3046847 NCBI GI BLAST score 41 E value 1.0e-13

Match length 135 % identity 90

NCBI Description

Arabidopsis thaliana genomic DNA, chromosome5, TAC clone:

K11J9, complete sequence [Arabidopsis thaliana]

Seq. No. 21965

Contig ID

90707 1.R1040

5'-most EST

LIB3170-032-Q1-J1-G7

Seq. No.

21966

Contig ID

90715 1.R1040

5'-most EST

LIB3170-032-Q1-J1-H5

Seq. No.

21967

Contig ID

90719 1.R1040

5'-most EST

LIB3170-032-Q1-J1-H9

Seq. No.

21968

Contig ID 5'-most EST 90774 1.R1040 k11701204969.h1

BLASTX Method g1352077 NCBI GI 852 BLAST score



E value 1.0e-91 Match length 224 % identity 68

% identity 68
NCBI Description BETA-GALACT

ription BETA-GALACTOSIDASE PRECURSOR (LACTASE)
(EXO-(1-->4)-BETA-D-GALACTANASE) >gi 971485 emb CAA58734

(X83854) putative beta-galactosidase/galactanase [Lycopersicon esculentum] >gi 4138139 emb CAA10174 (AJ012797) ss-galactosidase [Lycopersicon esculentum]

Seq. No.

21969

Contig ID

90792\_1.R1040

5'-most EST

LIB3170-034-Q1-J1-A4

Seq. No.

21970

Contig ID

90809\_1.R1040

5'-most EST

LIB3170-033-Q1-J1-C3 BLASTX

Method NCBI GI

g3738290 396

BLAST score E value Match length

4.0e-38

% identity

164 45

NCBI Description

(AC005309) unknown protein [Arabidopsis thaliana]

Seq. No.

Contig ID

21971 90814 1.R1040

5'-most EST

uC-gmropic074b02b1

Method NCBI GI BLASTX g1706110

BLAST score E value

511 1.0e-51

Match length

1.0e-51 129

% identity

78

NCBI Description

NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR

(CTPT) >gi\_1143713 (U13632) non-green plastid

phosphate/triose-phosphate translocator precursor [Brassica

oleracea]

Seq. No.

21972

Contig ID 5'-most EST

90814\_2.R1040 asn701134234.h1

Method

BLASTN

NCBI GI

g1778144

BLAST score

69

E value Match length 2.0e-30 217

Match lengt % identity

83

NCBI Description

Nicotiana tabacum plastid phosphate/phosphoenolpyruvate

translocator precursor (TABPPT10) mRNA, complete cds

Seq. No.

21973

Contig ID

90843\_1.R1040

5'-most EST

LIB3170-034-Q1-J1-C10

Seq. No.

21974

Contig ID

90856 1.R1040

5'-most EST

jC-gmf102220103e01d1



```
BLASTX
Method
                  g3355626
NCBI GI
                  785
BLAST score
                  1.0e-83
E value
                  230
Match length
                  81
                  (Y09204) histidinol-phosphate aminotransferase [Nicotiana
% identity
NCBI Description
                   tabacum]
                   21975
Seq. No.
                   90890 1.R1040
Contig ID
                   LIB3170-033-Q1-K1-D1
5'-most EST
                   21976
Seq. No.
                   90898 1.R1040
Contig ID
                   LIB3170-033-Q1-K1-D7
5'-most EST
                   BLASTX
Method
                   q2244981
NCBI GI
                   197
BLAST score
                   4.0e-15
E value
                   92
Match length
                   49
 % identity
                   (Z97340) similarity to proline-rich protein APG -
NCBI Description
                   Arabidopsis [Arabidopsis thaliana]
                   21977
 Seq. No.
                   90949_1.R1040
 Contig ID
                    jC-gmro02910049h08d1
 5'-most EST
                   BLASTN
 Method
                    g217910
 NCBI GI
                    43
 BLAST score
                    7.0e-15
 E value
                    91
 Match length
                    87
 % identity
 NCBI Description Carrot mRNA for nuclear antigen 21D7
                    21978
 Seq. No.
                    90957 1.R1040
 Contig ID
                    LIB3170-034-Q1-J1-B2
 5'-most EST
                    BLASTX
 Method
                    q3980417
 NCBI GI
                    185
 BLAST score
                    1.0e-13
 E value
                    46
 Match length
                    (AC004561) pumilio-like protein [Arabidopsis thaliana]
  % identity
  NCBI Description
                    21979
  Seq. No.
                    90958 1.R1040
  Contig ID
                    LIB3170-034-Q1-J1-B3
  5'-most EST
                     21980
  Seq. No.
                     90970 1.R1040
  Contig ID
                    LIB3170-034-Q1-J1-C6
  5'-most EST
```

Seq. No. 21981 Contig ID 90978\_1.R1040

3522



```
5'-most EST
                  LIB3170-034-Q1-J1-D2
Method
                  BLASTN
NCBI GI
                  g1381675
BLAST score
                  74
                  1.0e-33
E value
Match length
                  122
% identity
                  90
NCBI Description Glycine max small GTP-binding protein (sral) mRNA, partial
Seq. No.
                  21982
                  90983 1.R1040
Contig ID
5'-most EST
                  LIB3170-034-Q1-J1-D7
                  21983
Seq. No.
                  90991 1.R1040
Contig ID
                  LIB3170-047-Q1-J1-E8
5'-most EST
Method
                  BLASTX
                  q4539445
NCBI GI
BLAST score
                  183
E value
                  2.0e-13
Match length
                  56
% identity
NCBI Description (AL049523) putative protein [Arabidopsis thaliana]
Seq. No.
                  21984
                  91002 1.R1040
Contig ID
5'-most EST
                  LIB3170-034-Q1-J1-F5
Method
                  BLASTX
                  g2191194
NCBI GI
BLAST score
                  169
E value
                  1.0e-11
Match length
                   138
% identity
                   30
NCBI Description (AF007271) contains weak to the SAPB protein (TR:E236624)
                   [Arabidopsis thaliana]
                  21985
Seq. No.
                   91023 1.R1040
Contig ID
5'-most EST
                  jC-gmro02910061h09d1
Seq. No.
                  21986
                  91025 1.R1040
Contig ID
5'-most EST
                  LIB3170-034-Q1-J1-H6
Method
                  BLASTX
                  g1730502
NCBI GI
BLAST score
                  233
E value
                   3.0e-19
Match length
                  86
% identity
                  51
                  TRANSMEMBRANE PROTEIN PFT27 >gi 110903 pir A31351 probable
NCBI Description
                   transmembrane protein FT27 - mouse >gi 535682 (M23568)
                  transmembrane protein [Mus musculus]
```

Seq. No. 21987

Contig ID 91040\_1.R1040

5'-most EST LIB3170-034-Q1-K1-B11



```
21988
Seq. No.
Contig ID
                  91113 1.R1040
5'-most EST
                  LIB3170-035-Q1-J1-A10
Method
                  BLASTX
NCBI GI
                  q4490323
BLAST score
                  660
E value
                  4.0e-69
                  193
Match length
% identity
                  68
NCBI Description
                  (AJ131464) nitrate transporter [Arabidopsis thaliana]
Seq. No.
                  21989
                  91114 1.R1040
Contig ID
5'-most EST
                  LIB3170-035-Q1-J1-A12
Seq. No.
                  21990
Contig ID
                  91116 1.R1040
5'-most EST
                  LIB3170-035-Q1-J1-A3
Method
                  BLASTX
NCBI GI
                  q4580517
BLAST score
                  288
E value
                  6.0e-26
Match length
                  70
% identity
                  74
NCBI Description
                  (AF036302) scarecrow-like 5 [Arabidopsis thaliana]
                  21991
Seq. No.
Contig ID
                  91118 1.R1040
5'-most EST
                  LIB3170-035-Q1-J1-A5
Seq. No.
                  21992
Contig ID
                  91123 1.R1040
5'-most EST
                  LIB3170-057-Q1-J1-C4
                  21993
Seq. No.
Contig ID
                  91127 1.R1040
5'-most EST
                  LIB3170-035-Q1-J1-B2
Seq. No.
                  21994
                  91129 1.R1040
Contig ID
5'-most EST
                  jC-gmf102220101c09a1
                  BLASTX
Method
NCBI GI
                  g4325341
BLAST score
                  623
                  6.0e-65
E value
Match length
                  135
                  81
% identity
NCBI Description
                  (AF128393) similar to the Drosophila DES-1 protein
                  (GB:X94180) [Arabidopsis thaliana]
                  21995
Seq. No.
```

Contig ID 91133 1.R1040

5'-most EST LIB3170-035-Q1-J1-B9

Seq. No. 21996

Contig ID 91156 1.R1040

3524



5'-most EST LIB3170-035-Q1-J1-E9
Method BLASTX

NCBI GI g322801 BLAST score 164 E value 4.0e-11 Match length 80 % identity 55

NCBI Description promotes sex organ development protein ple - Antirrhinum majus >gi\_264223\_bbs\_123356 (S53900) promotes sex organ development=ple [Antirrhinum majus, Peptide, 239 aa]

[Antirrhinum majus]

Seq. No. 21997

Contig ID 91160 1.R1040

Method BLASTX
NCBI GI g4309741
BLAST score 616
E value 7.0e-64
Match length 165
% identity 72

NCBI Description (AC006439) hypothetical protein [Arabidopsis thaliana]

Seq. No. 21998

Contig ID 91197 1.R1040

5'-most EST LIB3170-035-Q1-K1-A7

Seq. No. 21999

Contig ID 91229 1.R1040

5'-most EST LIB3170-035-Q1-K1-D5

Seq. No. 22000

Contig ID 91281 1.R1040

5'-most EST LIB3170-036-Q1-K1-A2

Seq. No. 22001

Contig ID 91284 1.R1040

5'-most EST jC-gmle01810044e07d1

Method BLASTX
NCBI GI g3164222
BLAST score 167
E value 2.0e-11
Match length 109
% identity 36

NCBI Description (AB008518) RMA1 [Arabidopsis thaliana] >gi\_4206205

(AF071527) RMA1 RING zinc finger protein [Arabidopsis

thaliana]

Seq. No. 22002

Contig ID 91334 1.R1040

5'-most EST jC-gmro02910065g12d1

Method BLASTX
NCBI GI g3201554
BLAST score 510
E value 8.0e-52
Match length 111
% identity 81



NCBI Description (AJ006501) beta-D-glucosidase [Tropaeolum majus]

Seq. No. 22003

Contig ID 91336 1.R1040

5'-most EST uC-gmronoir0001h08a1

Seq. No. 22004

Contig ID 91340 1.R1040

5'-most EST LIB3170-036-Q1-K1-A1

Seq. No. 22005

Contig ID 91390 1.R1040

5'-most EST LIB3170-036-Q1-K2-F1

Seq. No. 22006

Contig ID 91430 1.R1040

5'-most EST LIB3170-036-Q1-K2-B4

Seq. No. 22007

Contig ID 91498 1.R1040

5'-most EST jC-gmle01810086e12d1

Seq. No. 22008

Contig ID 91524 1.R1040

5'-most EST LIB3170-037-Q1-J1-D1

Seq. No. 22009

Contig ID 91540 1.R1040

5'-most EST LIB3170-037-Q1-J1-E7

Seq. No. 22010

Contig ID 91542 1.R1040

5'-most EST jC-gmf102220115h08d1

Seq. No. 22011

Contig ID 91545\_1.R1040

5'-most EST LIB3170-064-Q1-J1-C4

Method BLASTX
NCBI GI g2462760
BLAST score 183
E value 2.0e-13
Match length 73
% identity 45

NCBI Description (AC002292) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 22012

Contig ID 91557\_1.R1040

5'-most EST LIB3170-037-Q1-J1-G12

Method BLASTX
NCBI GI g2460037
BLAST score 219
E value 2.0e-17
Match length 64
% identity 61

NCBI Description (AF014837) m6A methyltransferase [Homo sapiens]

Seq. No. 22013



Contig ID 91565\_1.R1040

5'-most EST jC-gmst02400068f11d1

Method BLASTX
NCBI GI g3493611
BLAST score 209
E value 2.0e-16
Match length 43
% identity 81

NCBI Description (AF068318) regulatory subunit of protein kinase CK2; CK2

beta-subunit [Arabidopsis thaliana]

Seq. No. 22014

Contig ID 91565 2.R1040

5'-most EST LIB3170-037-Q1-J1-H10

Method BLASTX
NCBI GI g729882
BLAST score 197
E value 3.0e-15
Match length 43
% identity 84

NCBI Description CASEIN KINASE II BETA' CHAIN (CK II)

>gi\_1076300\_pir\_\_S47968 casein kinase II (EC 2.7.1.-) beta chain CKB2 - Arabidopsis thaliana >gi\_467975 (U03984) casein kinase II beta subunit CKB2 [Arabidopsis thaliana] >gi\_2245122\_emb\_CAB10544\_ (Z97343) unnamed protein product

[Arabidopsis thaliana]

Seq. No. 22015

Contig ID 91627\_1.R1040

5'-most EST LIB3170-037-Q1-K1-F8

Method BLASTX
NCBI GI g1001263
BLAST score 239
E value 6.0e-20
Match length 186
% identity 31

NCBI Description (D64003) hypothetical protein [Synechocystis sp.]

Seq. No. 22016

Contig ID 91650\_1.R1040 5'-most EST uC-gmropic091a07b1

Method BLASTX
NCBI GI g2244970
BLAST score 158
E value 2.0e-14
Match length 50
% identity 70

NCBI Description (Z97340) hypothetical protein [Arabidopsis thaliana]

>gi\_2326365\_emb\_CAA74765\_ (Y14423) putative cell wall

protein [Arabidopsis thaliana]

Seq. No. 22017

Contig ID 91654\_1.R1040

5'-most EST LIB3170-038-Q1-J1-A9

Seq. No. 22018

Contig ID 91657 1.R1040



```
5'-most EST
                  LIB3170-038-Q1-J1-B12
                  22019
Seq. No.
Contig ID
                  91688 1.R1040
5'-most EST
                  LIB3170-038-Q1-J1-E5
Seq. No.
                  22020
                  91692 1.R1040
Contig ID
                  jC-gmro02910046f11a1
5'-most EST
Method
                  BLASTX
                  g2583136
NCBI GI
BLAST score
                  200
E value
                  2.0e-15
Match length
                  67
% identity
                  66
NCBI Description (AC002387) unknown protein [Arabidopsis thaliana]
                  22021
Seq. No.
                  91692 2.R1040
Contig ID
                  LIB3170-038-Q1-J1-F1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2583136
BLAST score
                  154
                  5.0e-10
E value
Match length
                  44
% identity
                  70
NCBI Description (AC002387) unknown protein [Arabidopsis thaliana]
                  22022
Seq. No.
Contig ID
                  91703 1.R1040
5'-most EST
                  LIB3170-038-Q1-J1-G12
                  22023
Seq. No.
                  91812 1.R1040
Contig ID
5'-most EST
                  LIB3170-039-Q1-J2-B1
Seq. No.
                  22024
                  91813 1.R1040
Contig ID
5'-most EST
                  LIB3170-039-Q1-J1-B11
                  BLASTX
Method
NCBI GI
                  q3785977
BLAST score
                  341
E value
                  5.0e-48
Match length
                  118
% identity
                  79
NCBI Description (AC005560) putative growth regulator protein [Arabidopsis
                  thaliana]
Seg. No.
                  22025
                  91814 1.R1040
Contig ID
5'-most EST
                  LIB3170-039-Q1-J1-B12
Seq. No.
                  22026
```

Contig ID 91823\_1.R1040

5'-most EST LIB3170-039-Q1-J2-C12

Method BLASTX NCBI GI g4098124



BLAST score 344 E value 3.0e-32 Match length 138 % identity 52

NCBI Description (U73522) AMSH [Homo sapiens]

Seq. No. 22027

Contig ID 91826\_1.R1040

5'-most EST LIB3170-039-Q1-J1-C7

Seq. No. 22028

Contig ID 91836 1.R1040

5'-most EST LIB3170-039-Q1-J1-E1

Method BLASTX
NCBI GI g2160173
BLAST score 392
E value 4.0e-54
Match length 249
% identity 10

NCBI Description (AC000132) Similar to N. tabacum salt-inducible protein

(gb U08285). [Arabidopsis thaliana]

Seq. No. 22029

Contig ID 91848 1.R1040

5'-most EST LIB3170-039-Q1-J1-F12

Seq. No. 22030

Contig ID 91850\_1.R1040 5'-most EST fC-gmse700853784d1

Method BLASTX
NCBI GI g1871526
BLAST score 312
E value 2.0e-28
Match length 128
% identity 20

NCBI Description (X81997) leucine-rich-repeat protein [Helianthus annuus]

Seq. No. 22031

Contig ID 91865 1.R1040

5'-most EST LIB3170-039-Q1-J1-H3

Seq. No. 22032

Contig ID 91865 2.R1040 5'-most EST rlr700898240.h1

Seq. No. 22033

Contig ID 91866\_1.R1040

5'-most EST LIB3170-039-Q1-J1-H4

Seq. No. 22034

Contig ID 91950 1.R1040

5'-most EST LIB3170-039-Q1-K2-A8

Method BLASTX
NCBI GI g3790441
BLAST score 299
E value 4.0e-27
Match length 94



% identity 63

NCBI Description (AF030515) chaperonin 60 alpha subunit [Canavalia lineata]

Seq. No. 22035

Contig ID 91960\_1.R1040 5'-most EST smc700748655.h1

Method BLASTX
NCBI GI g2462829
BLAST score 806
E value 4.0e-86
Match length 304
% identity 56

NCBI Description (AF000657) unknown protein [Arabidopsis thaliana]

Seq. No. 22036

Contig ID 91991\_1.R1040 5'-most EST uxk700673039.h1

Method BLASTX
NCBI GI g3894159
BLAST score 421
E value 2.0e-41
Match length 155
% identity 51

NCBI Description (AC005312) hypothetical protein [Arabidopsis thaliana]

Seq. No. 22037

Contig ID 91994 1.R1040

5'-most EST LIB3170-039-Q1-K1-F4

Seq. No. 22038

Contig ID 92103 1.R1040

5'-most EST LIB3170-040-Q1-J1-A9

Seq. No. 22039

Contig ID 92109\_1.R1040

5'-most EST jC-gmro02910066c11d1

Seq. No. 22040

Contig ID 92114 1.R1040

5'-most EST LIB3170-040-Q1-J1-C1

Seq. No. 22041

Contig ID 92119 1.R1040

5'-most EST jC-gmf102220092c02d1

Seq. No. 22042

Contig ID 92155\_1.R1040

5'-most EST jC-gmst02400037c02d2

Method BLASTX
NCBI GI 94056432
BLAST score 309
E value 4.0e-28
Match length 84
% identity 67

NCBI Description (AC005990) Similar to gi\_2245014 glucosyltransferase homolog from Arabidopsis thaliana chromosome 4 contig

gb\_Z97341. ESTs gb\_T20778 and gb\_AA586281 come from this



## gene. [Arabidopsis thaliana]

Seq. No. 22043

Contig ID 92161 1.R1040

5'-most EST LIB3170-040-Q1-J1-H3

Method BLASTX
NCBI GI g4558552
BLAST score 501
E value 1.0e-79
Match length 214
% identity 40

NCBI Description (AC007138) putative P-glycoprotein-like protein

[Arabidopsis thaliana]

Seq. No. 22044

Contig ID 92272 1.R1040

5'-most EST LIB3170-041-Q1-J1-D2

Seq. No. 22045

Contig ID 92280\_1.R1040
5'-most EST 94285734
Method BLASTX
NCBI GI 93080398
BLAST score 235
E value 1.0e-19
Match length 63
% identity 38

NCBI Description (AL022603) putative protein [Arabidopsis thaliana]

Seq. No. 22046

Contig ID 92289 1.R1040

5'-most EST LIB3170-041-Q1-J1-F3

Seq. No. 22047

Contig ID 92320\_1.R1040

5'-most EST LIB3170-041-Q1-K1-B5

Method BLASTX
NCBI GI g4539310
BLAST score 255
E value 8.0e-22
Match length 111
% identity 49

NCBI Description (AL035679) putative protein [Arabidopsis thaliana]

Seq. No. 22048

Contig ID 92364 1.R1040 5'-most EST fC-gmf1700903985d2

Method BLASTX
NCBI GI g1483228
BLAST score 139
E value 5.0e-12
Match length 66
% identity 68

NCBI Description (X99653) MADS3 protein [Betula pendula]

Seq. No. 22049

Contig ID 92447 1.R1040

3531



```
5'-most EST
                  jC-gmf102220070d05d1
Seq. No.
                  22050
Contig ID
                  92453 1.R1040
5'-most EST
                  fC-gmro700868783d1
Seq. No.
                  22051
Contig ID
                  92462 1.R1040
                  LIB3170-044-Q1-K1-E9
5'-most EST
                  BLASTN
Method
NCBI GI
                  g206371
BLAST score
                  103
E value
                  2.0e-50
Match length
                  581
% identity
                  100
NCBI Description Rat(Sprague-Dawley) prolactin gene: exons IV, V and flanks
                  22052
Seq. No.
                  92465 1.R1040
Contig ID
                  LIB3170-042-Q1-K1-C3
5'-most EST
Method
                  BLASTX
NCBI GI
                  q577301
BLAST score
                  146
                  4.0e-09
E value
                  143
Match length
                  33
% identity
NCBI Description (D42044) The ha3523 gene product is related to S.cerevisiae
                  gene product located in chromosome III. [Homo sapiens]
Seq. No.
                  22053
Contig ID
                  92469 1.R1040
                  fC-gmf1700906736a2
5'-most EST
Method
                  BLASTX
NCBI GI
                  g1531760
BLAST score
                  212
                  4.0e-17
E value
Match length
                  59
                  71
% identity
NCBI Description (X97075) proline oxidase [Arabidopsis thaliana]
Seg. No.
                  22054
Contig ID
                  92474 1.R1040
5'-most EST
                  LIB3170-042-Q1-K1-D4
Method
                  BLASTX
NCBI GI
                  g3176664
BLAST score
                  289
E value
                  6.0e-26
Match length
                  76
% identity
                  68
NCBI Description
                  (AC004393) Contains similarity to beta scruin gb Z47541
                  from Limulus polyphemus. ESTs gb_T04493 and gb_AA585955
                  come from this gene. [Arabidopsis thaliana]
```

Seq. No. 22055

Contig ID 92495\_1.R1040

5'-most EST LIB3170-042-Q1-K1-G10



22056 Seq. No.

92498 1.R1040 Contig ID

5'-most EST LIB3170-043-01-K1-H8

Seq. No.

22057

92526 1.R1040 Contig ID

5'-most EST LIB3170-043-Q1-J1-C1

Seq. No.

22058

92554 1.R1040 Contig ID

5'-most EST jC-gmro02910024a04d1

BLASTX Method NCBI GI q2832606 BLAST score 214 5.0e-17 E value Match length 63 70 % identity

(AL021635) predicted protein [Arabidopsis thaliana] NCBI Description

>gi 3292810 emb CAA19800 (AL031018) putative protein

[Arabidopsis thaliana]

Seq. No. 22059

Contig ID 92582 1.R1040 5'-most EST zhf700952445.hl

Seq. No. 22060

92601 1.R1040 Contig ID

LIB3170-043-Q1-K1-D9 5'-most EST

22061 Seq. No.

92614 1.R1040 Contig ID

5'-most EST LIB3170-043-Q1-K1-F12

Method BLASTX NCBI GI g125722 BLAST score 164 E value 4.0e-11 Match length 59 % identity 59

NCBI Description KUNITZ-TYPE TRYPSIN INHIBITOR KTI1 PRECURSOR

> >gi 81814 pir JQ1091 trypsin inhibitor KTi1 (Kunitz) soybean >gi 256635 bbs 115028 (S45035) Kunitz trypsin inhibitor KTil [soybeans, Peptide, 203 aa] [Glycine max]

Seq. No. 22062

92621 1.R1040 Contig ID leu701150223.hl 5'-most EST

Method BLASTX NCBI GI q3860020 BLAST score 246 E value 9.0e-21 Match length 102 50 % identity

NCBI Description (AF091091) unknown [Homo sapiens]

22063 Seq. No.

Contig ID 92643 1.R1040

LIB3170-046-Q1-J1-H8 5'-most EST



```
Method
                   BLASTX
NCBI GI
                   q2494329
                   165
BLAST score
                   4.0e-11
E value
Match length
                   161
                   34
% identity
```

NCBI Description GLUCAN 1,3-BETA-GLUCOSIDASE PRECURSOR

(EXO-1,3-BETA-GLUCANASE) >qi 1150694 emb CAA86952 (Z46872) exo-1,3-beta-glucanase/1,3-beta-D-glucan glucanohydrolase

[Yarrowia lipolytica]

```
22064
Seq. No.
Contig ID
                   92657 1.R1040
```

LIB3170-044-Q1-J1-C7 5'-most EST

```
22065
Seq. No.
```

92662 1.R1040 Contig ID

5'-most EST LIB3170-044-Q1-J1-D8

Method BLASTX NCBI GI g3927836 BLAST score 190 E value 6.0e-21 106 Match length 52 % identity

NCBI Description (AC005727) unknown protein [Arabidopsis thaliana]

Seq. No. 22066

Contig ID 92673 1.R1040

5'-most EST jC-qmf102220073e02d1

Seq. No.

% identity

22067

Contig ID 92745 1.R1040

5'-most EST LIB3170-044-Q1-K1-H12

Seq. No. 22068

Contig ID 92768 1.R1040 5'-most EST q5606376 Method BLASTX NCBI GI g1946360 BLAST score 476 1.0e-47 E value Match length 102 82

NCBI Description (U93215) elicitor response element binding protein WRKY3

isolog [Arabidopsis thaliana]

Seq. No. 22069

92785 1.R1040 Contig ID

5'-most EST LIB3170-045-Q1-J1-D6

Method BLASTX g629692 NCBI GI BLAST score 545 8.0e-56 E value Match length 149 % identity 73

NCBI Description hypothetical protein - common tobacco

>gi\_506471\_emb\_CAA56189 (X79794) unnamed protein product



## [Nicotiana tabacum]

Seq. No. 22070 Contig ID 92796\_1.R1040 5'-most EST LIB3170-045-Q1-J1-F11

22071

Seq. No.

Contig ID 92811\_1.R1040 5'-most EST LIB3170-045-Q1-J1-G7

5'-most EST LIB317 Method BLASTX

NCBI GI g3219938 BLAST score 159 E value 1.0e-10 Match length 86 % identity 36

NCBI Description HYPOTHETICAL 34.9 KD PROTEIN C57A10.11C IN CHROMOSOME I >gi 2058378 emb CAB08174 (Z94864) hypothetical protein

[Schizosaccharomyces pombe]

Seq. No. 22072

Contig ID 92816 1.R1040

5'-most EST LIB3170-045-Q1-J1-H12

Method BLASTX
NCBI GI g2529663
BLAST score 313
E value 1.0e-28
Match length 125
% identity 54

NCBI Description (AC002535) putative lysophospholipase [Arabidopsis

thaliana] >gi 3738277 (AC005309) putative lysophospholipase

[Arabidopsis thaliana]

Seq. No.

22073

Contig ID 92829\_1.R1040

5'-most EST LIB3170-045-Q1-K1-A5

Seq. No.

22074

Contig ID 92830\_1.R1040

5'-most EST jC-gmst02400006c11d1

Method BLASTX
NCBI GI g3522933
BLAST score 583
E value 5.0e-60
Match length 201
% identity 62

NCBI Description (AC004411) putative anion exchange protein 3 [Arabidopsis

thaliana]

Seq. No.

22075

Contig ID 92840\_1.R1040

5'-most EST jC-gmro02910014f07a1

Method BLASTX
NCBI GI g1946360
BLAST score 314
E value 2.0e-28
Match length 218
% identity 43



NCBI Description (U93215) elicitor response element binding protein WRKY3 isolog [Arabidopsis thaliana]

22076 Seq. No.

92845 1.R1040 Contig ID

LIB3170-045-Q1-K1-C3 5'-most EST

22077 Seq. No.

Contig ID 92861\_1.R1040

5'-most EST jC-gmf102220069d11d1

Method BLASTX q3759184 NCBI GI BLAST score 188 3.0e-14 E value Match length 48 % identity 71

NCBI Description (AB018441) phi-1 [Nicotiana tabacum]

Seq. No.

22078 92872 1.R1040 Contig ID 5'-most EST uC-gmropic019f03b1

Method BLASTX NCBI GI g1345773 BLAST score 217 4.0e-17 E value Match length 283 % identity 29

NCBI Description CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 1 (CHD-1)

>gi 455015 (L10410) DNA-binding protein [Mus musculus]

Seq. No. 22079

92875 1.R1040 Contig ID 5'-most EST uC-gmropic049h05b1

Method BLASTN NCBI GI q732912 BLAST score 308 E value 1.0e-173 598 Match length % identity 89

NCBI Description P.vulgaris mRNA for pectinesterase

Seq. No. 22080

Contig ID 92882 1.R1040

5'-most EST jC-gmf102220069h04d1

Seq. No. 22081

92884 1.R1040 Contig ID

LIB3170-045-Q1-K1-G6 5'-most EST

Method BLASTX NCBI GI g3319341 BLAST score 202 1.0e-15 E value Match length 36 % identity 92

NCBI Description (AF077407) similar to Medicago sativa nucleic acid binding

protein Alfin-1 (GB:L07291) [Arabidopsis thaliana]



```
Seq. No.
                  22082
Contig ID
                  92892 1.R1040
5'-most EST
                  jC-gmst02400015b01d1
Method
                  BLASTX
                  g2827658
NCBI GI
BLAST score
                  292
E value
                  3.0e-26
Match length
                  86
% identity
                  63
                  (AL021637) putative protein [Arabidopsis thaliana]
NCBI Description
                  22083
Seq. No.
Contig ID
                  92937 1.R1040
5'-most EST
                  LIB3170-046-Q1-J1-E7
Method
                  BLASTX
NCBI GI
                  g4006913
BLAST score
                  913
E value
                  7.0e-99
                  204
Match length
% identity
                  84
NCBI Description (299708) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  22084
Contig ID
                  92938 1.R1040
5'-most EST
                  LIB3170-046-Q1-J1-E8
Seq. No.
                  22085
Contig ID
                  92967 1.R1040
5'-most EST
                  LIB3170-046-Q1-K1-A4
Seq. No.
                  22086
                  92970 1.R1040
Contig ID
5'-most EST
                  jC-gmle01810091a01d1
Method
                  BLASTX
                  g3913439
NCBI GI
BLAST score
                  476
E value
                  1.0e-47
Match length
                  136
% identity
                   65
                  S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC)
NCBI Description
                   (SAMDC) >gi 1498080 (U64927) S-adenosylmethionine
                  decarboxylase [Ipomoea nil]
Seq. No.
                  22087
Contig ID
                  92973 1.R1040
5'-most EST
                  fua701039794.h1
Seq. No.
                  22088
Contig ID
                  92973 2.R1040
```

5'-most EST

uC-gmronoir027b11b1

Seq. No.

22089

Contig ID

92981 1.R1040

5'-most EST

LIB3170-046-Q1-K1-C11

Seq. No.

22090

Contig ID

92996 1.R1040



```
5'-most EST
                  bth700844723.h1
                  22091
Seq. No.
                  92998 1.R1040
Contig ID
5'-most EST
                  LIB3170-046-Q1-K1-D8
Method
                  BLASTX
NCBI GI
                  g3892204
BLAST score
                  324
E value
                  7.0e-30
Match length
                  160
% identity
                   44
                  (AF078105) site-1 protease of sterol regulatory element
NCBI Description
                  binding proteins [Cricetulus griseus]
Seq. No.
                  22092
                  93008 1.R1040
Contig ID
5'-most EST
                  jC-gmf102220085d10d1
Method
                  BLASTN
NCBI GI
                  g1947045
BLAST score
                  36
E value
                  1.0e-10
Match length
                  130
% identity
                  86
NCBI Description
                  Lotus japonicus late nodulin N1j16 (LjNOD16) gene, complete
                  22093
Seq. No.
                  93039 1.R1040
Contig ID
5'-most EST
                  zhf700965063.h1
                  22094
Seq. No.
Contig ID
                  93050 1.R1040
5'-most EST
                  LIB3170-048-Q1-J1-F11
Seq. No.
                  22095
                  93066 1.R1040
Contig ID
5'-most EST
                  LIB3170-050-Q1-J1-G9
Method
                  BLASTX
NCBI GI
                  q2137417
BLAST score
                  149
                  2.0e-09
E value
Match length
                  71
% identity
                  44
NCBI Description
                  Id-associated protein 1 - mouse >gi_1060925_dbj_BAA09854_
                   (D63784) MIDA1 [Mus musculus]
Seq. No.
                  22096
                  93116 1.R1040
Contig ID
5'-most EST
                  uC-gmflminsoy053e11b1
                  22097
Seq. No.
```

Contig ID 93118 1.R1040

5'-most EST LIB3170-047-Q1-K1-C7

22098 Seq. No.

Contig ID 93121 1.R1040

LIB3170-047-Q1-K1-D3 5'-most EST



Method BLASTX NCBI GI q2266672 BLAST score 397 E value 8.0e-39 Match length 106 74 % identity

(Y14214) phosphate transporter [Lycopersicon esculentum] NCBI Description

Seq. No.

22099

Contig ID 93128 1.R1040

5'-most EST LIB3170-047-Q1-K1-E2

Seq. No.

22100

93144 1.R1040 Contig ID

5'-most EST LIB3170-048-Q1-J1-A11

Seq. No.

22101 Contig ID 93153 1.R1040 ssr700553924.hl 5'-most EST

Seq. No.

22102

Contig ID 93153 2.R1040

5'-most EST LIB3170-048-Q1-J1-B1

Method BLASTX NCBI GI g4115534 BLAST score 462 4.0e-46 E value Match length 159 % identity 55

(AB012114) UDP-qlycose:flavonoid glycosyltransferase [Vigna NCBI Description

mungo]

Seq. No.

22103

Contig ID 93165 1.R1040

5'-most EST LIB3170-048-Q1-J1-C10

Seq. No.

22104

93174 1.R1040 Contig ID

5'-most EST LIB3170-048-Q1-J1-D11

Seq. No.

22105

93180\_1.R1040 Contig ID

5'-most EST LIB3170-048-Q1-J1-D6

Seq. No.

22106

93187 1.R1040 Contig ID

jC-gmst02400057c09d1 5'-most EST

Method BLASTX NCBI GI g2435511 BLAST score 524 E value 5.0e-53 Match length 151 % identity 64

(AF024504) contains similarity to prolyl 4-hydroxylase NCBI Description

alpha subunit [Arabidopsis thaliana]

Seq. No.

22107



```
Contig ID
                  93212_1.R1040
                  jC-gmst02400027c11a1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g4262230
BLAST score
                  141
E value
                  3.0e-18
Match length
                  68
% identity
                  72
                  (AC006200) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  22108
Contig ID
                  93224 1.R1040
5'-most EST
                  LIB3170-049-Q1-J1-A1
Seq. No.
                  22109
                   93232 1.R1040
Contig ID
5'-most EST
                  jC-gmle01810046d08d1
                  22110
Seq. No.
                  93237 1.R1040
Contig ID
5'-most EST
                  LIB3170-049-Q1-J1-B3
Method
                  BLASTN
NCBI GI
                  g3204102
BLAST score
                  150
E value
                  1.0e-78
Match length
                  262
% identity
                  89
NCBI Description
                  Cicer arietinum mRNA for hypothetical protein, clone Can35,
                  partial
                  22111
Seq. No.
Contig ID
                  93240 1.R1040
5'-most EST
                   jC-gmst02400046d12d1
Method
                  BLASTX
NCBI GI
                  q2244998
BLAST score
                   259
E value
                   5.0e-22
Match length
                   169
% identity
                  26
                  (Z97341) similarity to probable transcriptional adaptor
NCBI Description
                  ADA2 [Arabidopsis thaliana]
Seq. No.
                  22112
                   93259_1.R1040
Contig ID
5'-most EST
                  jC-gmst02400070b01d1
Seq. No.
                  22113
Contig ID
                   93273 2.R1040
5'-most EST
                  jC-gmle01810020c10d1
Method
                  BLASTX
NCBI GI
                  g2467273
```

BLAST score 228 2.0e-18 E value Match length 149 % identity 35

NCBI Description (Z99759) ubiquitin protein ligase [Schizosaccharomyces

pombe]



22114 Seq. No.

93288 1.R1040 Contig ID

5'-most EST LIB3170-049-Q1-J1-G6

22115 Seq. No.

93291 1.R1040 Contig ID

5'-most EST LIB3170-049-Q1-J1-H10

22116 Seq. No.

93298 1.R1040 Contig ID

5'-most EST jC-gmle01810020f02d1

Method BLASTX NCBI GI q1076291 BLAST score 282 E value 5.0e-25 Match length 105 53 % identity

amino acid transporter AAT1 - Arabidopsis thaliana NCBI Description

>gi\_2911069\_emb\_CAA17531\_ (AL021960) amino acid transport
protein AATI [Arabidopsis thaliana]

Seq. No. 22117

Contig ID 93308 1.R1040

5'-most EST LIB3170-049-Q1-K2-C6

Seq. No. 22118

Contig ID 93333 1.R1040

5'-most EST LIB3170-051-Q1-K2-C2

Seq. No. 22119

Contig ID 93364 1.R1040

5'-most EST LIB3170-049-Q1-K2-C7

Method BLASTX NCBI GI g4455287 BLAST score 414 E value 1.0e-40 Match length 111 % identity 72

(AL035527) putative protein [Arabidopsis thaliana] NCBI Description

Seq. No. 22120

93425 1.R1040 Contig ID

LIB3170-050-Q1-J1-A7 5'-most EST

22121 Seq. No.

Contig ID 93431 1.R1040

5'-most EST jC-gmst02400014c03d1

22122 Seq. No.

Contig ID 93440 1.R1040

5'-most EST LIB3170-050-Q1-J1-C3

22123 Seq. No.

93454 1.R1040 Contig ID

5'-most EST LIB3170-050-Q1-J1-D9

```
Seq. No.
                   22124
                   93457 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810041a12d1
                  22125
Seq. No.
                  93457 2.R1040
Contig ID
                  LIB3170-050-Q1-J1-F9
5'-most EST
Method
                  BLASTX
NCBI GI
                  g4062514
                  150
BLAST score
E value
                   2.0e-09
Match length
                   68
% identity
```

22126

93458 1.R1040

NCBI Description (D90732) Hypothetical protein 7.6 [Escherichia coli]

5'-most EST jC-gmro02910032f11d1
Method BLASTN
NCBI GI g3510339
BLAST score 48
E value 1.0e-17
Match length 148
% identity 87

Seq. No.

Contig ID

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K3K7, complete sequence [Arabidopsis thaliana]

Seq. No. 22127

Contig ID 93459 1.R1040
5'-most EST LIB3170-050-Q1-J1-E3

Method BLASTX

NCRI CI 21174470

NCBI GI g1174470
BLAST score 286
E value 2.0e-25
Match length 102
% identity 61

NCBI Description OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5)

(INTEGRAL MEMBRANE PROTEIN 1) >gi\_508543 (L34260) integral membrane protein 1 [Mus musculus] >gi\_1588285\_prf\_\_2208301A

integral membrane protein [Mus musculus]

Seq. No. 22128 Contig ID 93459 2

Contig ID 93459 2.R1040 5'-most EST kl1701205912.h1

Method BLASTX
NCBI GI g1174470
BLAST score 360
E value 1.0e-43
Match length 137
% identity 69

NCBI Description OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5)

(INTEGRAL MEMBRANE PROTEIN 1) >gi\_508543 (L34260) integral membrane protein 1 [Mus musculus] >gi\_1588285\_prf\_\_2208301A

integral membrane protein [Mus musculus]

Seq. No. 22129

Contig ID 93465 1.R1040



5'-most EST LIB3170-050-Q1-J1-F1

Method BLASTX
NCBI GI g1245182
BLAST score 857
E value 4.0e-95
Match length 211
% identity 81

NCBI Description (U49398) sterol delta-7 reductase [Arabidopsis thaliana]

Seq. No. 22130

Contig ID 93470\_1.R1040

5'-most EST jC-gmle01810072e05d1

Method BLASTX
NCBI GI g4539435
BLAST score 285
E value 4.0e-25
Match length 78
% identity 68

NCBI Description (AL049523) putative protein [Arabidopsis thaliana]

Seq. No. 22131

Contig ID 93472 1.R1040

5'-most EST jC-gmro02800039c05d1

Method BLASTX
NCBI GI g1871181
BLAST score 180
E value 9.0e-13
Match length 118
% identity 43

NCBI Description (U90439) ring zinc finger protein isolog [Arabidopsis

thaliana]

Seq. No. 22132

Contig ID 93482\_1.R1040

5'-most EST LIB3170-050-Q1-J1-G3

Seq. No. 22133

Contig ID 93483\_1.R1040

5'-most EST jC-gmro02910023d06a1

Method BLASTX
NCBI GI 94371285
BLAST score 552
E value 2.0e-56
Match length 122
% identity 82

NCBI Description (AC006260) hypothetical protein [Arabidopsis thaliana]

Seq. No. 22134

Contig ID 93483\_2.R1040 5'-most EST uxk700673240.h1

Method BLASTX
NCBI GI 94371285
BLAST score 273
E value 2.0e-24
Match length 83
% identity 69

NCBI Description (AC006260) hypothetical protein [Arabidopsis thaliana]



Seq. No. 22135

Contig ID 93484 1.R1040

5'-most EST LIB3170-054-Q1-J1-H7

Seq. No. 22136

Contig ID 93584 1.R1040

5'-most EST LIB3170-051-Q1-J1-B1

Method BLASTX
NCBI GI g2262173
BLAST score 460
E value 1.0e-45
Match length 100
% identity 89

NCBI Description (AC002329) NADPH thioredoxin reductase [Arabidopsis

thaliana]

Seq. No.

Contig ID 93586\_1.R1040

5'-most EST LIB3170-058-Q1-J1-B8

22137

Seq. No. 22138

Contig ID 93591 1.R1040

5'-most EST LIB3170-051-Q1-J1-B7

Seq. No. 22139

Contig ID 93601\_1.R1040

5'-most EST LIB3170-051-Q1-J1-C5

Seq. No. 22140

Contig ID 93614 1.R1040

5'-most EST jC-gmle01810009a05d1

Seq. No. 22141

Contig ID 93618 1.R1040

5'-most EST LIB3170-051-Q1-J1-E3

Seq. No. 22142

Contig ID 93626\_1.R1040

5'-most EST jC-gmst02400020dc02d1

Seq. No. 22143

Contig ID 93631 1.R1040

5'-most EST jC-gmf102220089d11d1

Seq. No. 22144

Contig ID 93635 1.R1040

5'-most EST LIB3170-051-Q1-J1-F9

Seq. No. 22145

Contig ID 93636\_1.R1040 5'-most EST smw700646167.h1

Seq. No. 22146

Contig ID 93652\_1.R1040

5'-most EST jC-gmro02910041011d1

Method BLASTX



NCBI GI g2435517 BLAST score 233 E value 3.0e-19 Match length 106 % identity 48

NCBI Description (AF024504) contains similarity to peptidase family A1

[Arabidopsis thaliana]

Seq. No. 22147

Contig ID 93655 1.R1040

5'-most EST LIB3170-051-Q1-K1-A10

Seq. No. 22148

Contig ID 93657\_1.R1040

5'-most EST LIB3170-051-Q1-K1-A12

Seq. No. 22149

Contig ID 93673 1.R1040

5'-most EST LIB3170-051-Q1-K2-B6

Seq. No. 22150

Contig ID 93682\_1.R1040 5'-most EST zsg701127750.h1

Method BLASTX
NCBI GI g2642436
BLAST score 151
E value 9.0e-10
Match length 92
% identity 55

NCBI Description (AC002391) hypothetical protein [Arabidopsis thaliana]

Seq. No. 22151

Contig ID 93694 1.R1040

5'-most EST LIB3170-051-Q1-K1-E10

Seq. No. 22152

Contig ID 93712 1.R1040

5'-most EST LIB3170-051-Q1-K1-G1

Seq. No. 22153

Contig ID 93727\_1.R1040

5'-most EST LIB3170-051-Q1-K2-H8

Seq. No. 22154

Contig ID 93814\_1.R1040

5'-most EST jC-gmf102220054g12a1

Seq. No. 22155

Contig ID 93819\_1.R1040 5'-most EST dpv701100407.h1

Method BLASTX
NCBI GI g3650033
BLAST score 220
E value 2.0e-17
Match length 128
% identity 42

NCBI Description (AC005396) unknown protein [Arabidopsis thaliana]



93820\_1.R1040 Contig ID

5'-most EST LIB3170-052-Q1-J1-B2

22157 Seg. No.

Contig ID 93836 1.R1040

5'-most EST g5342475 Method BLASTX NCBI GI q4220479 BLAST score 142 E value 1.0e-08

67 Match length 48 % identity

(AC006069) unknown protein [Arabidopsis thaliana] NCBI Description

Seq. No.

22158 Contig ID 93854 1.R1040 5'-most EST zsg701120839.h1

Seq. No.

Contig ID 93862 1.R1040

5'-most EST jC-gmle01810014b09d1

22159

22160

Seq. No.

Contig ID 93874 1.R1040

5'-most EST LIB3170-052-Q1-J1-G7

Seq. No. 22161

93881\_1.R1040 Contig ID zhf700964924.h1 5'-most EST

Method BLASTN q3641867 NCBI GI BLAST score 42 E value 4.0e-14 Match length 90 87 % identity

Cicer arietinum epicotyl EST, clone Cap30-2 NCBI Description

Seq. No. 22162

93892 1.R1040 Contig ID 5'-most EST leu701146057.h1

Method BLASTX NCBI GI q2342685 BLAST score 225 E value 2.0e-18 Match length 74 57 % identity

(AC000106) Contains similarity to Rhodococcus amidase NCBI Description

(gb\_D16207). ESTs gb\_T20504, gb\_H36650, gb\_N97423, gb\_H36595

come from this gene. [Arabidopsis thaliana]

22163 Seq. No.

Contig ID 93913 1.R1040

5'-most EST LIB3170-052-Q1-K1-C6

Method BLASTN NCBI GI g2062705



BLAST score 38 E value 8.0e-12 Match length 50 % identity 40

NCBI Description Human butyrophilin (BTF5) mRNA, complete cds

Seq. No. 22164

Contig ID 93972 1.R1040

5'-most EST jC-gmle01810028e11d1

Method BLASTX
NCBI GI g4006899
BLAST score 239
E value 6.0e-20
Match length 72
% identity 58

NCBI Description (Z99708) putative protein [Arabidopsis thaliana]

Seq. No. 22165

Contig ID 93976 1.R1040 5'-most EST g5688476 Method BLASTX NCBI GI g2791900 BLAST score 610 E value 2.0e-63 Match length 145 % identity 73

NCBI Description (AJ000057) PP7 [Arabidopsis thaliana]

Seq. No. 22166

Contig ID 93981\_1.R1040 5'-most EST fC-gmro700876555d1

Seq. No. 22167

Contig ID 93982 1.R1040

5'-most EST LIB3170-053-Q1-J1-B5

Seq. No. 22168

Contig ID 93998\_1.R1040

5'-most EST LIB3170-053-Q1-J1-D4

Seq. No. 22169

Contig ID 94016 1.R1040

5'-most EST LIB3170-053-Q1-J1-F12

Method BLASTX
NCBI GI g2623297
BLAST score 340
E value 1.0e-31
Match length 125
% identity 54

NCBI Description (AC002409) unknown protein [Arabidopsis thaliana]

>gi 3790583 (AF079180) RING-H2 finger protein RHC1a

[Arabidopsis thaliana]

Seq. No. 22170

Contig ID 94023\_1.R1040

5'-most EST LIB3170-053-Q1-J1-G1

Method BLASTX



NCBI GI g4104457 BLAST score 404 E value 3.0e-39 Match length 99 % identity 78

NCBI Description (AF036172) 2-oxoglutarate/malate translocator [Zea mays]

Seq. No. 22171

Contig ID 94029\_1.R1040

5'-most EST jC-gmf102220089b02d1

Method BLASTX
NCBI GI g4106515
BLAST score 471
E value 6.0e-47
Match length 160
% identity 57

NCBI Description (AF092743) CAK associated cyclinH homolog [Populus tremula

x Populus tremuloides]

Seq. No. 22172

Contig ID 94030 1.R1040

5'-most EST jC-gmfl02220104f04d1

Seq. No. 22173

Contig ID 94036 1.R1040

5'-most EST LIB3170-053-Q1-J1-H3

Method BLASTX
NCBI GI g2245000
BLAST score 234
E value 2.0e-19
Match length 74
% identity 58

NCBI Description (Z97341) hypothetical protein [Arabidopsis thaliana]

Seq. No. 22174

Contig ID 94052\_1.R1040

5'-most EST LIB3170-053-Q1-K1-B3

Method BLASTX
NCBI GI g1730771
BLAST score 322
E value 1.0e-29
Match length 195
% identity 28

NCBI Description HYPOTHETICAL 110.9 KD PROTEIN IN SPC98-TOM70 INTERGENIC

REGION >gi 2132752 pir S63064 probable membrane protein

YNL123w - yeast (Saccharomyces cerevisiae)

>gi\_1183950 emb CAA93384 (Z69382) N1897 [Saccharomyces
cerevisiae] >gi\_1302054 emb CAA96004 (Z71399) ORF YNL123w

[Saccharomyces cerevisiae]

Seq. No. 22175

Contig ID 94056\_1.R1040 5'-most EST asn701132215.h2

Method BLASTX
NCBI GI g486964
BLAST score 308
E value 1.0e-27



Match length 116 % identity 47

NCBI Description CCR4 protein - yeast (Saccharomyces cerevisiae) >gi 171854

(L05146) Ccr4p: Carbon catabolite repressor protein [Saccharomyces cerevisiae] >gi 386682 (L05027) repressor

protein [Saccharomyces cerevisiae]

Seq. No. 22176

Contig ID 94120\_1.R1040

5'-most EST LIB3170-054-Q1-J1-A5

Method BLASTN
NCBI GI g4039114
BLAST score 37
E value 4.0e-11
Match length 180
% identity 84

NCBI Description Glycine max alcohol-dehydrogenase (Adh-2) gene, partial cds

Seq. No.

22177

Contig ID 94128 1.R1040

5'-most EST uC-gmflminsoy026a09b1

Seq. No. 22178

Contig ID 94140 1.R1040

5'-most EST LIB3170-054-Q1-J1-C7

Method BLASTX NCBI GI g4335739 BLAST score 282 E value 6.0e-25 Match length 74 % identity 69

NCBI Description (AC006248) hypothetical protein [Arabidopsis thaliana]

Seq. No. 22179

Contig ID 94144 1.R1040 5'-most EST 94286798

Seq. No. 22180

Contig ID 94144 2.R1040

5'-most EST jC-gmle01810030b04d1

Seq. No. 22181

Contig ID 94164\_1.R1040

5'-most EST LIB3170-054-Q1-J1-G3

Seq. No. 22182

Contig ID 94169\_1.R1040

5'-most EST jC-gmst02400067c07d1

Seq. No. 22183

Contig ID 94202\_1.R1040

5'-most EST LIB3170-054-Q1-K1-C4

Method BLASTX
NCBI GI g2213600
BLAST score 1160
E value 1.0e-127
Match length 331



% identity 69

NCBI Description (AC000348) T7N9.20 [Arabidopsis thaliana]

Seq. No.

22184

Contig ID

94206 1.R1040

5'-most EST

LIB3170-054-Q1-K1-C8

Method NCBI GI BLASTX g3877439

BLAST score E value 128 2.0e-12

Match length % identity

103 43

NCBI Description

(Z72510) similarity to yeast UTR3 protein (Swiss Prot accession number P21374); cDNA EST EMBL:D72822 comes from this gene; cDNA EST EMBL:D75763 comes from this gene; cDNA EST yk274e3.3 comes from this gene; cDNA EST yk274e3.5 c

Seq. No.

22185

Contig ID 5'-most EST

94206\_2.R1040 seb700650923.h1

Seq. No.

22186

Contig ID

94228 1.R1040

5'-most EST

LIB3170-054-Q1-K1-E9

Method NCBI GI BLASTX q4467126

BLAST score

318

E value Match length 2.0e-29 140

% identity NCBI Description 48 (AL035538) guanine nucleotide-exchange protein-like

[Arabidopsis thaliana]

Seq. No.

22187

Contig ID

94247 1.R1040

5'-most EST

jC-gmst02400063c11a1

Method NCBI GI BLASTX g3047115

BLAST score E value 199

Match length

5.0e-15 174

35

% identity

NCBI Description (AF058919) No definition line found [Arabidopsis thaliana]

Seq. No.

22188

Contig ID 5'-most EST 94255\_1.R1040 zhf700955739.h1

Method

BLASTX

NCBI GI

g1730836

BLAST score E value 346 3.0e-32

Match length % identity

275 35

NCBI Description

HYPOTHETICAL 54.2 KD PROTEIN IN ZWF1-BLH1/LAP3 INTERGENIC

REGION >gi\_2131939\_pir\_\_\$63206 hypothetical protein YNL240c

- yeast (Saccharomyces cerevisiae)

>gi\_1183974\_emb\_CAA93358 (Z69381) N1114 [Saccharomyces



cerevisiae] >gi\_1302274\_emb\_CAA96145\_ (Z71516) ORF YNL240c [Saccharomyces cerevisiae]

Seq. No. 22189

Contig ID 94269 1.R1040

5'-most EST jC-gmro02800035g10d1

Seq. No. 22190

Contig ID 94276 1.R1040

5'-most EST LIB3170-055-Q1-J1-C7

Method BLASTX
NCBI GI g2252631
BLAST score 174
E value 5.0e-12
Match length 66
% identity 52

NCBI Description (U95973) hypothetical protein [Arabidopsis thaliana]

Seq. No. 22191

Contig ID 94278\_1.R1040

5'-most EST LIB3170-055-Q1-J1-E11

Seq. No. 22192

Contig ID 94297 1.R1040

5'-most EST jC-gmro02910008d08d1

Method BLASTX
NCBI GI g3212865
BLAST score 234
E value 2.0e-19
Match length 86
% identity 60

NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]

Seq. No. 22193

Contig ID 94334\_1.R1040 5'-most EST taw700659178.h1

Seq. No. 22194

Contig ID 94407 1.R1040

5'-most EST uC-gmrominsoy035e06b1

Method BLASTX
NCBI GI g2129918
BLAST score 150
E value 2.0e-09
Match length 46
% identity 59

NCBI Description BPF-1 protein - parsley >gi\_396197\_emb\_CAA48413\_ (X68337)

BPF-1 [Petroselinum crispum] >gi 441310 emb CAA44518

(X62653) BPF-1 [Petroselinum crispum]

Seq. No. 22195

Contig ID 94413 1.R1040

5'-most EST jC-gmf102220071e04d1

Seq. No. 22196

Contig ID 94451\_1.R1040 5'-most EST trc700565737.h1



Method BLASTX
NCBI GI g731284
BLAST score 318
E value 8.0e-29
Match length 228
% identity 35

NCBI Description HYPOTHETICAL 75.2 KD PROTEIN IN ACS1-GCV3 INTERGENIC REGION >gi\_1077482\_pir\_\_S51971 probable membrane protein YAL048c -

yeast (Saccharomyces cerevisiae) >gi\_595536 (U12980)

Yal048cp [Saccharomyces cerevisiae]

Seq. No. 22197

Contig ID 94451 2.R1040

5'-most EST jC-gmro02910009e10d1

Seq. No. 22198

Contig ID 94469\_1.R1040 5'-most EST jsh701066027.h1

Seq. No. 22199

Contig ID 94481\_1.R1040 5'-most EST 6HC-02-Q1-E1-G3

Method BLASTX
NCBI GI g4510376
BLAST score 413
E value 3.0e-40
Match length 172
% identity 47

NCBI Description (AC007017) unknown protein [Arabidopsis thaliana]

Seq. No.

Contig ID 94486 1.R1040

5'-most EST jC-gmst02400005c09d1

22200

Method BLASTX
NCBI GI 94467144
BLAST score 179
E value 6.0e-13
Match length 50
% identity 68

NCBI Description (AL035540) putative phosphatidylinositol synthase

[Arabidopsis thaliana]

Seq. No. 22201

Contig ID 94494\_1.R1040

5'-most EST LIB3170-057-Q1-J1-D1

Method BLASTN
NCBI GI g168579
BLAST score 184
E value 5.0e-99
Match length 348
% identity 90

NCBI Description Maize pyruvate, orthophosphate dikinase mRNA, complete cds

Seq. No. 22202

Contig ID 94497 1.R1040

5'-most EST  $jC-gm\overline{f}$ 1022220080d02d1



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22203
Seq. No.
                  94519 1.R1040
Contig ID
                  LIB3170-057-Q1-J1-F12
5'-most EST
                  22204
Seq. No.
                  94521 1.R1040
Contig ID
                  LIB3170-057-Q1-K1-F3
5'-most EST
                   22205
Seq. No.
                   94544 1.R1040
Contig ID
                   vwf700675270.hl
5'-most EST
                   BLASTX
Method
                   g2181180
NCBI GI
                   238
BLAST score
                   3.0e - 30
E value
                   226
Match length
                   40
% identity
NCBI Description (Z84377) xylosidase [Aspergillus niger]
                   22206
Seq. No.
                   94554 1.R1040
Contig ID
                   LIB3170-067-Q1-K1-B10
5'-most EST
                   BLASTX
Method
                   q3413716
NCBI GI
                   199
BLAST score
                   3.0e-15
E value
                   137
Match length
                   10
 % identity
                   (AC004747) unknown protein [Arabidopsis thaliana]
NCBI Description
                   >gi_3643589 (AC005395) unknown protein [Arabidopsis
                   thaliana]
                    22207
 Seq. No.
                    94569 1.R1040
 Contig ID
                    LIB3170-057-Q1-K1-C6
 5'-most EST
                    BLASTX
 Method
                    g1806144
 NCBI GI
                    568
 BLAST score
                    1.0e-58
 E value
                    165
 Match length
                    71
 % identity
                   (X97316) cdc2MsE [Medicago sativa]
 NCBI Description
                    22208
 Seq. No.
                    94597 1.R1040
 Contig ID
                    LIB3170-057-Q1-K1-F11
 5'-most EST
                    BLASTX
 Method
                    q3024425
 NCBI GI
                    821
 BLAST score
                    3.0e-88
 E value
                    188
 Match length
                    82
  % identity
 NCBI Description PYRUVATE, PHOSPHATE DIKINASE PRECURSOR
                    (PYRUVATE,ORTHOPHOSPHATE DIKINASE) >gi_1076700_pir__S53297
                    pyruvate, orthophosphate dikinase (EC 2.7.9.1) - Flaveria
```

pringlei >gi\_577776\_emb\_CAA53223\_ (X75516)

pyruvate, orthophosphate dikinase [Flaveria pringlei]



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22209
Seq. No.
                  94620 1.R1040
Contig ID
5'-most EST
                  LIB3170-057-Q1-K1-H3
                  BLASTX
Method
                  g1486472
NCBI GI
BLAST score
                  342
E value
                  6.0e - 32
Match length
                  71
% identity
NCBI Description (X99853) oxoglutarate malate translocator [Solanum
                  tuberosum]
                  22210
Seq. No.
Contig ID
                  94640 1.R1040
5'-most EST
                  dpv701103669.h1
Method
                  BLASTX
NCBI GI
                  g2499115
BLAST score
                  966
E value
                  1.0e-105
Match length
                  196
                  91
% identity
NCBI Description VACUOLAR ASSEMBLY PROTEIN VPS41 HOMOLOG >gi 1835788
                   (U86662) VPS41 [Lycopersicon esculentum]
Seq. No.
                  22211
Contig ID
                  94648 1.R1040
5'-most EST
                  LIB3170-058-Q1-J1-C7
Method
                  BLASTX
NCBI GI
                  g2731377
BLAST score
                  327
E value
                  6.0e-30
Match length
                  236
% identity
                  36
NCBI Description
                  (U28739) similar to alcohol dehydrogenase/ribitol
                  dehydrogenase [Caenorhabditis elegans]
Seq. No.
                  22212
Contig ID
                  94660 1.R1040
5'-most EST
                  jC-gmle01810005f09d1
                  22213
Seq. No.
Contig ID
                  94660 2.R1040
5'-most EST
                  jC-gmro02910070a09d1
                  22214
Seq. No.
Contig ID
                  94670 1.R1040
5'-most EST
                  g4290342
Seq. No.
                  22215
Contig ID
                  94688 1.R1040
5'-most EST
                  LIB3170-058-Q1-J1-H7
```

Contig ID 94732 1.R1040 5'-most EST

LIB3170-058-Q1-K1-E12

Method BLASTX



NCBI GI g122772 BLAST score 226 E value 2.0e-18 Match length 90 % identity 57

NCBI Description TRANSCRIPTION FACTOR HBP-1B >gi 100809 pir S15347

transcription factor HBP-1b - wheat >gi 21635 emb CAA40102

(X56782) HBP-1b [Triticum aestivum]

Seq. No. 22217

Contig ID 94765 1.R1040

5'-most EST LIB3170-058-Q1-K1-H8

Method BLASTX
NCBI GI g3172025
BLAST score 606
E value 1.0e-63
Match length 181
% identity 66

NCBI Description (AB005805) aldehyde oxidase [Arabidopsis thaliana]

Seq. No. 22218

Contig ID 94769\_1.R1040 5'-most EST dpv701103685.h1

Method BLASTX
NCBI GI g3548803
BLAST score 672
E value 2.0e-70
Match length 158
% identity 82

NCBI Description (AC005313) putative DNA-binding protein [Arabidopsis thaliana] >gi\_4335770\_gb\_AAD17447\_ (AC006284) putative

SMUBP-2 [mouse] DNA-binding protein [Arabidopsis thaliana]

Seq. No. 22219

Contig ID 94790 1.R1040

5'-most EST LIB3170-059-Q1-J1-C2

Seq. No. 22220

Contig ID 94791\_1.R1040

5'-most EST LIB3170-059-Q1-J1-C4

Method BLASTX
NCBI GI g1223579
BLAST score 330
E value 1.0e-30
Match length 105
% identity 65

NCBI Description (X96481) cDNA101 [Arabidopsis thaliana]

Seq. No. 22221

Contig ID 94792 1.R1040

Seq. No. 22222

Contig ID 94792 2.R1040

5'-most EST jC-gmro02910067b01d1

Seq. No. 22223



Contig ID 94805\_1.R1040 5'-most EST LIB3170-059-Q1-J1-E2

Seq. No. 22224

Contig ID 94813 1.R1040

5'-most EST jC-gmst02400050g12d1

Seq. No. 22225

Contig ID 94908\_1.R1040 5'-most EST uC-gmropic064b05b1

Seq. No. 22226

Contig ID 94909 1.R1040

5'-most EST jC-gmro02800031e05d1

Seq. No. 22227

Contig ID 94927 1.R1040

5'-most EST LIB3170-060-Q1-J1-E10

Method BLASTX
NCBI GI g4337189
BLAST score 205
E value 8.0e-16
Match length 59
% identity 63

NCBI Description (AC006403) putative calmodulin-binding protein [Arabidopsis

thaliana]

Seq. No. 22228

Contig ID 94929 1.R1040

5'-most EST jC-gmro02910020c04d1

Seg. No. 22229

Contig ID 94947 1.R1040

5'-most EST LIB3170-060-Q1-J1-G6

Method BLASTX
NCBI GI g461736
BLAST score 152
E value 7.0e-10
Match length 51
% identity 69

NCBI Description MITOCHONDRIAL CHAPERONIN HSP60-2 PRECURSOR

>gi\_478786\_pir\_\_S29316 chaperonin 60 - cucurbit

>gi\_12546\_emb\_CAA50218\_ (X70868) chaperonin 60 [Cucurbita

sp.]

Seq. No. 22230

Contig ID 95038\_1.R1040 5'-most EST bth700846680.h1

Method BLASTX
NCBI GI g4490297
BLAST score 174
E value 2.0e-12
Match length 166
% identity 31

NCBI Description (AL035678) putative protein [Arabidopsis thaliana]

Seq. No. 22231



Contig ID 95040\_1.R1040

5'-most EST LIB3170-061-Q1-J1-A9

Method BLASTX
NCBI GI g2262172
BLAST score 249
E value 5.0e-37
Match length 122
% identity 62

NCBI Description (AC002329) predicted protein of unknown function

[Arabidopsis thaliana]

Seq. No. 22232

Contig ID 95081 1.R1040 5'-most EST bth700848755.h1

Seq. No. 22233

Contig ID 95082 1.R1040

5'-most EST LIB3170-061-Q1-J1-F12

Seq. No. 22234

Contig ID 95084 1.R1040

5'-most EST jC-qmle01810042h05d1

Seq. No. 22235

Contig ID 95103\_1.R1040 5'-most EST fC-gmse700675662r1

Method BLASTX
NCBI GI g3047085
BLAST score 269
E value 3.0e-23
Match length 118
% identity 46

NCBI Description (AF058914) No definition line found [Arabidopsis thaliana]

Seq. No. 22236

Contig ID 95104\_1.R1040

5'-most EST LIB3170-061-Q1-J1-H11

Method BLASTX
NCBI GI g1617200
BLAST score 160
E value 1.0e-10
Match length 37
% identity 78

NCBI Description (Y08607) Shaggy-like kinase 6 [Nicotiana tabacum]

Seq. No. 22237

Contig ID 95105 1.R1040

5'-most EST jC-gmf102220051d04d1

Seq. No. 22238

Contig ID 95108 1.R1040

5'-most EST LIB3170-061-Q1-J1-H6

Method BLASTX
NCBI GI g3785995
BLAST score 247
E value 1.0e-20
Match length 77

3557



% identity 68
NCBI Description (AC005499) unknown protein [Arabidopsis thaliana]

Seq. No. 22239

Contig ID 95108 2.R1040

5'-most EST jC-gmst02400069d03d1

Seq. No. 22240

Contig ID 95115\_1.R1040 5'-most EST ncj700978480.h1

Seq. No. 22241

Contig ID 95122 1.R1040

5'-most EST LIB3170-061-Q1-K2-B11

Method BLASTX
NCBI GI g2244772
BLAST score 508
E value 1.0e-51
Match length 152
% identity 64

NCBI Description (Z97335) transport protein [Arabidopsis thaliana]

Seq. No. 22242

Contig ID 95185 1.R1040

5'-most EST LIB3170-061-Q1-K2-H12

Seq. No. 22243

Contig ID 95203 1.R1040

5'-most EST jC-gmf102220142g07d1

Seq. No. 22244

Contig ID 95205\_1.R1040

5'-most EST LIB3170-062-Q1-J1-B11

Method BLASTX
NCBI GI g4262174
BLAST score 813
E value 3.0e-87
Match length 193
% identity 50

NCBI Description (AC005508) 9058 [Arabidopsis thaliana]

Seq. No. 22245

Contig ID 95221\_1.R1040

5'-most EST LIB3170-085-Q1-J1-H5

Seq. No. 22246

Contig ID 95226 1.R1040

5'-most EST LIB3170-062-Q1-J1-D7

Seq. No. 22247

Contig ID 95238 1.R1040

5'-most EST LIB3170-062-Q1-J1-E5

Seq. No. 22248

Contig ID 95250 1.R1040

5'-most EST LIB3170-062-Q1-J1-G10



Contig ID 95261 1.R1040

5'-most EST LIB3170-062-Q1-J1-H10

Seq. No.

22250

22251

Contig ID 95281 1.R1040

5'-most EST LIB3170-062-Q1-K1-A9

Seq. No.

Contig ID 95282\_1.R1040

5'-most EST LIB3170-062-Q1-K1-B1

Method BLASTX
NCBI GI g4160573
BLAST score 207
E value 3.0e-16
Match length 84
% identity 48

NCBI Description (AL035226) guanine nucleotide binding protein beta

subunit-like [Schizosaccharomyces pombe]

Seq. No.

Contig ID 95326 1.R1040

5'-most EST LIB3170-062-Q1-K1-F5

22252

Seq. No.

22253 95351 1.R1040

Contig ID 95351\_1.R1040 5'-most EST ssr700555502.h1

Seq. No. 22254

Contig ID 95353 1.R1040

5'-most EST LIB3170-064-Q1-J1-B1

Method BLASTN
NCBI GI g1372965
BLAST score 48
E value 8.0e-18

Match length 104 % identity 87

NCBI Description Vicia faba CREB-like protein mRNA, complete cds

Seq. No. 22255

Contig ID 95363\_1.R1040

5'-most EST LIB3170-064-Q1-J1-B3

Seq. No. 22256

Contig ID 95372\_1.R1040 5'-most EST ncj700987326.h1

Seq. No. 22257

Contig ID 95390 1.R1040

5'-most EST LIB3170-066-Q1-J1-C6

Method BLASTN
NCBI GI g3925362
BLAST score 34
E value 2.0e-09
Match length 99
% identity 95

NCBI Description Malus domestica homeodomain protein (h3) mRNA, complete cds



Contig ID 95398\_1.R1040 5'-most EST fC-gmse700829816d1

Method BLASTX
NCBI GI g3413513
BLAST score 642
E value 4.0e-67
Match length 153
% identity 78

NCBI Description (AJ000266) glucose-6-phosphate isomerase [Spinacia

oleracea]

Seq. No. 22259

Contig ID 95460 1.R1040 5'-most EST fde700875403.h1

Method BLASTX
NCBI GI g2501612
BLAST score 432
E value 1.0e-42
Match length 130
% identity 60

NCBI Description HYPOTHETICAL 89.8 KD PROTEIN YPL207W

>gi\_2133000\_pir\_\_S65226 probable membrane protein YPL207w yeast (Saccharomyces cerevisiae) >gi 1370430 emb CAA97922

(Z73563) ORF YPL207w [Saccharomyces cerevisiae]

Seq. No. 22260

Contig ID 95496 1.R1040

5'-most EST LIB3170-065-Q1-J1-D6

Seq. No. 22261

Contig ID 95525\_1.R1040 5'-most EST fC-gmle7000786711a1

Method BLASTX
NCBI GI g3805845
BLAST score 1684
E value 0.0e+00
Match length 397
% identity 79

NCBI Description (AL031986) putative protein [Arabidopsis thaliana]

Seq. No. 22262

Contig ID 95588\_1.R1040

5'-most EST jC-gmf102220065a11d1

Method BLASTX
NCBI GI g4102839
BLAST score 550
E value 3.0e-56
Match length 149
% identity 69

NCBI Description (AF016713) LeOPT1 [Lycopersicon esculentum]

Seq. No. 22263

Contig ID 95588 2.R1040 5'-most EST wvk700681142.h2



22264

Contig ID 95589 1.R1040

5'-most EST LIB3170-066-Q1-J1-B4

Seq. No.

22265

Contig ID 95589 2.R1040

5'-most EST jC-qmst02400011h11d1

Seq. No.

22266

Contig ID 5'-most EST 95591 1.R1040 pxt700945131.hl

Seq. No.

22267

Contig ID

95604 1.R1040

5'-most EST

LIB3170-066-Q1-K1-D5

Seq. No.

22268

Contig ID

95614 1.R1040

5'-most EST

LIB3170-066-Q1-K1-E8

Method NCBI GI BLASTX g4336434

BLAST score

398

E value

1.0e-38

Match length

141

% identity

57

NCBI Description

(AF092431) nodule-enhanced protein phosphatase type 2C

[Lotus japonicus]

Seq. No.

22269

Contig ID

95620 1.R1040

5'-most EST

jC-gmle01810094g01d1

Seq. No.

22270

Contig ID

95625 1.R1040

5'-most EST

jC-gmle01810088d04d1

Seq. No.

22271

Contig ID

95629 1.R1040

5'-most EST

LIB3170-066-Q1-J1-H2

Seq. No.

22272

Contig ID

95664 1.R1040

5'-most EST

LIB3170-066-Q1-K1-D8

Seq. No.

22273

Contig ID

95686 1.R1040

5'-most EST

LIB3170-066-Q1-K1-G5

Method

BLASTX g1931650

NCBI GI

BLAST score E value

181

Match length

4.0e-13 118

% identity

41

NCBI Description

(U95973) disease resistance protein RPM1 isolog

[Arabidopsis thaliana]

Seq. No.

22274



Contig ID 95700 1.R1040 5'-most EST LIB3170-067-Q1-J1-A11

Seq. No. 22275

Contig ID 95719\_1.R1040

5'-most EST LIB3170-072-Q1-J1-C10

Seq. No. 22276

Contig ID 95726 1.R1040

5'-most EST LIB3170-067-Q1-J1-C8

Seq. No. 22277

Contig ID 95738 1.R1040

5'-most EST LIB3170-067-Q1-J1-E10

Method BLASTX
NCBI GI g3047082
BLAST score 393
E value 7.0e-38
Match length 85
% identity 78

NCBI Description (AF058914) similar to Vigna radiata pectinacetylesterase

precursor (GB:X99348) [Arabidopsis thaliana]

Seq. No. 22278

Contig ID 95854 1.R1040

5'-most EST uC-gmflminsoy069g04b1

Method BLASTX
NCBI GI g2281086
BLAST score 179
E value 5.0e-13
Match length 78
% identity 49

NCBI Description (AC002333) indole-3-acetate beta-glucosyltransferase isolog

[Arabidopsis thaliana]

Seq. No. 22279

Contig ID 95871\_1.R1040 5'-most EST uC-gmropic0001a04a1

Seq. No. 22280

Contig ID 95874 1.R1040

5'-most EST LIB3170-068-Q1-J1-F1

Seq. No. 22281

Contig ID 95907 1.R1040

5'-most EST LIB3170-068-Q1-K1-D9

Method BLASTX
NCBI GI g2597826
BLAST score 135
E value 3.0e-16
Match length 71
% identity 63

NCBI Description (Y14590) class IV chitinase [Arabidopsis thaliana]

Seq. No. 22282

Contig ID 95922 1.R1040

5'-most EST LIB3170-068-Q1-K1-E6



Method -BLASTX NCBI GI q1710032 BLAST score 300 1.0e-26 E value Match length 241 % identity 41 NCBI Description

RETINOBLASTOMA BINDING PROTEIN 2 (RBBP-2)

>gi\_2136106\_pir\_\_I78879 retinoblastoma binding protein 2 human >gi\_435778\_bbs\_138858 (S66431) retinoblastoma binding

protein 2, RBP2 [human, Nalm-6 pre-B cell leukemia,

Peptide, 1722 aa] [Homo sapiens]

Seq. No.

Contig ID 95924 1.R1040

5'-most EST LIB3170-068-Q1-K1-E9

Seq. No.

22284

22283

Contig ID

95946 1.R1040

5'-most EST

LIB3170-068-Q1-K1-H1

Method NCBI GI BLASTN g2264310

BLAST score

35

E value Match length 4.0e-10 115

% identity NCBI Description

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MKP11, complete sequence [Arabidopsis thaliana]

Seq. No.

22285

Contig ID 95957 1.R1040

5'-most EST

LIB3170-069-Q1-J1-B4

Seq. No.

22286

Contig ID

95969 1.R1040

5'-most EST

jC-gmf102220127f05d1

Method NCBI GI BLAST score

BLASTX g266567 557

E value Match length

5.0e-57 148

% identity

72 NCBI Description

MITOCHONDRIAL PROCESSING PEPTIDASE ALPHA SUBUNIT PRECURSOR (ALPHA-MPP) (UBIQUINOL-CYTOCHROME C REDUCTASE SUBUNIT II)

>gi 421956 pir S23558 mitochondrial processing peptidase

(EC 3.4.99.41) alpha chain precursor - potato

>qi 21493 emb CAA46990 (X66284) mitochondrial processing

peptidase [Solanum tuberosum]

Seq. No.

22287

Contig ID

95971 1.R1040

5'-most EST

LIB3170-069-Q1-J1-F4

Seq. No.

22288

Contig ID

95975 1.R1040

5'-most EST

jC-gmf102220065f11a1

Seq. No.

22289



Contig ID 95977 1.R1040 5'-most EST LIB3170-069-Q1-J1-D5

Seq. No. 22290

Contig ID 96012\_1.R1040

5'-most EST jC-gmf102220099b12d1

Seq. No. 22291

Contig ID 96015 1.R1040

5'-most EST LIB3170-069-Q1-J1-H9

Seq. No. 22292

Contig ID 96018\_1.R1040 5'-most EST wrg700787090.h2

Method BLASTN
NCBI GI g22445
BLAST score 223
E value 1.0e-122
Match length 253
% identity 98

NCBI Description Zea mays ZMPMS1 gene for 19 kDa zein protein

Seq. No. 22293

Contig ID 96018 2.R1040

5'-most EST jC-gmro02910022c05d1

Method BLASTN
NCBI GI g168675
BLAST score 756
E value 0.0e+00
Match length 804
% identity 99

NCBI Description Maize mutant zein (zE19) gene, complete cds

Seq. No. 22294

Contig ID 96025\_1.R1040 5'-most EST wrg700789204.h2

Method BLASTN
NCBI GI g22528
BLAST score 319
E value 1.0e-179
Match length 343
% identity 98

NCBI Description Zea mays mRNA encoding a zein (clone A20)

Seq. No. 22295

Contig ID 96034\_1.R1040

5'-most EST LIB3170-069-Q1-K1-E9

Method BLASTN
NCBI GI g22528
BLAST score 601
E value 0.0e+00
Match length 697
% identity 96

NCBI Description Zea mays mRNA encoding a zein (clone A20)

Seq. No. 22296

Contig ID 96046\_1.R1040

3564



5'-most EST jC-qmle01810002b04d1

Method BLASTX
NCBI GI g3395938
BLAST score 293
E value 5.0e-26
Match length 90
% identity 34

NCBI Description (AF076924) polypyrimidine tract-binding protein homolog

[Arabidopsis thaliana]

Seq. No. 22297

Contig ID 96051 1.R1040

5'-most EST LIB3170-070-Q1-J1-B12

Seq. No. 22298

Contig ID 96055 1.R1040

5'-most EST LIB3170-070-Q1-J1-B5

Method BLASTX
NCBI GI g2760839
BLAST score 161
E value 9.0e-11
Match length 80
% identity 46

NCBI Description (AC003105) putative receptor kinase [Arabidopsis thaliana]

Seq. No. 22299

Contig ID 96056\_1.R1040

5'-most EST jC-gmf102220092a02d1

Seq. No. 22300

Contig ID 96057 1.R1040

5'-most EST LIB3170-070-Q1-J1-B7

Method BLASTX
NCBI GI g4454026
BLAST score 294
E value 4.0e-36
Match length 133
% identity 62

NCBI Description (AL035394) phosphatase like protein [Arabidopsis thaliana]

Seq. No. 22301

Contig ID 96067\_1.R1040

5'-most EST LIB3170-070-Q1-J1-C7

Seq. No. 22302

Contig ID 96074 1.R1040

5'-most EST LIB3170-070-Q1-J1-D6

Seq. No. 22303

Contig ID 96077 1.R1040

5'-most EST jC-gmro02910074g10d1

Method BLASTX
NCBI GI g3643596
BLAST score 361
E value 3.0e-34
Match length 90
% identity 79



(AC005395) hypothetical protein [Arabidopsis thaliana] NCBI Description

22304 Seq. No.

96095 1.R1040 Contig ID

LIB3170-070-Q1-J1-G10 5'-most EST

22305 Seq. No.

96098 1.R1040 Contig ID

jC-gmst02400077h03d1 5'-most EST

22306 Seq. No.

96100 1.R1040 Contig ID

LIB3170-070-Q1-J1-G5 5'-most EST

22307 Seq. No.

96109 1.R1040 Contig ID

LIB3170-072-Q1-J1-A5 5'-most EST

22308 Seq. No.

96114 1.R1040 Contig ID

LIB3170-084-Q1-J1-F10 5'-most EST

22309 Seq. No.

96120 1.R1040 Contig ID

LIB3170-070-Q1-K2-B12 5'-most EST

22310 Seq. No.

96126 1.R1040 Contig ID

LIB3170-070-Q1-K1-E11 5'-most EST

22311 Seq. No.

96134 1.R1040 Contig ID

LIB3170-070-Q1-K2-H11 5'-most EST

22312 Seq. No.

96191 1.R1040 Contig ID trc700562023.hl 5'-most EST

22313 Seq. No.

96192 1.R1040 Contiq ID

LIB3170-071-Q1-K1-H6 5'-most EST

BLASTX Method q2217970 NCBI GI 211 BLAST score 6.0e-17 E value 120 Match length % identity

NCBI Description (Z97074) p40 [Homo sapiens]

22314 Seq. No.

96211\_1.R1040 Contig ID

LIB3170-071-Q1-J1-A12 5'-most EST

BLASTX Method q4263777 NCBI GI 992 BLAST score 0.0e+00E value 430 Match length



% identity 71

NCBI Description (AC006068) putative serine carboxypeptidase II (Arabidopsis

thaliana] >gi\_4510391\_gb\_AAD21479.1\_ (AC007017) putative

serine carboxypeptidase II [Arabidopsis thaliana]

Seq. No. 22315

Contig ID 96224 1.R1040

5'-most EST LIB3170-071-Q1-J1-C10

Seq. No. 22316

Contig ID 96226 1.R1040

5'-most EST LIB3170-071-Q1-J1-C5

Seq. No. 22317

Contig ID 96234 1.R1040

5'-most EST LIB3170-071-Q1-J1-D12

Seq. No. 22318

Contig ID 96240 1.R1040

5'-most EST LIB3170-071-Q1-J1-E10

Seg. No. 22319

Contig ID 96246 1.R1040

5'-most EST jC-gmst02400058e02d1

Seq. No. 22320

Contig ID 96260 1.R1040

5'-most EST LIB3170-071-Q1-J1-G8

Seq. No. 22321

Contig ID 96266 1.R1040

5'-most EST LIB3170-071-Q1-J1-H6

Method BLASTX
NCBI GI g586693
BLAST score 277
E value 1.0e-46
Match length 288
% identity 39

NCBI Description HYPOTHETICAL 86.0 KD PROTEIN IN DCTA-DPPF INTERGENIC REGION

PRECURSOR (F779) >gi\_1073472\_pir\_\_S47753 hypothetical protein f779 - Escherichia coli >gi 466670 (U00039) No

definition line found [Escherichia coli]

Seq. No. 22322

Contig ID 96271 1.R1040

5'-most EST jC-gmf102220091a10a1

Seq. No. 22323

Contig ID 96307 1.R1040

5'-most EST LIB3170-071-Q1-K1-F3

Seq. No. 22324

Contig ID 96313\_1.R1040 5'-most EST xpa700796924.h1

Method BLASTX NCBI GI g282881 BLAST score 202



E value 3.0e-16 Match length 74 % identity 46

NCBI Description receptor-like protein kinase precursor - Arabidopsis thaliana >gi 166846 (M84658) receptor-like protein kinase

[Arabidopsis thaliana]

Seq. No. 22325

Contig ID 96337\_1.R1040

5'-most EST jC-gmro02910065b07d1

Method BLASTX
NCBI GI g1620369
BLAST score 465
E value 2.0e-46
Match length 118
% identity 73

NCBI Description (Y08781) peroxidase ATP22a [Arabidopsis thaliana]

Seq. No.

22326

22327

Contig ID 96342 1.R1040

5'-most EST LIB3170-072-Q1-J1-B7

Seq. No.

Contig ID 96349 1.R1040

5'-most EST LIB3170-072-Q1-J1-C2

Seq. No. 22328

Contig ID 96377\_1.R1040

5'-most EST LIB3170-075-Q1-K1-G5

Method BLASTN
NCBI GI g3928074
BLAST score 39
E value 2.0e-12
Match length 75

% identity 88

NCBI Description Arabidopsis thaliana chromosome II BAC T7F6 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 22329

Contig ID 96388 1.R1040 5'-most EST uaw700664277.h1

Seq. No. 22330

Contig ID 96400\_1.R1040 5'-most EST pxt700942108.h1

Seq. No. 22331

Contig ID 96429\_2.R1040 5'-most EST vzy700756380.h1

Seq. No. 22332

Contig ID 96433\_1.R1040

5'-most EST LIB3170-072-Q1-K1-E10

Seq. No. 22333

Contig ID 96469\_1.R1040 5'-most EST pmv700888612.h1



Method BLASTX NCBI GI g3135611 BLAST score 721 E value 2.0e-76 Match length 150 % identity 86

(AF062485) cellulose synthase [Arabidopsis thaliana] NCBI Description

Seq. No.

22334

96480 1.R1040 Contig ID 5'-most EST

jC-gmst02400026b09d1

BLASTX Method NCBI GI g4432814 BLAST score 348 E value 1.0e-32 Match length 117 % identity 58

NCBI Description (AC006593) unknown protein [Arabidopsis thaliana]

Seq. No.

22335

Contiq ID

96485 1.R1040

5'-most EST

LIB3170-073-Q1-J1-C2

Method BLASTX NCBI GI g4510418 BLAST score 203 E value 7.0e-16 Match length 93 51 % identity

NCBI Description (AC006929) hypothetical protein [Arabidopsis thaliana]

Seq. No.

22336

Contig ID

96510 1.R1040

5'-most EST

LIB3170-073-Q1-J1-F1

Method BLASTX NCBI GI g4490341 BLAST score 374 4.0e-48 E value 105 Match length % identity

NCBI Description (AL035656) putative protein [Arabidopsis thaliana]

Seq. No.

22337

Contig ID

96515 1.R1040

5'-most EST

LIB3170-073-Q1-J1-F4

Method BLASTX NCBI GI g2983290 BLAST score 187 E value 7.0e-14 Match length 84 % identity 42

NCBI Description (AE000703) UMP kinase [Aquifex aeolicus]

Seq. No.

22338

Contig ID

96521 1.R1040

5'-most EST

jC-gmle01810063f05d1

Seq. No.

22339



Contig ID 96539 1.R1040 LIB3170-073-Q1-K1-A1 5'-most EST

22340 Seq. No.

Contig ID 96588 1.R1040

LIB3170-073-Q1-K1-F12 5'-most EST

Seq. No. 22341

Contig ID 96623 1,R1040

5'-most EST LIB3170-074-Q1-J1-A7

Method BLASTX NCBI GI g1168470 BLAST score 304 E value 1.0e-27 91 Match length 63 % identity

NCBI Description PROTEIN KINASE APK1A >gi 282877 pir S28615 protein kinase,

tyrosine/serine/threonine-specific (EC 2.7.1.-) -Arabidopsis thaliana >gi 217829 dbj BAA02092 (D12522) protein tyrosine-serine-threonine kinase [Arabidopsis

thaliana]

Seq. No.

22342

Contig ID 96630 1.R1040

LIB3170-074-Q1-J1-B9 5'-most EST

Method BLASTX NCBI GI q3413886 BLAST score 175 2.0e-12 E value Match length 148 31

% identity

NCBI Description (AB007931) KIAA0462 protein [Homo sapiens]

22343 Seq. No.

96638 1.R1040 Contig ID

LIB3170-074-Q1-J1-C4 5'-most EST

22344 Seq. No.

96652 1.R1040 Contig ID

LIB3170-074-Q1-J1-D8 5'-most EST

Method BLASTX NCBI GI q1514643 BLAST score 418 E value 7.0e-41Match length 153 % identity 58

(Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza] NCBI Description

22345 Seq. No.

Contig ID 96654 1.R1040

5'-most EST LIB3170-074-Q1-J1-E10

Seq. No. 22346

96664 1.R1040 Contig ID

5'-most EST LIB3170-074-Q1-J1-F12

Seq. No. 22347



Contig ID 96685\_1.R1040 5'-most EST pxt700946421.h1

Method BLASTX
NCBI GI g2842490
BLAST score 156
E value 2.0e-10
Match length 56
% identity 48

NCBI Description (AL021749) heat-shock protein [Arabidopsis thaliana]

Seq. No. 22348

Contig ID 96686 1.R1040

5'-most EST LIB3170-078-Q1-J1-C7

Seq. No. 22349

Contig ID 96749 1.R1040

5'-most EST jC-gmle01810051g03a1

Method BLASTX
NCBI GI g1777443
BLAST score 193
E value 9.0e-15
Match length 47
% identity 68

NCBI Description (U28422) CCA1 [Arabidopsis thaliana] >gi\_3510263 (AC005310)

DNA-binding protein CCA1 [Arabidopsis thaliana] >gi 4090569

(U79156) CCA1 [Arabidopsis thaliana]

Seq. No. 22350

Contig ID 96749 2.R1040

5'-most EST LIB3170-074-Q1-K1-F12

Method BLASTX
NCBI GI g3281846
BLAST score 243
E value 3.0e-20
Match length 54
% identity 78

NCBI Description (AJ006404) late elongated hypocotyl [Arabidopsis thaliana]

Seq. No. 22351

Contig ID 96778\_1.R1040

5'-most EST uC-gmflminsoy025h08b1

Method BLASTX
NCBI GI g1169544
BLAST score 391
E value 9.0e-38
Match length 146
% identity 55

NCBI Description ERD1 PROTEIN PRECURSOR >gi\_541859\_pir\_\_JN0901 ERD1 protein

- Arabidopsis thaliana >gi 497629 dbj BAA04506 (D17582)

ERD1 protein [Arabidopsis thaliana]

Seq. No. 22352

Contig ID 96785 1.R1040

5'-most EST LIB3170-075-Q1-K1-B10

Seq. No. 22353

Contig ID 96796\_1.R1040



5'-most EST LIB3170-075-Q1-K2-C11

Seq. No. 22354

Contig ID 96801 1.R1040

5'-most EST LIB3170-075-Q1-K2-C5

Method BLASTN
NCBI GI g4206101
BLAST score 273
E value 1.0e-152
Match length 357
% identity 94

NCBI Description Glycine max retroelement diaspora gag-pol polyprotein

(gag-pol) pseudogene, partial sequence

Seq. No. 22355

Contig ID 96806 1.R1040

5'-most EST LIB3170-075-Q1-K2-D1

Seq. No. 22356

Contig ID 96812 1.R1040

5'-most EST LIB3170-075-Q1-K2-D8

Seq. No. 22357

Contig ID 96820\_1.R1040 5'-most EST sat701003629.h1

Method BLASTX
NCBI GI g2673917
BLAST score 406
E value 6.0e-40
Match length 94
% identity 41

NCBI Description (AC002561) putative ATP-dependent RNA helicase [Arabidopsis

thaliana]

Seq. No. 22358

Contig ID 96827 1.R1040

5'-most EST LIB3170-075-Q1-K2-F10

Method BLASTX
NCBI GI g3892059
BLAST score 205
E value 3.0e-16
Match length 94
% identity 50

NCBI Description (AC002330) predicted protein of unknown function

[Arabidopsis thaliana]

Seq. No. 22359

Contig ID 96832 1.R1040

5'-most EST LIB3170-075-Q1-K2-F6

Seq. No. 22360

Contig ID 96851\_1.R1040

5'-most EST LIB3170-075-Q1-K2-H3

Seg. No. 22361

Contig ID 96853\_1.R1040

5'-most EST LIB3170-075-Q1-K2-H6



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Seq. No. 22362
Contig ID 96951 1.R1040
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5'-most EST LIB3170-076-Q1-J1-A9

Seq. No. 22363

Contig ID 96970\_1.R1040

5'-most EST LIB3170-076-Q1-J1-D10

Seq. No. 22364

Contig ID 96977\_1.R1040 5'-most EST fC-gmf1700895939d3

Method BLASTX
NCBI GI g2739383
BLAST score 218
E value 1.0e-17
Match length 46
% identity 93

NCBI Description (AC002505) unknown protein [Arabidopsis thaliana]

Seq. No. 22365

Contig ID 97003 1.R1040 5'-most EST fC-gmst700654123g2

Method BLASTX
NCBI GI g3121727
BLAST score 452
E value 3.0e-67
Match length 273
% identity 49

NCBI Description ALCOHOL DEHYDROGENASE CLASS III (GLUTATHIONE-DEPENDENT

FORMALDEHYDE DEHYDROGENASE) (FDH) (FALDH)

Seq. No. 22366

Contig ID 97012 1.R1040

5'-most EST LIB3170-076-Q1-K1-A3

Seq. No. 22367

Contig ID 97032 1.R1040

5'-most EST LIB3170-076-Q1-K1-D1

Seq. No. 22368

Contig ID 97034\_1.R1040

5'-most EST jC-gmst02400014b08d1

Method BLASTX
NCBI GI g3738332
BLAST score 199
E value 3.0e-15
Match length 110
% identity 43

NCBI Description (AC005170) putative eukaryotic initiation factor

[Arabidopsis thaliana]

Seq. No. 22369

Contig ID 97037\_1.R1040

5'-most EST LIB3170-076-Q1-K1-D9

Method BLASTX NCBI GI g2632254



BLAST score 1.0e-28 E value 103 Match length 69 % identity

NCBI Description (Y12465) serine/threonine kinase [Sorghum bicolor]

Seq. No. Contig ID 22370 97057 1.R1040

5'-most EST

LIB3170-076-Q1-K1-G9

Seq. No.

22371

Contig ID

97067 1.R1040

5'-most EST

LIB3170-077-Q1-J1-A11

Seq. No.

22372

Contig ID

97073 1.R1040

5'-most EST

LIB3170-077-Q1-J1-A5

Seq. No.

22373

Contig ID

97091 1.R1040

5'-most EST

LIB3170-077-Q1-J1-C12

Seq. No.

22374

Contig ID

97099 1.R1040

5'-most EST

LIB3170-077-Q1-J1-D10

Seq. No.

22375

Contig ID

97115 1.R1040

5'-most EST

LIB3170-078-Q1-J1-A6

Seq. No.

22376

Contig ID

97144 1.R1040

5'-most EST

LIB3170-077-Q1-J1-H6

Method NCBI GI BLASTX g4468817

BLAST score E value

256

Match length

3.0e-22 60

% identity

46

NCBI Description (AL035601) putative protein [Arabidopsis thaliana]

Seq. No.

22377

Contig ID 5'-most EST 97154 1.R1040 jsh701065560.h1

Seq. No.

22378

Contig ID

97178 1.R1040

5'-most EST

LIB3170-077-Q1-K1-C8

Seq. No.

22379

Contig ID

97242 1.R1040

5'-most EST

jC-gmf102220098h05d1

Seq. No.

22380

Contig ID

97261 1.R1040

5'-most EST

jC-gmf102220125h11d1

Method

BLASTX



NCBI GI g1711618 BLAST score 167 E value 1.0e-11 Match length 54 % identity 63

NCBI Description LOW AFFINITY SULPHATE TRANSPORTER 3 >gi\_1085993\_pir\_\_S51765

low affinity sulphate transporter - Stylosanthes hamata >gi\_607188\_emb\_CAA57831\_ (X82454) low affinity sulphate

transporter [Stylosanthes hamata]

Seq. No. 22381

Contig ID 97262 1.R1040 5'-most EST g4288071

Seq. No.

22382

Contig ID 97265\_1.R1040

5'-most EST uC-gmrominsoy121f10b1

Method BLASTX
NCBI GI g1483150
BLAST score 574
E value 5.0e-59
Match length 118
% identity 87

NCBI Description (D84417) monodehydroascorbate reductase [Arabidopsis

thaliana]

22383

Seq. No.

Contig ID 97285\_1.R1040

5'-most EST LIB3170-078-Q1-J1-G11

Method BLASTX
NCBI GI g3335367
BLAST score 156
E value 3.0e-10
Match length 53
% identity 49

% identity 49

NCBI Description (AC003028) unknown protein [Arabidopsis thaliana]

Seq. No. 22384

Contig ID 97288 1.R1040

5'-most EST jC-gmro02910027b03d1

Seq. No. 22385

Contig ID 97309\_1.R1040 5'-most EST pcp700989122.h1

Seq. No. 22386

Contig ID 97312\_1.R1040 5'-most EST hrw701057724.h1

Seq. No. 22387

Contig ID 97341\_1.R1040

5'-most EST jC-gmf102220065c06d1

Method BLASTX
NCBI GI g1171577
BLAST score 214
E value 7.0e-20
Match length 103



% identity 50
NCBI Description (X95343) hypersensitivity-related gene [Nicotiana tabacum]

Seq. No. 22388

Contig ID 97352 1.R1040

5'-most EST LIB3170-078-Q1-K1-F6

Method BLASTX
NCBI GI g4325324
BLAST score 211
E value 9.0e-24
Match length 70
% identity 83

NCBI Description (AF125574) lysyl-tRNA synthetase; LysRS [Arabidopsis

thaliana]

Seq. No. 22389

Contig ID 97362\_1.R1040 5'-most EST rca700996195.h1

Seq. No. 22390

Contig ID 97369\_1.R1040

5'-most EST LIB3170-078-Q1-K1-H12

Method BLASTX
NCBI GI g4467151
BLAST score 307
E value 1.0e-33
Match length 214
% identity 41

NCBI Description (AL035540) putative protein [Arabidopsis thaliana]

Seq. No. 22391

Contig ID 97375 1.R1040

5'-most EST LIB3170-079-Q1-J1-A10

Seq. No. 22392

Contig ID 97383\_1.R1040 5'-most EST hyd700726535.h1

Seq. No. 22393

Contig ID 97386\_1.R1040

5'-most EST LIB3170-079-Q1-J1-B3

Seq. No. 22394

Contig ID 97387 1.R1040

5'-most EST LIB3170-079-Q1-J1-B4

Seq. No. 22395

Contig ID 97406 1.R1040

5'-most EST jC-gmro02910007b02d1

Seq. No. 22396

Contig ID 97437\_1.R1040

5'-most EST LIB3170-079-Q1-K1-B4

Method BLASTN NCBI GI g2351070 BLAST score 44

BLAST score 44 E value 2.0e-15



Match length 160 % identity 85

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:

MTH12, complete sequence [Arabidopsis thaliana]

Seq. No. 22397

Contig ID 97447 1.R1040 g4313274 5'-most EST Method BLASTX q1853968 NCBI GI BLAST score 383 E value 7.0e-37 Match length 115 % identity 68

NCBI Description (D88121) CPRD12 protein [Vigna unguiculata]

Seq. No. 22398

Contig ID 97448 1.R1040

5'-most EST LIB3170-079-Q1-K1-C5

Seq. No. 22399

Contig ID 97489\_1.R1040 5'-most EST trc700563604.h1

Method BLASTX
NCBI GI g4454567
BLAST score 298
E value 2.0e-26
Match length 374
% identity 27

NCBI Description (AF128407) lipase homolog [Arabidopsis thaliana]

Seq. No. 22400

Contig ID 97500 1.R1040

5'-most EST LIB3170-080-Q1-J1-A11

Seq. No. 22401

Contig ID 97513 1.R1040

5'-most EST LIB3170-080-Q1-J1-D12

Seq. No. 22402

Contig ID 97526\_1.R1040

5'-most EST LIB3170-080-Q1-J1-H11

Seq. No. 22403

Contig ID 97539 1.R1040

5'-most EST LIB3170-080-Q1-K1-B11

Method BLASTX
NCBI GI g2623301
BLAST score 459
E value 1.0e-45
Match length 119
% identity 71

NCBI Description (AC002409) putative kinase [Arabidopsis thaliana]

Seq. No. 22404

Contig ID 97541 1.R1040

5'-most EST LIB3170-080-Q1-K1-B2



```
22405
Seq. No.
Contig ID
                  97553 1.R1040
5'-most EST
                  LIB3170-080-Q1-K1-G6
Method
                  BLASTX
NCBI GI
                  q4455213
BLAST score
                  742
E value
                  5.0e-79
Match length
                  164
% identity
                  86
                  (AL035440) glutamine amidotransferase/cyclase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  22406
Contig ID
                  97554 1.R1040
                  LIB3170-080-Q1-K1-C7
```

5'-most EST Method BLASTX NCBI GI q1168548 BLAST score 143

E value 6.0e-09 Match length 32 % identity 91

NCBI Description HOMEOBOX-LEUCINE ZIPPER PROTEIN ATHB-7 (HD-ZIP PROTEIN ATHB-7) >gi\_629527 pir \_S47137 homeotic protein Athb-7 -

Arabidopsis thaliana >gi 499164 emb CAA47425 (X67032) orf

[Arabidopsis thaliana]

22407 Seq. No.

97609 1.R1040 Contig ID

5'-most EST LIB3170-081-Q1-J1-A11

Seq. No. 22408

Contig ID 97619 1.R1040

5'-most EST LIB3170-081-01-J1-B10

Method BLASTX NCBI GI g4580394 BLAST score 124 7.0e-11 E value Match length 62 % identity 65

NCBI Description (AC007171) putative fatty acid elongase [Arabidopsis

thaliana]

Seq. No. 22409

Contig ID 97643 1.R1040

5'-most EST LIB3170-081-Q1-J1-E10

Method BLASTX NCBI GI g3738315 BLAST score 240 E value 5.0e-20 Match length 80 % identity

NCBI Description (AC005170) unknown protein [Arabidopsis thaliana]

Seq. No. 22410

Contig ID 97648 1.R1040

LIB3170-081-Q1-J1-E8 5'-most EST



```
22411
Seq. No.
                  97656 1.R1040
Contig ID
5'-most EST
                  jC-qmro02910007c11d1
Method
                  BLASTX
NCBI GI
                  q2832616
BLAST score
                  247
E value
                  6.0e-21
                  120
Match length
% identity
                  48
                  (AL021711) heat shock transcription factor - like protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  22412
                  97658 1.R1040
Contig ID
5'-most EST
                  jC-gmf102220090a03d1
Seq. No.
                  22413
Contig ID
                  97738 1.R1040
5'-most EST
                  LIB3170-082-Q1-J1-A11
Seq. No.
                  22414
Contig ID
                  97760 1.R1040
5'-most EST
                  LIB3170-082-Q1-J1-C11
Seq. No.
                  22415
                  97790 1.R1040
Contig ID
5'-most EST
                  LIB3170-082-Q1-J1-E9
                  BLASTX
Method
NCBI GI
                  q4220480
BLAST score
                  154
E value
                  5.0e-10
Match length
                  56
                   66
% identity
NCBI Description (AC006069) unknown protein [Arabidopsis thaliana]
                  22416
Seq. No.
Contig ID
                  97790_2.R1040
5'-most EST
                  jC-gmle01810090b09d1
Method
                  BLASTX
NCBI GI
                  q4220480
BLAST score
                  234
E value
                   2.0e-19
Match length
                  94
% identity
                   61
NCBI Description (AC006069) unknown protein [Arabidopsis thaliana]
```

Contig ID 97804 1.R1040

5'-most EST LIB3170-082-Q1-J1-G2

Seq. No. 22418

Contig ID 97815 1.R1040

5'-most EST LIB3170-082-Q1-J1-H4

Method BLASTX
NCBI GI g4249411
BLAST score 246



E value 7.0e-21 Match length 78 % identity 58

NCBI Description (AC006072) unknown protein [Arabidopsis thaliana]

Seq. No. 22419

Contig ID 97826\_1.R1040 5'-most EST vzy700752039.h1

Seq. No. 22420

Contig ID 97839\_1.R1040 5'-most EST rca700997639.h1

Method BLASTX
NCBI GI g2864618
BLAST score 275
E value 2.0e-24
Match length 96
% identity 55

NCBI Description (AL021811) putative protein [Arabidopsis thaliana]

Seq. No. 22421

Contig ID 97876 1.R1040

5'-most EST LIB3170-085-Q1-K1-E11

Seq. No. 22422

Contig ID 97912\_1.R1040

5'-most EST LIB3170-083-Q1-J1-B5

Seq. No. 22423

Contig ID 97913 1.R1040

5'-most EST LIB3170-083-Q1-J1-B6

Seq. No. 22424

Contig ID 97917 1.R1040

5'-most EST jC-gmro02800029g03d1

Method BLASTX
NCBI GI g3128177
BLAST score 313
E value 2.0e-28
Match length 131
% identity 48

NCBI Description (AC004521) unknown protein [Arabidopsis thaliana]

Seq. No. 22425

Contig ID 97925 1.R1040

5'-most EST LIB3170-083-Q1-J1-D11

Seq. No. 22426

Contig ID 97933\_1.R1040 5'-most EST epx701107549.h1

Seq. No. 22427

Contig ID 97937 1.R1040

5'-most EST LIB3170-083-Q1-J1-E3

Seq. No. 22428

Contig ID 97940\_1.R1040



5'-most EST zsg701124832.h1

Seq. No. 22429

Contig ID 97986 1.R1040

5'-most EST LIB3170-083-Q1-K1-C9

Seq. No. 22430

Contig ID 97997 1.R1040

5'-most EST LIB3170-087-Q1-K1-E10

Method BLASTX
NCBI GI g731528
BLAST score 202
E value 1.0e-15
Match length 146
% identity 36

NCBI Description HYPOTHETICAL 38.2 KD PROTEIN IN BEM2-NCB1 INTERGENIC REGION

>gi\_1077718\_pir\_\_S50659 hypothetical protein YER156c -

yeast (Saccharomyces cerevisiae) >gi\_603396 (U18917)

Yer156cp [Saccharomyces cerevisiae]

Seq. No. 22431

Contig ID 98054 1.R1040

5'-most EST LIB3170-084-Q1-J1-B7

Seq. No. 22432

Contig ID 98060 1.R1040

5'-most EST LIB3170-084-Q1-J1-C11

Seq. No. 22433

Contig ID 98075 1.R1040

5'-most EST LIB3170-084-Q1-J1-D8

Method BLASTX
NCBI GI g2980781
BLAST score 573
E value 4.0e-59
Match length 149
% identity 72

NCBI Description (AL022198) putative protein [Arabidopsis thaliana]

Seq. No. 22434

Contig ID 98118\_1.R1040 5'-most EST fC-gmst700666011i1

Method BLASTX
NCBI GI g2181180
BLAST score 525
E value 7.0e-53
Match length 365
% identity 35

NCBI Description (Z84377) xylosidase [Aspergillus niger]

Seq. No. 22435

Contig ID 98140\_1.R1040 5'-most EST epx701106138.h1

Seq. No. 22436

Contig ID 98151\_1.R1040 5'-most EST ssr700554413.h1

NCBI Description

22443

98253 1.R1040

Seq. No.

Contig ID

```
Method
                   BLASTX
NCBI GI
                   g2738752
BLAST score
                   500
                   6.0e-67
E value
Match length
                  171
                   77
% identity
NCBI Description
                  (AF016306) sulfate permease [Zea mays]
                   22437
Seq. No.
                   98170 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy207e01b1
Method
                   BLASTX
NCBI GI
                   g2252634
BLAST score
                   379
E value
                   2.0e-36
Match length
                   129
% identity
                  (U95973) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   22438
Seq. No.
                   98187 1.R1040
Contig ID
5'-most EST
                  LIB3170-085-Q1-J1-B7
Seq. No.
                   22439
                   98209 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220079c06d1
                   BLASTX
Method
NCBI GI
                   q2842689
BLAST score
                   224
E value
                   4.0e-18
Match length
                   142
                   39
% identity
                   HYPOTHETICAL 50.4 KD PROTEIN C1F8.04C IN CHROMOSOME I
NCBI Description
                   >gi 1638851 emb CAB03598 (Z81312) unknown
                   [Schizosaccharomyces pombe]
Seq. No.
                   22440
Contig ID
                   98214 1.R1040
5'-most EST
                   LIB3170-085-Q1-J1-G5
Seq. No.
                   22441
Contig ID
                   98221 1.R1040
5'-most EST
                   jC-gmro02910063f11d1
Seq. No.
                   22442
                   98229 1.R1040
Contig ID
5'-most EST
                   uC-gmropic056e06b1
Method
                   BLASTX
                   g3980417
NCBI GI
BLAST score
                   254
E value
                   1.0e-21
Match length
                   131
% identity
                   44
```

(AC004561) pumilio-like protein [Arabidopsis thaliana]



5'-most EST LIB3170-085-Q1-K1-D3

Seq. No. 22444

Contig ID 98286\_1.R1040 5'-most EST uC-gmropic098h02b1

Seq. No. 22445

Contig ID 98293\_1.R1040 5'-most EST zsg701127547.h1

Seq. No. 22446

Contig ID 98294 1.R1040

5'-most EST LIB3170-085-Q1-K1-H6

Method BLASTX
NCBI GI g2880043
BLAST score 370
E value 3.0e-35
Match length 159
% identity 46

NCBI Description (AC002340) putative 3-hydroxyisobutyryl-coenzyme A

hydrolase [Arabidopsis thaliana]

Seq. No. 22447

Contig ID 98296\_1.R1040

5'-most EST LIB3170-086-Q1-J1-A3

Seq. No. 22448

Contig ID 98298 1.R1040 5'-most EST vzy700754051.h1

Seq. No. 22449

Contig ID 98302\_1.R1040

5'-most EST LIB3170-086-Q1-J1-B1

Seq. No. 22450

Contig ID 98365\_1.R1040

5'-most EST LIB3170-086-Q1-K1-H2

Method BLASTX
NCBI GI g2342679
BLAST score 329
E value 2.0e-30
Match length 113
% identity 66

NCBI Description (AC000106) Similar to Vicia sativa ENBP1 (gb X95995).

[Arabidopsis thaliana]

Seq. No. 22451

Contig ID 98381 1.R1040

5'-most EST LIB3170-087-Q1-J1-B6

Seq. No. 22452

Contig ID 98392\_1.R1040

5'-most EST LIB3170-087-Q1-J1-D1

Seq. No. 22453

Contig ID 98394\_1.R1040

5'-most EST LIB3170-087-Q1-J1-D4



22454 Seq. No.

98397 1.R1040 Contig ID

LIB3170-087-Q1-J1-D7 5'-most EST

22455 Seq. No.

98400 1.R1040 Contig ID

LIB3170-087-Q1-J1-E1 5'-most EST

22456 Seq. No.

98414 1.R1040 Contig ID

LIB3170-087-Q1-J1-G6 5'-most EST

22457 Seq. No.

98427 1.R1040 Contig ID jex700905405.hl 5'-most EST

22458 Seq. No.

98472 1.R1040 Contig ID

LIB3170-087-Q1-K1-G7 5'-most EST

22459 Seq. No.

98509 1.R1040 Contig ID fC-gmse700862853h3 5'-most EST

BLASTX Method q3786005 NCBI GI 1172 BLAST score 1.0e-129 E value 287 Match length

% identity

(AC005499) putative phosphoethanolamine NCBI Description cytidylyltransferase [Arabidopsis thaliana]

22460 Seq. No.

98638 1.R1040 Contig ID 2DC-01-Q1-B1-B10 5'-most EST

22461 Seq. No.

98640\_1.R1040 Contig ID uC-gmropic109c12b1 5'-most EST

BLASTX Method g3176674 NCBI GI BLAST score 1269 1.0e-140 E value 322 Match length 73

(AC003671) Contains similarity to Ste20-like kinase homolog % identity NCBI Description

from A. thaliana chromosome 4 contig gb\_Z97336.

Single

[Arabidopsis thaliana]

22462 Seq. No.

98645\_1.R1040 Contig ID

jC-gmf102220148b04a1 5'-most EST

BLASTX Method q3913425 NCBI GI 640 BLAST score 3.0e-85 E value



Match length 166 % identity 93

NCBI Description PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA

HELICASE >gi\_2275203 (AC002337) RNA helicase isolog

[Arabidopsis thaliana]

Seq. No. 22463

Contig ID 98675\_1.R1040 5'-most EST vzy700754031.h1

Seq. No. 22464

Contig ID 98678\_1.R1040 5'-most EST pxt700941907.h1

Seq. No. 22465

Contig ID 98689 1.R1040 5'-most EST epx701105422.h1

Method BLASTX
NCBI GI g3402689
BLAST score 400
E value 4.0e-39
Match length 103
% identity 75

NCBI Description (AC004697) unknown protein [Arabidopsis thaliana]

Seq. No. 22466

Contig ID 98693 1.R1040 5'-most EST 2DC-01-Q1-B1-G12

Seq. No. 22467

Contig ID 98704\_1.R1040 5'-most EST 2DC-01-Q1-B1-H11

Seq. No. 22468

Contig ID 98712\_1.R1040 5'-most EST 2DC-01-Q1-E1-H9

Method BLASTX
NCBI GI g123563
BLAST score 176
E value 5.0e-13
Match length 77
% identity 40

NCBI Description CHLOROPLAST SMALL HEAT SHOCK PROTEIN >gi\_81786\_pir\_\_S00375

heat shock 22K protein - soybean (fragment)

>gi\_18659\_emb\_CAA30168\_ (X07188) hsp22 (181 AA) [Glycine

max]

Seq. No. 22469

Contig ID 98771\_1.R1040 5'-most EST 2DC-01-Q1-E1-F1

Seq. No. 22470

Contig ID 98781\_1.R1040 5'-most EST 2DC-01-Q1-E1-F8

Seq. No. 22471

Contig ID 98806\_1.R1040



```
5'-most EST
                  vzy700753547.hl
Method
                  BLASTX
NCBI GI
                  q3063464
                  948
BLAST score
E value
                  1.0e-103
                  202
Match length
                  89
% identity
NCBI Description (AC003981) F22013.26 [Arabidopsis thaliana]
                  22472
Seq. No.
Contig ID
                  98810 1.R1040
5'-most EST
                  2DC-02-Q1-B1-A3
                  BLASTX
Method
NCBI GI
                  g2507346
BLAST score
                  281
E value
                  1.0e-24
Match length
                  162
% identity
                  41
NCBI Description DNA-DIRECTED RNA POLYMERASE I 190 KD POLYPEPTIDE (A190)
                  >qi 2131238 pir S67250 DNA-directed RNA polymerase (EC
                  2.7.7.6) I 190K chain - yeast (Saccharomyces cerevisiae)
                  >qi 1199844 emb CAA65029 (X95720) 06276 [Saccharomyces
                  cerevisiae] >gi 1420741 emb CAA99665 (Z75249) ORF YOR341w
                  [Saccharomyces cerevisiae]
Seq. No.
                  22473
Contig ID
                  98819 1.R1040
5'-most EST
                  2DC-02-Q1-B1-B12
                  22474
Seq. No.
                  98821_1.R1040
Contig ID
5'-most EST
                  g5677961
Method
                  BLASTX
                  g3047064
NCBI GI
BLAST score
                  153
E value
                  6.0e-10
Match length
                  35
                  77
% identity
NCBI Description
                  (AF058825) contains similarity to peptidyl-prolyl cis-trans
                  isomerase (Pfam: pro isomerase.hmm, score: 23.86 and 28.41
                  [Arabidopsis thaliana]
Seq. No.
                  22475
Contig ID
                  98831 1.R1040
5'-most EST
                  uC-gmflminsoy065b02b1
Method
                  BLASTX
NCBI GI
                  g4510373
BLAST score
                  143
                  8.0e-09
E value
Match length
                  73
% identity
                  (AC007017) putative harpin-induced protein [Arabidopsis
NCBI Description
                  thaliana]
```

22476 Seq. No.

Contig ID 98832 1.R1040 5'-most EST pmv700889023.h1



```
Method
                  q2622862
NCBI GI
                  259
BLAST score
                  4.0e-22
E value
                  163
Match length
                  44
% identity
                  (AE000929) phosphate transport system ATP-binding
NCBI Description
                   [Methanobacterium thermoautotrophicum]
                  22477
Seq. No.
                  98833 1.R1040
Contig ID
                  pxt700942957.h1
5'-most EST
```

22478 Seq. No. 98835 1.R1040 Contig ID pxt700943880.hl 5'-most EST

22479 Seq. No. 98835 2.R1040 Contig ID zsg701120665.hl 5'-most EST

22480 Seq. No. 98840 1.R1040 Contig ID 5'-most EST jsh701066231.h1

22481 Seq. No. 98853 1.R1040 Contig ID

5'-most EST Method BLASTX q3158376 NCBI GI 217 BLAST score 2.0e-17 E value 91 Match length

% identity 48

(AF035385) unknown [Arabidopsis thaliana] NCBI Description

epx701110359.h1

22482 Seq. No. 98859 1.R1040 Contig ID 5'-most EST zpv700760356.hl BLASTN Method g4519193 NCBI GI

37 BLAST score 3.0e-11 E value Match length 93 % identity 85

Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: NCBI Description

MDC11, complete sequence

22483 Seq. No. 98861 1.R1040 Contig ID  $2DC - 0\overline{2} - Q1 - B1 - E7$ 5'-most EST

22484 Seq. No. 98875 1.R1040 Contig ID g4291<del>9</del>96 5'-most EST BLASTX Method g3413424 NCBI GI



BLAST score 275 E value 3.0e-24 Match length 157 % identity 38

NCBI Description (AJ006309) hypothetical protein [Arabidopsis thaliana]

Seq. No. 22485

Contig ID 98877\_1.R1040 5'-most EST 2DC-02-Q1-B1-G2

Seq. No. 22486

Contig ID 98899\_1.R1040 5'-most EST gsv701046939.h1

Method BLASTX
NCBI GI g3885334
BLAST score 609
E value 3.0e-63
Match length 192
% identity 62

NCBI Description (AC005623) putative argonaute protein [Arabidopsis

thaliana]

Seq. No. 22487

Contig ID 98902\_1.R1040 5'-most EST 6HA-01-Q1-B1-A6

Method BLASTX
NCBI GI 94038035
BLAST score 234
E value 3.0e-19
Match length 101
% identity 49

NCBI Description (AC005936) putative DNA-binding protein [Arabidopsis

thaliana]

Seq. No. 22488

Contig ID 98915\_1.R1040 5'-most EST 6HA-01-Q1-B1-B7

Seq. No. 22489

Contig ID 98941\_1.R1040 5'-most EST kl1701205704.h1

Seq. No. 22490

Contig ID 98942\_1.R1040 5'-most EST epx701108953.h1

Seq. No. 22491

Contig ID 98943\_1.R1040 5'-most EST 6HA-01-Q1-B1-E12

Seq. No. 22492

Contig ID 98947\_1.R1040

5'-most EST uC-gmrominsoy047a11b1

Method BLASTX
NCBI GI g3402711
BLAST score 283
E value 4.0e-25



Match length % identity

(AC004261) putative RNA-binding protein [Arabidopsis NCBI Description

Seq. No.

22493

Contig ID 5'-most EST

98948 1.R1040 uC-gmropic027h08b1

Method NCBI GI BLASTN g170645 383

BLAST score E value Match length

0.0e + 00483

95

% identity

NCBI Description

Vigna aconitifolia pyrroline-5-carboxylate synthetase associated mRNA sequence. >gi\_2471746\_gb\_I47781\_I47781

Sequence 1 from patent US

Seq. No.

22494

Contig ID 5'-most EST 98956 1.R1040 6HA-01-Q1-B1-F2

Method BLASTX q4544402 NCBI GI BLAST score 475 1.0e-47 E value 150 Match length

% identity

(AC007047) putative leucine rich repeat protein NCBI Description

[Arabidopsis thaliana]

22495 Seq. No.

Contig ID 98958 1.R1040 dpv701096975.hl 5'-most EST

BLASTX Method g2760324 NCBI GI 427 BLAST score 6.0e-42E value 194 Match length % identity

(AC002130) F1N21.9 [Arabidopsis thaliana] NCBI Description

Seq. No.

22496

Contig ID

98984 1.R1040

5'-most EST

uC-gmflminsoy054f06b1

Seq. No.

22497

Contig ID

98995 1.R1040

5'-most EST

 $jC-gm\overline{l}e01810008c07d1$ 

BLASTX Method NCBI GI g3461814 BLAST score 282 E value 7.0e-25

Match length % identity

106

NCBI Description

(AC004138) hypothetical protein [Arabidopsis thaliana]

Seq. No.



fC-gmro700873542d1

```
98998 1.R1040
Contig ID
5'-most EST
                   seb700649322.hl
                   22499
Seq. No.
                   99011 1.R1040
Contig ID
```

BLASTN Method g1103711 NCBI GI 37 BLAST score 3.0e-11 E value 195 Match length

80 % identity

5'-most EST

NCBI Description N.tabacum mRNA for inorganic pyrophosphatase (TVP31 clone)

Seq. No. 22500

99011 2.R1040 Contig ID  $6HA - 0\overline{1} - Q1 - E1 - C2$ 5'-most EST

22501 Seq. No.

99019 1.R1040 Contig ID  $6HA - 0\overline{1} - Q1 - E1 - D10$ 5'-most EST

BLASTN Method g3483707 NCBI GI 324 BLAST score E value 0.0e + 00340 Match length 99 % identity

Homo sapiens full length insert cDNA clone ZD66A09 NCBI Description

22502 Seq. No.

99037\_1.R1040 Contig ID g4395663 5'-most EST BLASTN Method NCBI GI g170645 BLAST score 211 E value 1.0e-115 314

Match length % identity

Vigna aconitifolia pyrroline-5-carboxylate synthetase NCBI Description associated mRNA sequence. >qi 2471746 gb I47781 I47781

Sequence 1 from patent US

22503 Seq. No.

99044 1.R1040 Contig ID 6HA-01-Q1-E1-F12 5'-most EST

Method BLASTN NCBI GI g347385 BLAST score 339 0.0e + 00E value Match length 351 99 % identity

NCBI Description Human ribosomal protein L37a mRNA sequence

22504 Seq. No.

99046 2.R1040 Contig ID

jC-gmf102220132ac01d1 5'-most EST

BLASTX Method



```
NCBI GI
                   q3881976
BLAST score
                   411
                   5.0e-40
E value
Match length
                   92
% identity
                   83
```

NCBI Description (AJ012409) hypothetical protein [Homo sapiens]

Seq. No. 22505

Contig ID 99062 1.R1040

5'-most EST ASG3244V4L-01-Q1-E1-E1

Seq. No. 22506

Contig ID 99072 1.R1040

5'-most EST jC-qmro02800029f03d1

Seq. No. 22507

99080 1.R1040 Contig ID 5'-most EST 6HA - 02 - Q1 - B1 - A2

Seq. No. 22508

99086 1.R1040 Contig ID 5'-most EST q5606146 Method BLASTX NCBI GI q4455274 BLAST score 309 E value 5.0e-28

Match length 76 76 % identity

NCBI Description (AL035527) spliceosome associated protein-like [Arabidopsis

thaliana]

22509 Seq. No.

Contig ID 99104 1.R1040 5'-most EST  $6HA - 0\overline{2} - Q1 - B1 - C3$ 

Method BLASTX NCBI GI q3924611 BLAST score 270 2.0e-23 E value Match length 220 % identity 34

(AF069442) hypothetical protein [Arabidopsis thaliana] NCBI Description

Seq. No.

22510 99107 1.R1040 Contig ID 5'-most EST  $6HA - 0\overline{2} - Q1 - E1 - C6$ 

Seq. No. 22511

99136 1.R1040 Contig ID 5'-most EST  $6HA - 0\overline{2} - Q1 - B1 - F10$ 

22512 Seq. No.

99138 1.R1040 Contig ID 5'-most EST sat701013724.hl

22513 Seq. No.

Contig ID 99141 1.R1040 5'-most EST 6HA-02-Q1-B1-F4



Method BLASTX
NCBI GI g2914703
BLAST score 343
E value 2.0e-32
Match length 114
% identity 54

NCBI Description (AC003974) unknown protein [Arabidopsis thaliana]

Seq. No. 22514

Contig ID 99142\_1.R1040 5'-most EST 6HA-02-Q1-B1-F5

Method BLASTX
NCBI GI g3608154
BLAST score 293
E value 2.0e-26
Match length 124
% identity 57

NCBI Description (AC005314) unknown protein [Arabidopsis thaliana]

Seq. No. 22515

Contig ID 99144 1.R1040

5'-most EST uC-gmflminsoy022a02b1

Method BLASTX
NCBI GI g4455171
BLAST score 247
E value 9.0e-21
Match length 60
% identity 68

NCBI Description (AL035521) hypothetical protein [Arabidopsis thaliana]

Seq. No. 22516

Contig ID 99145\_1.R1040 5'-most EST taw700659854.h1

Seq. No. 22517

Contig ID 99157\_1.R1040 5'-most EST 6HA-02-Q1-B1-G9

Seq. No. 22518

Contig ID 99164 1.R1040

5'-most EST  $jC-gm\overline{f}102220054a01a1$ 

Method BLASTX
NCBI GI g2499087
BLAST score 449
E value 2.0e-44
Match length 119
% identity 66

NCBI Description UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR

(DUGT) >gi\_1085170\_pir\_\_S54723 UDP-glucose--glycoprotein glucosyltransferase - fruit fly (Drosophila sp.) >gi\_790585

(U20554) UDP-glucose:glycoprotein glucosyltransferase

precursor [Drosophila melanogaster]

Seq. No. 22519

Contig ID 99170\_1.R1040 5'-most EST 6HA-02-Q1-E1-A1

Method BLASTX



NCBI GI q4580466 BLAST score 455 E value 2.0e-45 Match length 132 % identity

NCBI Description (AC006081) putative 50S ribosomal protein L4 [Arabidopsis

thaliana]

Seq. No. 22520

Contig ID 99173 1.R1040 5'-most EST q5510357 Method BLASTX NCBI GI q3785994 BLAST score 270 E value 2.0e-23

Match length 103 % identity 52

NCBI Description (AC005499) hypothetical protein [Arabidopsis thaliana]

Seq. No. 22521

Contig ID 99207 1.R1040 5'-most EST  $6HA - 0\overline{2} - Q1 - E1 - D11$ 

Seq. No. 22522

Contig ID 99233 1.R1040

jC-gmro02910014f03d1 5'-most EST

Seq. No. 22523

Contig ID 99234 1.R1040 5'-most EST 6HA-02-Q1-E1-F4

Method BLASTX NCBI GI g2914703 BLAST score 286 E value 2.0e-25 79 Match length

67 % identity

NCBI Description (AC003974) unknown protein [Arabidopsis thaliana]

Seq. No. 22524

99235 1.R1040 Contig ID 5'-most EST  $epx70\overline{1}106089.h1$ 

Method BLASTX NCBI GI g3608154 BLAST score 572 E value 1.0e-58 Match length 297 53 % identity

NCBI Description (AC005314) unknown protein [Arabidopsis thaliana]

Seq. No. 22525

Contig ID 99236 1.R1040 5'-most EST 6HA - 02 - Q1 - E1 - F6

Method BLASTX NCBI GI q3176686 BLAST score 419 E value 5.0e-41 Match length 110



% identity 70

NCBI Description (AC003671) Similar to high affinity potassium transporter, HAK1 protein gb\_U22945 from Schwanniomyces occidentalis.

[Arabidopsis thaliana]

Seq. No. 22526

Contig ID 99247\_1.R1040

5'-most EST  $g5752\overline{8}49$ 

Seq. No. 22527

Contig ID 99261\_1.R1040 5'-most EST hyd700726649.h1

Method BLASTX
NCBI GI g2982293
BLAST score 146
E value 3.0e-09
Match length 31
% identity 84

NCBI Description (AF051231) ISP42-like protein [Picea mariana]

Seq. No. 22528

Contig ID 99279 1.R1040

5'-most EST jC-gmf102220057d10a1

Seq. No. 22529

Contig ID 99280\_1.R1040 5'-most EST 6HC-02-Q1-B1-H8

Seq. No. 22530

Contig ID 99286\_1.R1040 5'-most EST wvk700684866.h1

Seq. No. 22531

Contig ID 99289\_1.R1040 5'-most EST 6HC-01-Q1-B1-C2

Seq. No. 22532

Contig ID 99289 4.R1040 5'-most EST awf700838706.h1

Seq. No. 22533

Contig ID 99291\_1.R1040 5'-most EST gsv701046220.h1

Seq. No. 22534

Contig ID 99325\_1.R1040

5'-most EST jC-gmf102220127g10a1

Seq. No. 22535

Contig ID 99329 1.R1040

5'-most EST uC-gmrominsoy128c09b1

Method BLASTX
NCBI GI g4324597
BLAST score 549
E value 2.0e-56
Match length 141
% identity 77



(AF106324) sodium proton exchanger Nhx1 [Arabidopsis thaliana]

Seq. No. 22536

NCBI Description

Contig ID 99339\_1.R1040 5'-most EST zzp700834519.h1

Seq. No. 22537

Contig ID 99354 1.R1040

5'-most EST jC-gmst02400064f04d1

Method BLASTX
NCBI GI 94580455
BLAST score 199
E value 2.0e-15
Match length 48
% identity 81

NCBI Description (AC006081) unknown protein [Arabidopsis thaliana]

Seq. No. 22538

Contig ID 99361\_1.R1040 5'-most EST 6HC-01-Q1-E1-A7

Seq. No. 22539

Contig ID 99370 1.R1040

5'-most EST jC-gmle01810034d01d1

Seq. No. 22540

Contig ID 99370\_2.R1040 5'-most EST 6HC-01-Q1-E1-B4

Seq. No. 22541

Contig ID 99374 1.R1040

5'-most EST jC-gmle01810083d12d1

Seq. No. 22542

Contig ID 99380\_1.R1040

5'-most EST jC-gmf102220077b09d1

Seq. No. 22543

Contig ID 99385\_1.R1040

5'-most EST jC-gmst02400054e04d1

Method BLASTX
NCBI GI g294845
BLAST score 210
E value 1.0e-16
Match length 55
% identity 62

NCBI Description (L13655) membrane protein [Saccharum hybrid cultivar

H65-7052]

Seq. No. 22544

Contig ID 99389\_1.R1040 5'-most EST zpv700759330.h1

Seq. No. 22545

Contig ID 99397 1.R1040 5'-most EST 6HC-01-Q1-E1-D9



Method BLASTX
NCBI GI g4115536
BLAST score 262
E value 7.0e-23
Match length 70
% identity 74

NCBI Description (AB012115) UDP-glycose:flavonoid glycosyltransferase [Vigna

mungo]

Seq. No. 22546

Contig ID 99400\_1.R1040 5'-most EST 6HC-01-Q1-E1-E12

Method BLASTX
NCBI GI 94220529
BLAST score 367
E value 5.0e-35
Match length 86
% identity 79

NCBI Description (AL035356) putative protein [Arabidopsis thaliana]

Seq. No. 22547

Contig ID 99406\_1.R1040 5'-most EST 6HC-01-Q1-E1-E7

Seq. No. 22548

Contig ID 99413 1.R1040

5'-most EST jC-gmro02910004h02d1

Method BLASTX
NCBI GI g2129726
BLAST score 468
E value 8.0e-47
Match length 112
% identity 81

NCBI Description RNA polymerase II third largest chain RPB35.5A -

Arabidopsis thaliana >gi\_514318 (L34770) RNA polymerase II

third largest subunit [Arabidopsis thaliana]

>gi\_4544370\_gb\_AAD22281.1\_AC006920\_5 (AC006920) RNA

polymerase II, third largest subunit [Arabidopsis thaliana]

Seq. No. 22549

Contig ID 99414\_1.R1040

5'-most EST jC-gmf102220127g10d1

Method BLASTX
NCBI GI g4522011
BLAST score 242
E value 2.0e-20
Match length 92
% identity 52

NCBI Description (AC007069) hypothetical protein [Arabidopsis thaliana]

Seq. No. 22550

Contig ID 99427 1.R1040

5'-most EST jC-gmle01810010d11d1

Seq. No. 22551

Contig ID 99428\_1.R1040 5'-most EST g5676975



Seq. No. 22552

Contig ID 99445 1.R1040 5'-most EST sat701013886.h1

Seq. No. 22553

Contig ID 99447\_1.R1040 5'-most EST 6HC-02-Q1-B1-A4

Seq. No. 22554

Contig ID 99469\_1.R1040 5'-most EST fua701040375.h1

Method BLASTX
NCBI GI g3643611
BLAST score 963
E value 1.0e-104
Match length 202
% identity 90

NCBI Description (AC005395) putative casein kinase [Arabidopsis thaliana]

Seq. No. 22555

Contig ID 99475\_1.R1040 5'-most EST 6HC-02-Q1-B1-D1

Method BLASTX
NCBI GI g3935184
BLAST score 258
E value 2.0e-22
Match length 79
% identity 63

NCBI Description (AC004557) F17L21.27 [Arabidopsis thaliana]

Seq. No. 22556

Contig ID 99483\_1.R1040 5'-most EST ncj700983262.h1

Method BLASTX
NCBI GI g4432823
BLAST score 362
E value 6.0e-34
Match length 162
% identity 50

NCBI Description (AC006593) hypothetical protein [Arabidopsis thaliana]

Seq. No. 22557

Contig ID 99483\_2.R1040 5'-most EST xpa700797040.h1

Seq. No. 22558

Contig ID 99492 1.R1040 5'-most EST trc700565561.h1

Method BLASTX
NCBI GI g1079136
BLAST score 250
E value 4.0e-21
Match length 116
% identity 50

NCBI Description RNA-binding protein cabeza - fruit fly (Drosophila melanogaster) >gi\_532788 (U13178) RNA binding protein



[Drosophila melanogaster] >gi\_567106 (L37083) RNA binding protein [Drosophila melanogaster]

Seq. No. 22559
Contig ID 99495 1.R1040
5'-most EST 6HC-02-Q1-B1-E9

Seq. No. 22560

Contig ID 99496\_1.R1040 5'-most EST dpv701102470.h1

Method BLASTX
NCBI GI g4455151
BLAST score 356
E value 1.0e-33
Match length 178
% identity 43

NCBI Description (AL022603) putative serine/threonine kinase (fragment)

[Arabidopsis thaliana]

Seq. No. 22561

Contig ID 99503\_1.R1040 5'-most EST hrw70\overline{1}059838.h1

Method BLASTX
NCBI GI g4105798
BLAST score 659
E value 4.0e-69
Match length 175
% identity 57

NCBI Description (AF049930) PGP237-11 [Petunia x hybrida]

Seq. No. 22562

Contig ID 99504 1.R1040 5'-most EST kl1701212561.h1

Seq. No. 22563

Contig ID 99507\_1.R1040 5'-most EST 6HC-02-Q1-B1-G1

Seq. No.

22564

Contig ID 99507 2.R1040 5'-most EST leu701147696.h1

Seq. No.

22565

Contig ID 99508\_1.R1040 5'-most EST zzp700831876.h1

Seq. No.

22566

Contig ID 99550\_1.R1040 5'-most EST 6HC-02-Q1-E1-C6

Seq. No.

22567

Contig ID 99555\_1.R1040

5'-most EST jC-gmst02400049h09d1

Method BLASTX
NCBI GI g3367534
BLAST score 155
E value 4.0e-10



Match length 35 % identity 77

NCBI Description (AC004392) Strong similarity to coatamer alpha subunit

(HEPCOP) homolog gb\_U24105 from Homo sapiens. [Arabidopsis

thaliana]

Seq. No. 22568

Contig ID 99557\_1.R1040

5'-most EST jC-gmle01810063b11d1

Method BLASTX
NCBI GI g3549672
BLAST score 385
E value 6.0e-37
Match length 134

Match length 134 % identity 61

NCBI Description (AL031394) putative protein [Arabidopsis thaliana]

Seq. No. 22569

Contig ID 99557 2.R1040

5'-most EST jC-gmf102220091b12d1

Seq. No. 22570

Contig ID 99558 1.R1040 5'-most EST 6HC-02-Q1-E1-D8

Seq. No. 22571

Contig ID 99564 1.R1040 5'-most EST taw700656723.h1

Seq. No. 22572

Contig ID 99569 1.R1040 5'-most EST gsv701050372.h1

Seq. No. 22573

Contig ID 99571 1.R1040 5'-most EST bth700846395.h1

Seq. No. 22574

Contig ID 99592\_1.R1040 5'-most EST g5606831 Method BLASTX

NCBI GI g3688600 BLAST score 502 E value 9.0e-51 Match length 129 % identity 69

NCBI Description (AB009030) beta-Amyrin Synthase [Panax ginseng]

Seq. No. 22575

Contig ID 99600\_1.R1040 5'-most EST 23-V4L-01-Q1-E1-F11

Seq. No. 22576

Contig ID 99602\_1.R1040 5'-most EST 27-V4L-01-Q1-E1-G11

Seq. No. 22577



Contig ID 99603 1.R1040 5'-most EST wrg700790863.h1

Seq. No. 22578

Contig ID 99616\_1.R1040 5'-most EST 94299353

Seq. No. 22579

Contig ID 99623\_1.R1040

5'-most EST jC-gmf102220138f06d1

Seq. No. 22580

Contig ID 99626 1.R1040

5'-most EST ASG3244V4L-01-Q1-E1-B1

Seq. No. 22581

Contig ID 99630\_1.R1040

5'-most EST ASG3244V4L-01-Q1-E1-B6

Seq. No. 22582

Contig ID 99636 1.R1040

5'-most EST ASG3244V4L-01-Q1-E1-C4

Seq. No. 22583

Contig ID 99638 1.R1040

5'-most EST ASG3244V4L-01-Q1-E1-C6

Method BLASTX
NCBI GI g2760830
BLAST score 398
E value 1.0e-38
Match length 82

% identity 87

NCBI Description (AC003105) putative beta-ketoacyl-CoA synthase [Arabidopsis

thaliana]

Seq. No. 22584

Contig ID 99638\_2.R1040 5'-most EST gsv701055420.h1

Seq. No. 22585

Contig ID 99641\_1.R1040

5'-most EST jC-gmle01810059h12d1

Seq. No. 22586

Contig ID 99642 1.R1040

5'-most EST ASG3244V4L-01-Q1-E1-D3

Method BLASTX
NCBI GI g2501056
BLAST score 251
E value 2.0e-21
Match length 64
% identity 77

NCBI Description SERYL-TRNA SYNTHETASE (SERINE--TRNA LIGASE) (SERRS)

>gi\_2129737\_pir\_\_S71293 seryl-tRNA synthetase - Arabidopsis

thaliana >gi\_1359497\_emb\_CAA94388\_ (Z70313) seryl-tRNA

Synthetase [Arabidopsis thaliana]

% identity

61



```
22587
                                                                             Sales .
Seq. No.
                   99651 1.R1040
Contig ID
5'-most EST
                   fC-qmse700850128d1
                   22588
Seq. No.
                   99664 1.R1040
Contig ID
5'-most EST
                  ASG3244V4L-01-Q1-E1-G3
Method
                  BLASTX
NCBI GI
                  q3688170
BLAST score
                  302
E value
                   2.0e-27
Match length
                  72
% identity
NCBI Description (AL031804) putative protein [Arabidopsis thaliana]
Seq. No.
                  22589
Contig ID
                  99668 1.R1040
                  q4405546
5'-most EST
Method
                  BLASTX
NCBI GI
                   g2315153
BLAST score
                   778
                   6.0e-83
E value
Match length
                   191
% identity
                   73
NCBI Description (Y14316) MAP3K gamma protein kinase [Arabidopsis thaliana]
                   22590
Seq. No.
Contig ID
                   99688 1.R1040
5'-most EST
                   jex700909101.h1
                   BLASTX
Method
NCBI GI
                   g2576255
BLAST score
                   324
                   7.0e-30
E value
                   98
Match length
% identity
                   67
NCBI Description (AJ001729) TH65 protein [Arabidopsis thaliana]
                   22591
Seq. No.
                   99710 1.R1040
Contig ID
5'-most EST
                   ncj700978602.h1
Method
                   BLASTX
                   g4056495
NCBI GI
BLAST score
                   178
                   3.0e-13
E value
Match length
                   98
% identity
                   43
NCBI Description (AC005896) putative TKRP125 [Arabidopsis thaliana]
                   22592
Seq. No.
                   99728 1.R1040
Contig ID
5'-most EST
                   V4L-01-Q1-B1-H1
                   BLASTX
Method
                   g3033400
NCBI GI
BLAST score
                   423
E value
                   2.0e-41
Match length
                   140
```



NCBI Description (AC004238) putative Ser/Thr protein kinase [Arabidopsis thaliana]

Seq. No. 22593

Contig ID 99730\_1.R1040 5'-most EST cf1700863610.h1

Seq. No. 22594

Contig ID 99730\_2.R1040 5'-most EST V4L-01-Q1-B1-H3

Seq. No. 22595

Contig ID 99740 1.R1040 5'-most EST sat701010895.h1

Seq. No. 22596

Contig ID 99754\_1.R1040 5'-most EST V4L-02-Q1-B1-B8

Method BLASTX
NCBI GI g3482882
BLAST score 188
E value 1.0e-13
Match length 150
% identity 35

NCBI Description (U63816) unknown [Pseudomonas aeruginosa]

Seq. No. 22597

Contig ID 99755\_1.R1040 5'-most EST V4L-02-Q1-B1-B9

Method BLASTX
NCBI GI g2583133
BLAST score 297
E value 7.0e-27
Match length 72

% identity 82

NCBI Description (AC002387) unknown protein [Arabidopsis thaliana]

Seq. No. 22598

Contig ID 99756\_1.R1040 5'-most EST ncj700984051.h1

Method BLASTX
NCBI GI g2498882
BLAST score 258
E value 5.0e-22
Match length 121
% identity 25

NCBI Description SPLICEOSOME ASSOCIATED PROTEIN 114 (SAP 114) (SF3A120)

>gi\_2146975\_pir\_\_S60735 splicing factor SF3a 120K chain human >gi\_899298\_emb\_CAA59494 (X85237) human splicing
factor [Homo sapiens] >gi\_3212998 (AC004997) spliceosome

associated protein 114 (SF3a) [Homo sapiens]

Seq. No. 22599

Contig ID 99761\_1.R1040

5'-most EST jC-gmro02910026f11d1

Method BLASTX NCBI GI g3176680



BLAST score 378 E value 3.0e-36 Match length 121 % identity 45

NCBI Description (AC003671) Identical to polygalacuronase isoenzyme 1 beta subunit homolog mRNA gb\_U63373. EST gb\_AA404878 comes from

this gene. [Arabidopsis thaliana]

Seq. No. 22600

Contig ID 99767\_1.R1040 5'-most EST V4L-02-Q1-B1-C9

Method BLASTX
NCBI GI g1173638
BLAST score 306
E value 5.0e-37
Match length 124
% identity 65

NCBI Description (U35779) 1-aminocyclopropane-1-carboxylate synthase

[Triticum aestivum]

Seq. No. 22601

Contig ID 99779 1.R1040

5'-most EST jC-gmro02800025g02a1

Method BLASTX
NCBI GI g4539458
BLAST score 126
E value 3.0e-12
Match length 90
% identity 42

NCBI Description (AL049500) hypothetical protein [Arabidopsis thaliana]

Seq. No. 22602

Contig ID 99779\_2.R1040 5'-most EST 94396948

Seq. No. 22603

Contig ID 99784 1.R1040 5'-most EST rca701001082.h1

Method BLASTX
NCBI GI g4455182
BLAST score 287
E value 1.0e-25
Match length 112
% identity 53

NCBI Description (AL035521) putative protein [Arabidopsis thaliana]

Seq. No. 22604

Contig ID 99787 1.R1040

5'-most EST jC-gmf102220056h07a1

Seq. No. 22605

Contig ID 99790 1.R1040 5'-most EST gsv701044712.h1

Seq. No. 22606

Contig ID 99793 1.R1040 5'-most EST gsv70\overline{1}052985.h1



Method BLASTX
NCBI GI 94558659
BLAST score 428
E value 4.0e-42
Match length 145
% identity 58

NCBI Description (AC007063) unknown protein [Arabidopsis thaliana]

Seq. No.

22607

Contig ID 99795\_1.R1040 5'-most EST awf700843074.h1

Seq. No.

22608

Contig ID 99802\_1.R1040 5'-most EST gsv701056328.h1

Seq. No.

22609

Contig ID 99803\_1.R1040 5'-most EST gsv701052595.h1

Method BLASTX
NCBI GI g4539423
BLAST score 393
E value 6.0e-38
Match length 102
% identity 75

NCBI Description (AL049171) pyrophosphate-dependent phosphofructo-1-kinase

[Arabidopsis thaliana]

Seq. No. 22610

Contig ID 99803\_2.R1040 5'-most EST ssr700557814.h1

Method BLASTX
NCBI GI g4539423
BLAST score 152
E value 7.0e-10
Match length 84
% identity 45

NCBI Description (AL049171) pyrophosphate-dependent phosphofructo-1-kinase

[Arabidopsis thaliana]

Seq. No. 22611

Contig ID 99811\_1.R1040

5'-most EST uC-gmrominsoy180d03b1

Method BLASTX
NCBI GI g2660670
BLAST score 509
E value 1.0e-51
Match length 165
% identity 59

NCBI Description (AC002342) putative Cu2+-transporting ATPase [Arabidopsis

thaliana]

Seq. No. 22612

Contig ID 99818\_1.R1040

5'-most EST jC-gmst02400041c08a1

Method BLASTX NCBI GI g2244868



BLAST score 261 E value 2.0e-22 Match length 133 % identity 43

NCBI Description (Z97337) cytochrome P450 [Arabidopsis thaliana]

Seq. No. 22613

Contig ID 99820\_1.R1040 5'-most EST V4L-02-Q1-B1-H6

Seq. No. 22614

Contig ID 99822\_1.R1040 5'-most EST smc700749392.h1

Method BLASTN
NCBI GI g3449321
BLAST score 49
E value 2.0e-18
Match length 121
% identity 85

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MTG10, complete sequence [Arabidopsis thaliana]

Seq. No. 22615

Contig ID 99824 1.R1040 5'-most EST V4L-02-Q1-E1-A1

Seq. No. 22616

Contig ID 99838 1.R1040 5'-most EST g4397411

Method BLASTX
NCBI GI g2244914
BLAST score 221
E value 1.0e-17
Match length 100
% identity 57

NCBI Description (297339) similarity to probable splicing factor Ceprp21

[Arabidopsis thaliana]

Seq. No. 22617

Contig ID 99838 2.R1040 5'-most EST V4L-02-Q1-E1-C1

Method BLASTX
NCBI GI g2498882
BLAST score 213
E value 6.0e-17
Match length 102
% identity 48

NCBI Description SPLICEOSOME ASSOCIATED PROTEIN 114 (SAP 114) (SF3A120)

>gi\_2146975\_pir\_\_S60735 splicing factor SF3a 120K chain human >gi\_899298\_emb\_CAA59494\_ (X85237) human splicing factor [Homo sapiens] >gi\_3212998 (AC004997) spliceosome

associated protein 114 (SF3a) [Homo sapiens]

Seq. No. 22618

Contig ID 99844\_1.R1040

5'-most EST jC-gmle01810044e10d1

Method BLASTX



NCBI GI

g2967687

```
BLAST score
                   211
E value
                   8.0e-17
Match length
                  86
% identity
                  48
NCBI Description (AF035630) epidermal germacrene C synthase [Lycopersicon
                  esculentum]
Seq. No.
                  22619
                  99859 1.R1040
Contig ID
5'-most EST
                  wvk700682913.h1
                  22620
Seq. No.
                  99861 1.R1040
Contig ID
5'-most EST
                  V4L-02-Q1-E1-F1
Seq. No.
                  22621
Contig ID
                  99874 1.R1040
5'-most EST
                  pmv700893822.h1
Method
                  BLASTX
NCBI GI
                  q2660670
BLAST score
                  694
E value
                  6.0e-73
Match length
                  260
% identity
                  55
NCBI Description (AC002342) putative Cu2+-transporting ATPase [Arabidopsis
                  thaliana]
Seq. No.
                  22622
Contig ID
                   99877 1.R1040
                  V4L-02-Q1-E1-H2
5'-most EST
Seq. No.
                  22623
                  99879 1.R1040
Contig ID
5'-most EST
                  V4L-02-Q1-E1-H4
Method
                  BLASTX
NCBI GI
                  q2738996
BLAST score
                  185
                  7.0e-14
E value
Match length
                  73
% identity
NCBI Description (AF022457) CYP97B2p [Glycine max]
                  22624
Seq. No.
Contig ID
                  99890 1.R1040
5'-most EST
                  eep700868218.hl
Seq. No.
                  22625
Contig ID
                  99895_1.R1040
5'-most EST
                  fC-gmro7000746124r1
Method
                  BLASTX
NCBI GI
                  g2146735
BLAST score
                  1025
E value
                  1.0e-141
                  289
Match length
% identity
                  88
```

NCBI Description glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) (clone



E5) - Arabidopsis thaliana (fragment) >gi\_1166405\_emb\_CAA59011\_ (X84229) glucose-6-phosphate 1-dehydrogenase [Arabidopsis thaliana]

Seq. No. 22626

99895 2.R1040 Contig ID

5'-most EST jC-gmst02400002b02d1

Method BLASTX NCBI GI g3023818 BLAST score 235 E value 2.0e-19 59 Match length 73

NCBI Description GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CHOLOROPLAST ISOFORM

PRECURSOR (G6PD) >gi 1197385 emb CAA58775 (X83923) glucose-6-phosphate dehydrogenase [Solanum tuberosum]

Seq. No. 22627

% identity

99895 4.R1040 Contig ID 5'-most EST rca700998437.h1

Method BLASTX NCBI GI g3023818 BLAST score 419 E value 2.0e-41 Match length 95 % identity 95

NCBI Description GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CHOLOROPLAST ISOFORM

PRECURSOR (G6PD) >gi\_1197385\_emb\_CAA58775\_ (X83923) glucose-6-phosphate dehydrogenase [Solanum tuberosum]

Seq. No. 22628

99896 1.R1040 Contig ID

5'-most EST 36-V4R-02-Q1-E1-A12

Seq. No. 22629

99897 1.R1040 Contig ID 5'-most EST 38-V4R-02-Q1-E1-B10

Seq. No. 22630

Contig ID 99909 1.R1040

5'-most EST jC-qmle01810020h08d1

Method BLASTX NCBI GI g2088648 BLAST score 181 6.0e-13 E value Match length 126 % identity

NCBI Description (AF002109) hypothetical protein [Arabidopsis thaliana]

Seq. No. 22631

Contig ID 99909 2.R1040

5'-most EST jC-qmst02400023c01a1

Seq. No. 22632

99914 1.R1040 Contig ID

5'-most EST ASG3244V4R-02-Q1-E1-A6



22633 Seq. No. Contig ID 99925 1.R1040 5'-most EST a4313552 Method BLASTX NCBI GI g1170619 BLAST score 468

E value 8.0e-47 Match length 105 % identity 87

NCBI Description KINESIN-LIKE PROTEIN A >gi 479594 pir S34830

kinesin-related protein katA - Arabidopsis thaliana >gi 303502 dbj BAA01972 (Dl1371) kinesin-like motor

protein heavy chain [Arabidopsis thaliana]

>gi 2911084 emb CAA17546 (AL021960) kinesin-related protein katA [Arabidopsis thaliana]

Seq. No. 22634

99926 1.R1040 Contig ID

5'-most EST ASG3244V4R-02-Q1-E1-C2

BLASTX Method NCBI GI q3510264 BLAST score 506 E value 3.0e-51 Match length 125 % identity 72

NCBI Description (AC005310) hypothetical protein, 5' partial [Arabidopsis

thaliana]

Seq. No.

Contig ID 99946 1.R1040

5'-most EST ASG3244V4R-02-Q1-E1-E7

22635

Method BLASTX NCBI GI g2982309 BLAST score 213 E value 5.0e-17 Match length 47 85 % identity

NCBI Description (AF051239) probable ubiquitin activating enzyme 2 [Picea

mariana]

Seq. No.

22636

Contig ID 99950 1.R1040

5'-most EST jC-gmst02400011f07d1

Seq. No. 22637

99969 1.R1040 Contig ID

5'-most EST jC-gmro02800027c11d1

22638 Seq. No.

99978\_1.R1040 Contig ID 5'-most EST V4R-01-Q1-B1-A6

Method BLASTX NCBI GI q1256509 BLAST score 250 E value 6.0e - 3292 Match length % identity 66

Match length

NCBI Description

% identity

160

24



```
NCBI Description
                  (X92943) pectate lyase [Musa acuminata]
                  22639
Seq. No.
Contig ID
                  99982 1.R1040
5'-most EST
                  fua701039974.h1
Method
                  BLASTX
NCBI GI
                  g1931654
BLAST score
                  340
E value
                  9.0e-32
Match length
                  105
                  65
% identity
                  (U95973) BRCA1-associated RING domain protein isolog
NCBI Description
                  [Arabidopsis thaliana]
                  22640
Seq. No.
Contig ID
                  99991 1.R1040
5'-most EST
                  rlr700898545.h1
Seq. No.
                  22641
Contig ID
                  99991 2.R1040
5'-most EST
                  V4R-01-Q1-B1-B7
Seq. No.
                  22642
Contig ID
                  99994 1.R1040
5'-most EST
                  taw700654753.h1
                  BLASTX
Method
                  g2736155
NCBI GI
BLAST score
                  647
E value
                  2.0e-68
Match length
                  146
% identity
                  88
NCBI Description
                  (AF022082) sulfolipid biosynthesis protein [Arabidopsis
                  thaliana] >gi_3688184_emb_CAA21212_ (AL031804) sulfolipid
                  biosynthesis protein SQD1 [Arabidopsis thaliana]
Seq. No.
                  22643
                  99995 1.R1040
Contig ID
5'-most EST
                  V4R-01-Q1-B1-C10
                  BLASTX
Method
NCBI GI
                  g2191149
BLAST score
                  331
                  8.0e-31
E value
Match length
                  108
% identity
NCBI Description
                  (AF007269) Similar to protein kinase [Arabidopsis thaliana]
                  22644
Seq. No.
                  100002_1.R1040
Contig ID
5'-most EST
                  V4R-01-Q1-B1-C7
Method
                  BLASTX
NCBI GI
                  g1086263
BLAST score
                  140
E value
                  1.0e-11
```

>gi\_558887 (U15605) N [Nicotiana glutinosa]

TMV resistance protein N - tobacco (Nicotiana glutinosa)



Seq. No. 22645

Contig ID 100005\_1.R1040 5'-most EST kl1701208620.h1

Seq. No. 22646

Contig ID 100006 1.R1040

5'-most EST uC-gmflminsoy011d10b1

Seq. No. 22647

Contig ID 100008\_1.R1040 5'-most EST vzy700754481.h1

Seq. No. 22648

Contig ID 100015\_1.R1040 5'-most EST jC-gmle01810006b06a1

Method BLASTX
NCBI GI g3413700
BLAST score 1506
E value 1.0e-168
Match length 440
% identity 70

NCBI Description (AC004747) putative YME1 protein [Arabidopsis thaliana]

Seq. No. 22649

Contig ID 100016\_1.R1040 5'-most EST V4R-01-Q1-B1-E1

Seq. No. 22650

Contig ID 100018\_1.R1040 5'-most EST V4R-01-Q1-B1-E11

Method BLASTX
NCBI GI g3482974
BLAST score 179
E value 3.0e-13
Match length 52
% identity 69

NCBI Description (AL031369) ATP-dependent Clp proteinase-like protein

[Arabidopsis thaliana]

Seq. No. 22651

Contig ID 100020\_1.R1040 5'-most EST V4R-01-Q1-B1-E2

Seq. No. 22652

Contig ID 100033\_1.R1040 5'-most EST V4R-01-Q1-B1-F3

Method BLASTX
NCBI GI g731675
BLAST score 528
E value 1.0e-53
Match length 189
% identity 52

NCBI Description HYPOTHETICAL 80.7 KD PROTEIN IN ERG7-NMD2 INTERGENIC REGION

>gi\_626631\_pir\_\_S46811 hypothetical protein YHR074w - yeast
(Saccharomyces cerevisiae) >gi\_500832 (U10556) Yhr074wp

[Saccharomyces cerevisiae]



```
22653
Seq. No.
                  100037 1.R1040
Contig ID
                  V4R-01-Q1-B1-F8
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4544412
BLAST score
                  476
E value
                  7.0e-48
Match length
                  145
% identity
                  70
                  (AC006955) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  22654
Contig ID
                  100054 1.R1040
5'-most EST
                  jC-qmst02400056e09a1
Method
                  BLASTX
NCBI GI
                  g3337361
BLAST score
                  1245
                  1.0e-137
E value
Match length
                  370
% identity
                  68
                  (AC004481) ankyrin-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  22655
                  100057_1.R1040
Contig ID
5'-most EST
                  V4R-01-Q1-B1-H5
Seq. No.
                  22656
                  100082 1.R1040
Contig ID
5'-most EST
                  g5509659
Seq. No.
                  22657
Contig ID
                  100111 2.R1040
5'-most EST
                  V4R-01-Q1-E1-G8
                  22658
Seq. No.
Contig ID
                  100113 1.R1040
5'-most EST
                  V4R-01-Q1-E1-H5
Method
                  BLASTX
NCBI GI
                  q2598269
BLAST score
                  166
E value
                  2.0e-11
Match length
                  78
% identity
                  44
                  (Y14285) extracellular S domain: 8-1342; transmembrane
NCBI Description
                  domain: 1343-1411; intracellular kinase domain: 1412-2554
                  [Brassica oleracea]
                  22659
Seq. No.
Contig ID
                  100115_1.R1040
5'-most EST
                  V4R-01-Q1-E1-H7
Method
                  BLASTX
```

NCBI GI q3287696 BLAST score 188 E value 3.0e-14

Match length 41 % identity 80



NCBI Description (AC003979) Strong similarity to phosphoribosylanthranilate transferase gb\_D86180 from Pisum sativum. This ORF may be part of a larger gene that lies in the overlapping region. [Arabidopsis thaliana]

Seq. No. 22660

Contig ID 100116\_1.R1040 5'-most EST jC-gmr002800024d11d1

Method BLASTX
NCBI GI g114176
BLAST score 705
E value 2.0e-74
Match length 151
% identity 87

NCBI Description 3-PHOSPHOSHIKIMATE 1-CARBOXYVINYLTRANSFERASE PRECURSOR

(5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE SYNTHASE) (EPSP SYNTHASE) >gi 66620 pir XUPJVS 3-phosphoshikimate

1 applications for a contract (70.0 5 - phosphosnikimace

1-carboxyvinyltransferase (EC 2.5.1.19) precursor - garden

petunia >gi\_169191 (M21084)

5-enolpyruvylshikimate-3-phosphate synthase precursor

[Petunia hybrida]

Seq. No. 22661

Contig ID 100118 1.R1040 5'-most EST V4R-01-Q1-E1-A11

Seq. No. 22662

Contig ID 100125\_2.R1040 5'-most EST eep700868351.h1

Seq. No. 22663

Contig ID 100128\_1.R1040 5'-most EST V4R-01-Q1-E1-C9

Method BLASTX
NCBI GI g1172556
BLAST score 444
E value 8.0e-44
Match length 115
% identity 73

NCBI Description 36 KD OUTER MITOCHONDRIAL MEMBRANE PROTEIN PORIN

(VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN) (VDAC) (POM 36) >gi\_629729\_pir\_\_S46925 porin II, 36K - potato >gi\_1076681\_pir\_\_B55364 porin (clone pPOM 36.2) - potato mitochondrion >gi\_515360\_emb\_CAA56600\_ (X80387) 36kDA porin

II [Solanum tuberosum]

Seq. No. 22664

Contig ID 100129\_1.R1040 5'-most EST V4R-01-Q1-E1-D10

Method BLASTX
NCBI GI g3193288
BLAST score 1118
E value 1.0e-122
Match length 311
% identity 64

NCBI Description (AF069298) similar to bacterial and fungi pectinesterases

[Arabidopsis thaliana]



Seq. No. 22665 100132 1.R1040 Contig ID 5'-most EST jC-gmro02910001a06d1 22666 Seq. No. Contig ID 100132 2.R1040 5'-most EST jC-gmst02400051b12d1 22667 Seq. No. Contig ID 100138 1.R1040

jC-gmle01810085h11d1 5'-most EST BLASTX Method NCBI GI g2979548 BLAST score 385

E value 3.0e-37 Match length 110 59 % identity

NCBI Description (AC003680) putative 7-ethoxycoumarin O-deethylase

[Arabidopsis thaliana]

22668 Seq. No.

100145\_1.R1040 Contig ID 5'-most EST V4R-01-Q1-E1-H12

Method BLASTX NCBI GI g2245066 505 BLAST score E value 9.0e-51 Match length 238 % identity 44

NCBI Description (Z97342) Beta-Amylase [Arabidopsis thaliana]

Seq. No. 22669

100147 1.R1040 Contig ID

5'-most EST uC-gmrominsoy109f02b1

Method BLASTX NCBI GI q2088648 BLAST score 172 E value 4.0e-12 Match length 58 62

% identity

NCBI Description (AF002109) hypothetical protein [Arabidopsis thaliana]

22670 Seq. No.

100154 1.R1040 Contig ID 5'-most EST V4R-02-Q1-B1-A6

BLASTX Method NCBI GI g3123161 BLAST score 277 E value 1.0e-24Match length 129 17 % identity

NCBI Description HYPOTHETICAL 77.0 KD TRP-ASP REPEATS CONTAINING PROTEIN

F35G12.4 IN CHROMOSOME III >gi 3876723 emb CAA86335

(Z46242) similar to beta-transducin; cDNA EST EMBL:Z14703 comes from this gene; cDNA EST EMBL: D67532 comes from this gene; cDNA EST EMBL:D69055 comes from this gene; cDNA EST



EMBL: D64515 comes from this gene; cDNA EST EMBL: D655

Seq. No. 22671

Contig ID 100169\_1.R1040 5'-most EST sat701014226.h1

Method BLASTX
NCBI GI g1170619
BLAST score 553
E value 1.0e-56
Match length 209
% identity 57

NCBI Description KINESIN-LIKE PROTEIN A >gi\_479594\_pir\_\_S34830

kinesin-related protein katA - Arabidopsis thaliana >gi\_303502\_dbj\_BAA01972\_ (D11371) kinesin-like motor

protein heavy chain [Arabidopsis thaliana]

>gi\_2911084\_emb\_CAA17546\_ (AL021960) kinesin-related

protein katA [Arabidopsis thaliana]

Seq. No. 22672

Contig ID 100174\_1.R1040 5'-most EST V4R-02-Q1-B1-C3

Seq. No. 22673

Contig ID 100179 1.R1040 5'-most EST zzp700830489.h1

Seq. No. 22674

Contig ID 100182\_1.R1040 5'-most EST bth700848171.h1

Seq. No. 22675

Contig ID 100182\_2.R1040 5'-most EST fua701042543.h1

Seq. No. 22676

Contig ID 100190 1.R1040 5'-most EST gsv701043762.h1

Seq. No. 22677

Contig ID 100193 1.R1040 5'-most EST trc700563875.h1

Method BLASTX
NCBI GI g2462834
BLAST score 207
E value 2.0e-16
Match length 95
% identity 44

NCBI Description (AF000657) hypothetical protein [Arabidopsis thaliana]

Seq. No. 22678

Contig ID 100196\_1.R1040 5'-most EST V4R-02-Q1-B1-E3

Method BLASTX
NCBI GI g2244790
BLAST score 233
E value 2.0e-19
Match length 89



% identity

NCBI Description (Z97336) kinesin homolog [Arabidopsis thaliana]

Seq. No.

22679

Contig ID 5'-most EST

100201 1.R1040 V4R-02-Q1-B1-E9

Seq. No.

22680

Contig ID 5'-most EST

100212 1.R1040 V4R-02-Q1-B1-F8

Seq. No.

22681

Contig ID

100214 1.R1040

5'-most EST jC-gmle01810043g06a1

Seq. No.

22682

Contig ID 5'-most EST 100231 1.R1040 zzp700834753.h1

Seq. No.

Seq. No.

22683

Contig ID 5'-most EST

100233 1.R1040 dpv701102390.h1

22684

Contig ID 5'-most EST 100235\_1.R1040

uC-gmropic089f01b1 BLASTX Method

NCBI GI

q2052383

BLAST score

906

E value

5.0e-98

Match length % identity

186 85

NCBI Description (U66345) calreticulin [Arabidopsis thaliana]

Seq. No.

22685

Contig ID 5'-most EST 100235 2.R1040

Method

hrw701063435.h1 BLASTX

NCBI GI

g2052383

BLAST score

261

6.0e-23

E value

53

Match length

83

% identity

NCBI Description (U66345) calreticulin [Arabidopsis thaliana]

Seq. No.

22686

Contig ID

100247 1.R1040

5'-most EST

gbt700547917.h1

Seq. No.

22687

Contig ID 5'-most EST 100253 1.R1040 wvk700680181.h2

Method

BLASTX

NCBI GI

g2316016

BLAST score

E value

1578

Match length

1.0e-176



% identity 47
NCBI Description (U92650) MRP-like ABC transporter [Arabidopsis thaliana]

Seq. No. 22688

Contig ID 100273\_1.R1040 5'-most EST jC-gmfl02220070e02d1

Seq. No. 22689

Contig ID 100296\_1.R1040 5'-most EST jex700906964.h1

Seq. No. 22690

Contig ID 100310\_1.R1040 5'-most EST vzy700752425.h1

Seq. No. 22691

Contig ID 100315\_1.R1040 5'-most EST gbt700548016.h1

Method BLASTX
NCBI GI g1771158
BLAST score 277
E value 2.0e-24
Match length 176
% identity 35

NCBI Description (Y07861) MFP1 protein [Lycopersicon esculentum]

Seq. No. 22692

Contig ID 100335\_1.R1040 5'-most EST gbt700548042.h1

Method BLASTX
NCBI GI g3668092
BLAST score 511
E value 4.0e-52
Match length 122
% identity 79

NCBI Description (AC004667) unknown protein [Arabidopsis thaliana]

Seq. No. 22693

Contig ID 100340\_1.R1040 5'-most EST gbt700548050.h1

Seq. No. 22694

Contig ID 100340\_2.R1040 5'-most EST dpv701097087.h1

Seq. No. 22695

Contig ID 100354\_1.R1040 5'-most EST gbt700548066.h1

Seq. No. 22696

Contig ID 100359\_1.R1040 5'-most EST leu701149296.h1

Method BLASTX
NCBI GI g1778145
BLAST score 146
E value 1.0e-20
Match length 64



% identity 78

NCBI Description (U66402) phosphate/phosphoenolpyruvate translocator

precursor [Nicotiana tabacum]

Seq. No. 22697

Contig ID 100360\_1.R1040 5'-most EST epx701106430.h1

Method BLASTX
NCBI GI 94204311
BLAST score 172
E value 2.0e-13
Match length 83
% identity 53

NCBI Description (AC003027) 1cl prt seq No definition line found

[Arabidopsis thaliana]

Seq. No. 22698

Contig ID 100374\_1.R1040 5'-most EST uC-gmronoir036h07b1

Method BLASTX
NCBI GI g4415920
BLAST score 279
E value 9.0e-25
Match length 95
% identity 62

NCBI Description (AC006282) putative glucosyl transferase [Arabidopsis

thaliana]

Seq. No. 22699

Contig ID 100383\_1.R1040 5'-most EST zhf700952775.h1

Method BLASTX
NCBI GI g3618316
BLAST score 213
E value 4.0e-17
Match length 48
% identity 43

NCBI Description (AB001886) zinc finger protein [Oryza sativa]

Seq. No. 22700

Contig ID 100386\_1.R1040 5'-most EST ssr700553507.h1

Seq. No. 22701

Contig ID 100387\_1.R1040 5'-most EST pcp700991645.h1

Seq. No. 22702

Contig ID 100388\_1.R1040 5'-most EST ssr700560808.h1

Seq. No. 22703

Contig ID 100394\_1.R1040 5'-most EST jC-qmro02910041038a1

Method BLASTX
NCBI GI g4539435
BLAST score 506

3617



E value 2.0e-51 Match length 140 % identity 66

NCBI Description (AL049523) putative protein [Arabidopsis thaliana]

Seq. No. 22704

Contig ID 100396\_1.R1040 5'-most EST ssr700553523.h1

Seq. No. 22705

Contig ID 100397\_1.R1040 5'-most EST ssr700553871.h1

Seq. No. 22706

Contig ID 100401\_1.R1040 5'-most EST eep700869812.h1

Seq. No. 22707

Contig ID 100401\_2.R1040 5'-most EST xpa700794572.h1

Seq. No. 22708

Contig ID 100403\_1.R1040 5'-most EST ssr700553530.h1

Method BLASTX
NCBI GI g1839022
BLAST score 254
E value 8.0e-22
Match length 154
% identity 25

NCBI Description (Y11121) amino acid carrier [Ricinus communis]

Seq. No. 22709

Contig ID 100410\_1.R1040 5'-most EST ssr700553537.h1

Method BLASTX
NCBI GI g1169782
BLAST score 147
E value 1.0e-09
Match length 61
% identity 56

% identity 56
NCBI Description FUSCA PROTEIN FUS6 >gi\_432446 (L26498) FUS6 [Arabidopsis

thaliana]

Seq. No. 22710

Contig ID 100436\_1.R1040 5'-most EST uC-gmronoir044b12b1

Method BLASTX
NCBI GI g3367576
BLAST score 225
E value 3.0e-18
Match length 54
% identity 74

NCBI Description (AL031135) NAM / CUC2 -like protein [Arabidopsis thaliana]

Seq. No. 22711

Contig ID 100436\_2.R1040

Match length

NCBI Description

% identity

126

thaliana]



```
5'-most EST
                  qsv701050039.h1
                  22712
Seq. No.
                  100440 1.R1040
Contig ID
                  ssr700\overline{5}53579.h1
5'-most EST
Method
                  BLASTN
NCBI GI
                  g4519188
BLAST score
                  64
                  2.0e-27
E value
Match length
                  280
                  85
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K21L19, complete sequence
                  22713
Seq. No.
Contig ID
                  100451 1.R1040
5'-most EST
                  uxk700671215.hl
Seq. No.
                  22714
Contig ID
                  100458 1.R1040
5'-most EST
                  ncj700986952.h1
Method
                  BLASTX
                  g3108075
NCBI GI
BLAST score
                  234
E value
                  2.0e-19
Match length
                  120
% identity
                  43
                  (AF060797) putative beta-ureidopropionase [Manduca sexta]
NCBI Description
Seq. No.
                  22715
                  100472 1.R1040
Contig ID
5'-most EST
                  uC-qmflminsoy089e04b1
Seq. No.
                  22716
                  100496 1.R1040
Contig ID
5'-most EST
                  ssr700553656.h1
Seq. No.
                  22717
                  100502 1.R1040
Contig ID
5'-most EST
                  wrg700786760.h2
Seq. No.
                  22718
Contig ID
                   100518 1.R1040
                   fC-qmle700553684a3
5'-most EST
                  22719
Seq. No.
                  100540 1.R1040
Contig ID
5'-most EST
                  fC-gmle700553715a3
Method
                  BLASTX
NCBI GI
                  g3885336
BLAST score
                  229
E value
                   1.0e-18
```

(AC005623) receptor-like protein kinase [Arabidopsis

```
22720
Seq. No.
                  100542 1.R1040
Contig ID
5'-most EST
                  ssr700553718.hl
                  22721
Seq. No.
                  100545 1.R1040
Contig ID
5'-most EST
                  fC-gmle700553723a3
Seq. No.
                  22722
                  100546 1.R1040
Contig ID
5'-most EST
                  jC-gmst02400071d06a1
Method
                  BLASTX
                  g3986289
NCBI GI
BLAST score
                  349
E value
                  1.0e-35
Match length
                  140
% identity
NCBI Description (AB017357) L-Galactono-1,4-lactone dehydrogenase [Ipomoea
                  batatas]
                  22723
Seq. No.
                  100546 2.R1040
Contig ID
5'-most EST
Method
                  BLASTX
NCBI GI
                  q2760543
BLAST score
                  292
```

jC-gmro02910057e04a1

E value 2.0e-26 Match length 67 % identity 82

NCBI Description (297060) L-galactono-1,4-lactone dehydrogenase [Brassica

oleracea]

Seq. No. 22724

Contig ID 100557 2.R1040 5'-most EST kl1701205269.h1

22725 Seq. No.

100564 1.R1040 Contig ID

5'-most EST jC-gmst02400051f02a1

22726 Seq. No.

100566 1.R1040 Contig ID 5'-most EST ssr700557704.h1

Seq. No. 22727

100577 1.R1040 Contig ID 5'-most EST jsh701064908.h1

Seq. No. 22728

100586 1.R1040 Contig ID 5'-most EST ssr700553772.hl Method BLASTX

NCBI GI q4539335 BLAST score 255 E value 9.0e-28 Match length 146 48 % identity

3620



NCBI Description (AL035539) putative protein [Arabidopsis thaliana]

Seq. No. 22729

Contig ID 100602\_1.R1040 5'-most EST ssr700553804.h1

Method BLASTX
NCBI GI g2864608
BLAST score 252
E value 1.0e-28
Match length 84
% identity 75

NCBI Description (AL021811) ferredoxin--NADP+ reductase - like protein

[Arabidopsis thaliana] >gi\_4049338\_emb\_CAA22563\_ (AL034567)

ferredoxin-NADP+ reductase-like protein [Arabidopsis

thaliana]

Seq. No. 22730

Contig ID 100612\_1.R1040 5'-most EST ssr700553816.h1

Method BLASTX
NCBI GI g2191150
BLAST score 151
E value 8.0e-10
Match length 122
% identity 16

NCBI Description (AF007269) similar to mitochondrial carrier family

[Arabidopsis thaliana]

Seq. No. 22731

Contig ID 100617\_1.R1040 5'-most EST awf700837081.h1

Seq. No. 22732

Contig ID 100623 1.R1040 5'-most EST hrw701062277.h1

Seq. No. 22733

Contig ID 100625\_1.R1040 5'-most EST ssr700553834.h1

Method BLASTX
NCBI GI g3646126
BLAST score 329
E value 1.0e-30
Match length 91
% identity 65

NCBI Description (AJ010840) ATP-dependent RNA helicase [Homo sapiens]

Seq. No. 22734

Contig ID 100631\_1.R1040 5'-most EST ssr700553841.h1

Seq. No. 22735

Contig ID 100633\_1.R1040 5'-most EST tku700646434.h1

Seq. No. 22736

Contig ID 100635 1.R1040



5'-most EST ssr700553845.h1

Method BLASTX
NCBI GI g4580394
BLAST score 375
E value 4.0e-36
Match length 120
% identity 53

NCBI Description (AC007171) putative fatty acid elongase [Arabidopsis

thaliana]

Seq. No. 22737

Contig ID 100637\_1.R1040 5'-most EST ssr700553847.h1

Method BLASTX
NCBI GI g1698548
BLAST score 918
E value 5.0e-99
Match length 351
% identity 56

NCBI Description (U58971) calmodulin-binding protein [Nicotiana tabacum]

Seq. No. 22738

Contig ID 100638\_1.R1040 5'-most EST ssr700553848.h1

Seq. No. 22739

Contig ID 100643\_1.R1040 5'-most EST ssr700553856.h1

Method BLASTX
NCBI GI g2384675
BLAST score 386
E value 2.0e-74
Match length 177
% identity 81

NCBI Description (AF012659) putative potassium transporter AtKT4p

[Arabidopsis thaliana]

Seq. No. 22740

Contig ID 100653\_1.R1040 5'-most EST kl1701208678.h1

Method BLASTN
NCBI GI g2098248
BLAST score 200
E value 1.0e-108
Match length 444
% identity 86

NCBI Description Arabidopsis thaliana DNA repair protein homolog (XPBara)

mRNA, complete cds

Seq. No. 22741

Contig ID 100661\_1.R1040 5'-most EST ssr700553879.h1

Method BLASTX
NCBI GI g119640
BLAST score 172
E value 7.0e-25
Match length 118



% identity 51

NCBI Description 1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE HOMOLOG (PROTEIN E8) >gi 82109 pir S01642 ripening protein E8 - tomato

E8) >gi\_82109\_pir\_\_S01642 ripening protein E8 - tomato >gi\_19199\_emb\_CAA31789\_ (X13437) E8 protein [Lycopersicon

esculentum]

Seq. No. 22742

Contig ID 100664\_1.R1040 5'-most EST ssr700557482.h1

Seq. No. 22743

Contig ID 100676\_1.R1040 5'-most EST hrw701057311.h1

Method BLASTX
NCBI GI g3548802
BLAST score 332
E value 2.0e-33
Match length 118
% identity 64

NCBI Description (AC005313) axi 1-like protein [Arabidopsis thaliana]

>gi\_4335769\_gb\_AAD17446\_ (AC006284) putative axi1 protein

[Nicotiana tabacum] [Arabidopsis thaliana]

Seq. No. 22744

Contig ID 100683\_1.R1040 5'-most EST kl1701207574.h1

Seq. No. 22745

Contig ID 100689 1.R1040 5'-most EST leu701149658.h1

Method BLASTX
NCBI GI g286009
BLAST score 156
E value 7.0e-22
Match length 217
% identity 32

NCBI Description (D13645) KIAA0020 [Homo sapiens]

Seq. No. 22746

Contig ID 100696\_1.R1040 5'-most EST fua701043244.h1

Method BLASTN
NCBI GI g3985934
BLAST score 40
E value 5.0e-13
Match length 104
% identity 85

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MJE7, complete sequence [Arabidopsis thaliana]

Seq. No. 22747

Contig ID 100729\_1.R1040 5'-most EST ssr700553977.h1

Seq. No. 22748

Contig ID 100733\_1.R1040

5'-most EST uC-gmflminsoy041h04b1



Method BLASTX
NCBI GI g2347199
BLAST score 235
E value 1.0e-19
Match length 80
% identity 59

NCBI Description (AC002338) protein kinase isolog [Arabidopsis thaliana]

Seq. No. 22749

Contig ID 100733\_2.R1040 5'-most EST ssr700553982.h1

Method BLASTX
NCBI GI g2347199
BLAST score 222
E value 5.0e-18
Match length 60
% identity 73

NCBI Description (AC002338) protein kinase isolog [Arabidopsis thaliana]

Seq. No. 22750

Contig ID 100735\_1.R1040 5'-most EST seb700649201.h1

Seq. No. 22751

Contig ID 100742\_1.R1040 5'-most EST dpv701102944.h1

Method BLASTX
NCBI GI g2760839
BLAST score 226
E value 2.0e-18
Match length 174
% identity 26

NCBI Description (AC003105) putative receptor kinase [Arabidopsis thaliana]

Seq. No. 22752

Contig ID 100743\_1.R1040 5'-most EST vzy700751051.h1

Seq. No. 22753

Contig ID 100745\_1.R1040 5'-most EST asn701141722.h1

Seq. No. 22754

Contig ID 100746\_1.R1040 5'-most EST zpv700761744.h1

Method BLASTX
NCBI GI g799177
BLAST score 197
E value 6.0e-15
Match length 185
% identity 31

NCBI Description (U22055) 100 kDa coactivator [Homo sapiens]

Seq. No. 22755

Contig ID 100751\_1.R1040 5'-most EST ssr700554008.h1

Method BLASTX



NCBI GI g4115938 BLAST score 214 E value 4.0e-25 Match length 126 % identity 56

NCBI Description (AF118223) contains similarity several bacterial

glutathione-regulated potassium efflux system proteins

[Arabidopsis thaliana]

Seq. No. 22756

Contig ID 100765\_1.R1040 5'-most EST epx701107843.h1

Method BLASTX
NCBI GI g2088651
BLAST score 1395
E value 1.0e-155
Match length 464
% identity 61

NCBI Description (AF002109) hypersensitivity-related gene 201 isolog

[Arabidopsis thaliana]

Seq. No. 22757

Contig ID 100774\_1.R1040 5'-most EST ssr700554060.h1

Seq. No. 22758

Contig ID 100779\_1.R1040 5'-most EST ssr700554053.h1

Method BLASTX
NCBI GI g2244988
BLAST score 382
E value 6.0e-37
Match length 113
% identity 66

NCBI Description (Z97340) hypothetical protein [Arabidopsis thaliana]

Seq. No. 22759

Contig ID 100799\_1.R1040 5'-most EST ssr700554082.h1

Seq. No. 22760

Contig ID 100802\_1.R1040 5'-most EST uC-gmronoir000e03b1

Method BLASTX
NCBI GI g2832632
BLAST score 149
E value 2.0e-14
Match length 113
% identity 41

NCBI Description (AL021711) hypothetical protein [Arabidopsis thaliana]

Seq. No. 22761

Contig ID 100822\_1.R1040 5'-most EST ssr700554533.h1

Seq. No. 22762

Contig ID 100825\_1.R1040



```
kmv700743696.h1
5'-most EST
                   22763
Seq. No.
                   100826 1.R1040
Contig ID
5'-most EST
                   epx701109693.h1
Seq. No.
                   22764
                   100840 1.R1040
Contig ID
                   dpv701\overline{0}98116.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q2289786
BLAST score
                   149
E value
                   8.0e-10
Match length
                   85
% identity
                   39
NCBI Description (D88153) HYA22 [Homo sapiens]
Seq. No.
                   22765
                   100873 1.R1040
Contig ID
5'-most EST
                   ssr700\overline{5}54177.h1
                   22766
Seq. No.
                   100881 1.R1040
Contig ID
5'-most EST
                   hrw701058303.h1
Method
                   BLASTX
NCBI GI
                   g4539326
BLAST score
                   420
                   4.0e-41
E value
Match length
                   139
% identity
                   61
                   (AL035679) putative zinc finger protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   22767
                   100881 2.R1040
Contig ID
5'-most EST
                   zzp700832588.h1
                   BLASTX
Method
NCBI GI
                   g4539326
BLAST score
                   160
                   2.0e-11
E value
Match length
                   57
% identity
                   40
NCBI Description
                   (AL035679) putative zinc finger protein [Arabidopsis
                   thaliana]
Seq. No.
                   22768
Contig ID
                   100891 1.R1040
5'-most EST
                   fC-gmle700554207a3
```

Seq. No. 22769

Contig ID 100895\_1.R1040 5'-most EST ssr700554212.h1

Seq. No. 22770

Contig ID 100903\_1.R1040

5'-most EST jC-gmro02910074h09a1

Method BLASTX



```
q3695019
NCBI GI
BLAST score
                  385
                  4.0e-37
E value
                  129
Match length
% identity
                  (AF055848) subtilisin-like protease [Arabidopsis thaliana]
NCBI Description
                   22771
Seq. No.
                   100905 1.R1040
Contig ID
                   fC-gmle700554222a3
5'-most EST
Method
                   BLASTN
                   g1663548
NCBI GI
                   118
BLAST score
                   1.0e-59
E value
                   286
Match length
                   85
% identity
                   Glycine max clone RLG6 disease resistance protein homolog
NCBI Description
                   gene, partial cds
                   22772
Seq. No.
                   100906 1.R1040
Contig ID
                   ssr700554223.h1
5'-most EST
                   BLASTX
Method
                   g4218002
NCBI GI
                   261
BLAST score
                   1.0e-22
E value
Match length
                   134
                   41
% identity
                   (AC006135) putative UTP-glucose glucosyltransferase
NCBI Description
                   [Arabidopsis thaliana]
                   22773
Seq. No.
                   100936 1.R1040
Contig ID
                   uxk700672370.h1
5'-most EST
                   BLASTX
Method
                   g2398527
NCBI GI
                   552
BLAST score
                   2.0e-56
E value
                   143
Match length
                   76
 % identity
                   (Y13723) Transcription factor [Arabidopsis thaliana]
 NCBI Description
                   22774
 Seq. No.
                   100937 1.R1040
 Contig ID
                   wvk700684254.h1
 5'-most EST
                   BLASTX
 Method
                   g2462832
 NCBI GI
                    475
 BLAST score
                    9.0e-48
 E value
 Match length
                   145
                    62
 % identity
                   (AF000657) similar to Bacillus CotA [Arabidopsis thaliana]
 NCBI Description
```

22775

100939 1.R1040

 $ssr700\overline{5}54272.h1$ 

Seq. No.

Contig ID

5'-most EST



```
Seq. No.
                   22776
                   100941 1.R1040
Contig ID
5'-most EST
                  ncj700982186.h1
Method
                  BLASTX
NCBI GI
                  g3170525
BLAST score
                  448
E value
                  2.0e-44
Match length
                  113
                  79
% identity
NCBI Description (AF054615) cellulase [Fragaria x ananassa]
Seq. No.
                  22777
                  100941 2.R1040
Contig ID
5'-most EST
                  hyd700728050.h1
Seq. No.
                   22778
Contig ID
                  100943 1.R1040
5'-most EST
                  ssr700556939.h1
Seq. No.
                   22779
Contig ID
                  100977 1.R1040
5'-most EST
                  g5509238
Seq. No.
                  22780
Contig ID
                  100977 2.R1040
5'-most EST
                  zpv700757849.h1
Method
                  BLASTX
NCBI GI
                  g1055161
BLAST score
                   166
                   1.0e-24
E value
Match length
                   365
                   28
% identity
NCBI Description
                   (U40029) similar to human 100 kDa coactivator (U22055)
                   [Caenorhabditis elegans]
Seq. No.
                  22781
                  100977 3.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy110g10b1
                  BLASTN
Method
                  g2760165
NCBI GI
BLAST score
                  35
E value
                   4.0e-10
Match length
                  71
                   94
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MAC9, complete sequence [Arabidopsis thaliana]
                   22782
Seq. No.
                  100978 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810091f12a1
Method
                  BLASTX
```

Method BLASTX
NCBI GI g3249105
BLAST score 447
E value 5.0e-44
Match length 150
% identity 59

NCBI Description (AC003114) Contains similarity to protein phosphatase 2C



(ABI1) gb\_X78886 from A. thaliana. [Arabidopsis thaliana]

22783 Seq. No. 100978 2.R1040 Contig ID smc700748527.h15'-most EST BLASTX Method q3249105 NCBI GI 477 BLAST score 3.0e-48E value 110 Match length % identity 83 (AC003114) Contains similarity to protein phosphatase 2C NCBI Description (ABI1) gb\_X78886 from A. thaliana. [Arabidopsis thaliana] 22784 Seq. No. 100995 1.R1040 Contig ID uC-gmflminsoy025d04b1 5'-most EST BLASTX Method g3980380 NCBI GI 470 BLAST score 4.0e-47 E value 110 Match length % identity (AC004561) putative enolase [Arabidopsis thaliana] NCBI Description 22785 Seq. No. 101017 1.R1040 Contig ID gsv701045867.hl 5'-most EST 22786 Seq. No. 101034 1.R1040 Contig ID smc700750051.h15'-most EST BLASTX Method g3004551 NCBI GI 162 BLAST score 6.0e-11 E value 87 Match length 43 % identity (AC003673) hypothetical protein [Arabidopsis thaliana] NCBI Description 22787 Seq. No. 101056 1.R1040 Contig ID g5677904 5'-most EST BLASTX Method g4510400 NCBI GI 375 BLAST score 5.0e-36 E value 79 Match length % identity (AC006587) putative vacuolar-type H(+)-ATPase [Arabidopsis NCBI Description thaliana] Seq. No. 22788 101057 1.R1040 Contig ID

Seq. No. 22789

pcp700991702.hl

5'-most EST



101058 1.R1040 Contig ID 5'-most EST epx701106931.hl Method BLASTX NCBI GI g4204267

BLAST score 283 E value 5.0e-25 Match length 148 % identity 45

NCBI Description (AC005223) 55585 [Arabidopsis thaliana]

Seq. No. 22790

Contig ID 101074 1.R1040 5'-most EST ssr700554459.hl

22791 Seq. No.

Contig ID 101075 1.R1040 5'-most EST ssr700554901.hl

Method BLASTX NCBI GI g3281851 BLAST score 839 E value 3.0e~90 185 Match length 80 % identity

(AL031004) RNA lariat debranching enzyme - like protein NCBI Description

[Arabidopsis thaliana]

22792 Seq. No.

Contig ID 101080 1.R1040 5'-most EST ssr700554471.h1

Method BLASTX NCBI GI q1170619 BLAST score 356 E value 4.0e-34 Match length 95

% identity 73

KINESIN-LIKE PROTEIN A >gi 479594 pir S34830 NCBI Description

> kinesin-related protein katA - Arabidopsis thaliana >gi\_303502\_dbj\_BAA01972\_ (D11371) kinesin-like motor

protein heavy chain [Arabidopsis thaliana]

>gi 2911084 emb CAA17546 (AL021960) kinesin-related

protein katA [Arabidopsis thaliana]

22793 Seq. No.

101094 1.R1040 Contig ID 5'-most EST ssr700554494.hl

Seq. No. 22794

101098 1.R1040 Contig ID

5'-most EST g5678081

22795 Seq. No.

101103 1.R1040 Contig ID 5'-most EST ssr700554514.h1

Method BLASTX g1724112 NCBI GI BLAST score 198 E value 6.0e-15



Match length 176 % identity 31

NCBI Description (U80037) ABA induced plasma membrane protein PM 19

[Triticum aestivum]

Seq. No. 22796

Contig ID 101110\_1.R1040 5'-most EST ssr700555092.h1

Seq. No. 22797

Contig ID 101126\_1.R1040 5'-most EST hyd700726187.h1

Seq. No. 22798

Contig ID 101132\_1.R1040 5'-most EST zhf700956540.h1

Seq. No. 22799

Contig ID 101133 1.R1040 5'-most EST ssr700554563.h1

Seq. No. 22800

Contig ID 101171\_1.R1040 5'-most EST fua701041333.h1 Method BLASTX

NCBI GI g4544464
BLAST score 367
E value 2.0e-35
Match length 92
% identity 67

NCBI Description (AC006580) putative chloroplast nucleoid DNA binding

protein [Arabidopsis thaliana]

Seq. No. 22801

Contig ID 101178\_1.R1040 5'-most EST uC-gmropic020h09b1

Seq. No. 22802

Contig ID 101191 1.R1040 5'-most EST ssr700554644.h1

Method BLASTX
NCBI GI g1905775
BLAST score 474
E value 2.0e-47
Match length 205
% identity 52

NCBI Description (Y11930) putative protein kinase [Arabidopsis thaliana]

Seq. No. 22803

Contig ID 101194\_1.R1040 5'-most EST jC-qmr002910032e02a1

Method BLASTX
NCBI GI g3482978
BLAST score 578
E value 1.0e-59
Match length 146

% identity 78



NCBI Description (AL031369) putative protein [Arabidopsis thaliana]

Seq. No. 22804

Contig ID 101222\_1.R1040 5'-most EST zhf700956516.h1

Seq. No. 22805

Contig ID 101232\_1.R1040 5'-most EST pcp700995134.h1

Method BLASTX
NCBI GI g2642159
BLAST score 515
E value 3.0e-52
Match length 105
% identity 88

NCBI Description (AC003000) putative mannose-1-phosphate guanyltransferase

[Arabidopsis thaliana] >gi\_3598958 (AF076484) GDP-mannose

pyrophosphorylase [Arabidopsis thaliana] >gi\_4151925

(AF108660) CYT1 protein [Arabidopsis thaliana]

Seq. No. 22806

Contig ID 101234\_1.R1040 5'-most EST ssr700554733.h1

Seq. No. 22807

Contig ID 101275 1.R1040 5'-most EST ssr700554765.h1

Seq. No. 22808

Contig ID 101281\_1.R1040 5'-most EST zzp700834036.h1

Method BLASTX
NCBI GI g4160532
BLAST score 724
E value 1.0e-76
Match length 286
% identity 47

NCBI Description (AJ011304) sphingosine-1-phosphate lyase [Homo sapiens]

Seq. No. 22809

Contig ID 101294 1.R1040 5'-most EST hyd700726212.h1

Seq. No. 22810

Contig ID 101295\_1.R1040 5'-most EST ssr700554801.h1

Method BLASTX
NCBI GI g2191135
BLAST score 453
E value 8.0e-45
Match length 145
% identity 58

NCBI Description (AF007269) A\_IG002N01.14 gene product [Arabidopsis

thaliana]

Seq. No. 22811

Contig ID 101302\_1.R1040



5'-most EST ssr700554809.hl

22812 Seq. No.

101305 1.R1040 Contig ID 5'-most EST zhf700954018.hl

Seq. No. 22813

Contig ID 101307 1.R1040 5'-most EST ssr700554814.hl

BLASTX Method g3776015 NCBI GI BLAST score 313 E value 6.0e-29 Match length 109 % identity

NCBI Description (AJ010471) RNA helicase [Arabidopsis thaliana]

>gi 4249378 gb AAD14475 (AC005966) Identical to

gb AJ010471 mRNA for DEAD box RNA helicase (RH22) from Arabidopsis thaliana. EST gb\_Y11191 comes from this gene.

[Arabidopsis thaliana]

Seq. No. 22814

Contig ID 101308 1.R1040 5'-most EST  $epx701\overline{1}09979.h1$ 

Seq. No. 22815

101310 1.R1040 Contig ID 5'-most EST wvk700686301.hl

Method BLASTX NCBI GI g3702337 BLAST score 426 E value 4.0e-48 Match length 165 % identity 66

NCBI Description (AC005397) unknown protein [Arabidopsis thaliana]

Seq. No. 22816

Contig ID 101314 1.R1040 5'-most EST  $ssr700\overline{5}57043.h1$ 

Method BLASTX NCBI GI g2982431 BLAST score 193 E value 7.0e-15 Match length 93

% identity 3

NCBI Description (AL022224) leucine rich repeat-like protein [Arabidopsis

thaliana]

Seq. No. 22817

Contig ID 101320 1.R1040 5'-most EST ssr700555205.h1

Seq. No. 22818

101320 2.R1040 Contig ID zhf700953018.hl 5'-most EST

Seq. No. 22819



Contig ID 101322\_1.R1040 5'-most EST trc700566865.h1

Seq. No. 22820

Contig ID 101322\_2.R1040 5'-most EST uC-gmropic033h05b1

Seq. No. 22821

Contig ID 101335\_1.R1040 5'-most EST leu701151191.h1

Seq. No. 22822

Contig ID 101351\_1.R1040

5'-most EST g5126412
Method BLASTX
NCBI GI g3096935
BLAST score 552
E value 2.0e-56
Match length 136
% identity 80

NCBI Description (AL023094) putative protein [Arabidopsis thaliana]

Seq. No. 22823

Contig ID 101351\_2.R1040

5'-most EST uC-gmrominsoy228b05b1

Method BLASTX
NCBI GI g3096935
BLAST score 894
E value 2.0e-96
Match length 237
% identity 76

NCBI Description (AL023094) putative protein [Arabidopsis thaliana]

Seq. No. 22824

Contig ID 101351\_3.R1040 5'-most EST zsg701125922.h1

Method BLASTX
NCBI GI g3096935
BLAST score 172
E value 3.0e-12
Match length 59
% identity 68

NCBI Description (AL023094) putative protein [Arabidopsis thaliana]

Seq. No. 22825

Contig ID 101351\_4.R1040 5'-most EST taw700654519.h1

Seq. No. 22826

Contig ID 101359\_1.R1040 5'-most EST ssr700554893.h1

Seq. No. 22827

Contig ID 101360\_1.R1040 5'-most EST leu701149847.h1

Seq. No. 22828

```
101366 1.R1040
Contig ID
                  ncj700\overline{9}87962.h1
5'-most EST
                  22829
Seq. No.
                  101367 1.R1040
Contig ID
                  ssr700\overline{5}54910.h1
5'-most EST
                  BLASTX
Method
                  g3075399
NCBI GI
                   233
BLAST score
                   1.0e-19
E value
                   75
Match length
                   61
% identity
                  (AC004484) SF16-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   22830
                   101374 1.R1040
Contig ID
                   ssr700554919.hl
5'-most EST
                   BLASTN
Method
                   g1155204
NCBI GI
                   124
BLAST score
                   2.0e-63
E value
                   280
Match length
                   86
% identity
NCBI Description P.vulgaris mRNA for plasma membrane H+-ATPase
                   22831
Seq. No.
                   101379 1.R1040
Contig ID
                   uC-gmronoir054f05b1
5'-most EST
                   BLASTX
Method
                   g4512667
NCBI GI
                   923
BLAST score
                   1.0e-100
E value
                   195
Match length
                   87
% identity
                   (AC006931) putative MAP kinase [Arabidopsis thaliana]
NCBI Description
                   22832
Seq. No.
                   101382 1.R1040
Contig ID
                   fC-gmle700557179f3
5'-most EST
                   BLASTX
Method
                   a1871182
NCBI GI
                   457
BLAST score
                   2.0e-45
E value
                   110
Match length
 % identity
                   (U90439) phospholipase D isolog [Arabidopsis thaliana]
NCBI Description
                    22833
 Seq. No.
                    101383 1.R1040
 Contig ID
                    jC-qmro02910040h02a1
 5'-most EST
                    22834
 Seq. No.
                    101404 1.R1040
 Contia ID
                    awf700836921.hl
 5'-most EST
```

22835

101406\_1.R1040

Seq. No.

Contig ID

Seq. No.

Contig ID

22840

101429 1.R1040

```
5'-most EST
                  ssr700554968.h1
Method
                  BLASTX
NCBI GI
                  q4309889
BLAST score
                  144
E value
                  6.0e-09
                  77
Match length
                  36
% identity
NCBI Description (AC004983) similar to PID:g3877944 [Homo sapiens]
                  22836
Seq. No.
                  101408 1.R1040
Contig ID
5'-most EST
                  crh700850624.h1
                  BLASTX
Method
                  q2827141
NCBI GI
BLAST score
                  1142
E value
                  1.0e-125
Match length
                  225
% identity
                  90
NCBI Description (AF027173) cellulose synthase catalytic subunit
                  [Arabidopsis thaliana]
                  22837
Seq. No.
                  101411 1.R1040
Contig ID
5'-most EST
                  ncj700985449.h1
Method
                  BLASTX
NCBI GI
                  g4538993
BLAST score
                  129
                  8.0e-16
E value
Match length
                  58
% identity
                  61
                  (AL049481) putative host response protein [Arabidopsis
NCBI Description
                  thaliana]
                  22838
Seq. No.
                  101411 2.R1040
Contig ID
5'-most EST
                  wvk700680920.h1
Method
                  BLASTX
                  q4538994
NCBI GI
BLAST score
                  155
                  1.0e-10
E value
Match length
                  81
                  53
% identity
NCBI Description (ALO49481) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  22839
                  101419 1.R1040
Contig ID
5'-most EST
                  g4289978
Method
                  BLASTX
NCBI GI
                  g3128186
BLAST score
                  199
                  3.0e-15
E value
Match length
                  66
% identity
                  59
NCBI Description (AC004521) hypothetical protein [Arabidopsis thaliana]
```



```
jC-gmf102220063c08a1
5'-most EST
                  BLASTX
Method
                  q4185136
NCBI GI
                  610
BLAST score
                  2.0e-73
E value
                  212
Match length
% identity
                  (AC005724) putative trehalose-6-phosphate synthase
NCBI Description
                  [Arabidopsis thaliana]
                  22841
Seq. No.
                  101444 1.R1040
Contig ID
                  uC-gmropic061e09b1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q4164576
BLAST score
                  632
                   4.0e-66
E value
                  146
Match length
                   75
% identity
                   (AF098946) CTF2A [Arabidopsis thaliana]
NCBI Description
                   22842
Seq. No.
                   101458 1.R1040
Contig ID
                   uC-gmropic114d06b1
5'-most EST
                   BLASTX
Method
                   g4063751
NCBI GI
                   168
BLAST score
                   9.0e-12
E value
                   98
Match length
                   39
% identity
                   (AC005851) putative white protein [Arabidopsis thaliana]
NCBI Description
                   >gi 4510409 gb AAD21495.1 (AC006929) putative white
                   protein [Arabidopsis thaliana]
                   22843
Seq. No.
                   101468 1.R1040
Contig ID
                   ssr700555045.hl
5'-most EST
                   BLASTX
Method
                   q4432846
NCBI GI
BLAST score
                   266
                   3.0e-23
E value
                   88
Match length
                   56
% identity
                   (AC006283) unknown protein [Arabidopsis thaliana]
NCBI Description
                   22844
 Seq. No.
                   101511 1.R1040
 Contig ID
                   ssr700555102.hl
 5'-most EST
 Seq. No.
                   22845
                   101530 1.R1040
 Contig ID
                   uC-gmrominsoy214g11b1
 5'-most EST
                   BLASTX
 Method
                   g3212865
 NCBI GI
                   434
 BLAST score
```

4.0e-43

103

E value Match length



% identity 81

NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]

Seq. No. 22846

Contig ID 101530 2.R1040 5'-most EST zsg701127925.h1

Method BLASTX
NCBI GI g3212865
BLAST score 382
E value 3.0e-37
Match length 91
% identity 84

NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]

Seq. No. 22847

Contig ID 101533 1.R1040 5'-most EST txt700736163.h1

Method BLASTX
NCBI GI g4115949
BLAST score 340
E value 8.0e-32
Match length 139
% identity 53

NCBI Description (AF118223) contains similarity to adenosine deaminases

[Arabidopsis thaliana]

Seq. No. 22848

Contig ID 101533\_2.R1040 5'-most EST ncj700975674.h1

Method BLASTX
NCBI GI 94115949
BLAST score 283
E value 3.0e-25
Match length 116
% identity 55

NCBI Description (AF118223) contains similarity to adenosine deaminases

[Arabidopsis thaliana]

Seq. No. 22849

Contig ID 101533\_3.R1040 5'-most EST kl1701207914.h1

Method BLASTX
NCBI GI g4115949
BLAST score 170
E value 3.0e-12
Match length 47
% identity 68

NCBI Description (AF118223) contains similarity to adenosine deaminases

[Arabidopsis thaliana]

Seq. No. 22850

Contig ID 101536\_1.R1040

5'-most EST uC-gmflminsoy061d03b1

Seq. No. 22851

Contig ID 101564\_1.R1040 5'-most EST dpv701100905.h1



Method BLASTX
NCBI GI g4432857
BLAST score 402
E value 2.0e-39
Match length 159
% identity 51

NCBI Description (AC006300) hypothetical protein [Arabidopsis thaliana]

Seq. No. 22852

Contig ID 101566 1.R1040

5'-most EST uC-gmrominsoy205h04b1

Seq. No. 22853

Contig ID 101573\_1.R1040 5'-most EST ssr700555195.h1

Seq. No. 22854

Contig ID 101574\_1.R1040 5'-most EST ssr700555196.h1

Seq. No. 22855

Contig ID 101576\_1.R1040 5'-most EST rca701002105.h1

Seq. No. 22856

Contig ID 101577\_1.R1040 5'-most EST fua701041592.h1

Seq. No. 22857

Contig ID 101590\_1.R1040 5'-most EST vwf700676448.h1

Seq. No. 22858

Contig ID 101602 1.R1040 5'-most EST sat701004445.h1

Seq. No. 22859

Contig ID 101612\_1.R1040 5'-most EST pcp700995829.h1

Method BLASTX
NCBI GI g4467133
BLAST score 718
E value 9.0e-76
Match length 253
% identity 62

NCBI Description (AL035540) geranylgeranyl pyrophosphate synthase-related

protein [Arabidopsis thaliana]

Seq. No. 22860

Contig ID 101624 1.R1040 5'-most EST ssr700555263.h1

Seq. No. 22861

Contig ID 101643\_1.R1040 5'-most EST zsg701128864.h1

Seq. No. 22862



```
Contig ID 101650 1.R1040 5'-most EST ssr700555305.h1 Method BLASTX
```

NCBI GI g559713 BLAST score 260 E value 9.0e-23 Match length 109 % identity 48

NCBI Description (D38552) The half39 protein is related to cyclophilin.

[Homo sapiens]

Seq. No. 22863

Contig ID 101653\_1.R1040 5'-most EST pxt700943394.h1

Seq. No. 22864

Contig ID 101670 1.R1040 5'-most EST fC-gmle700555329a1

Method BLASTX
NCBI GI g3249064
BLAST score 597
E value 6.0e-62
Match length 170
% identity 62

NCBI Description (AC004473) Strong similarity to trehalose-6-phosphate

synthase homolog gb\_2245136 from A. thaliana chromosome 4

contig gb Z97344. [Arabidopsis thaliana]

Seq. No. 22865

Contig ID 101672 1.R1040 5'-most EST zzp700832814.h1

Method BLASTX
NCBI GI g3434967
BLAST score 250
E value 3.0e-21
Match length 115
% identity 50

NCBI Description (AB008103) ethylene responsive element binding factor 1

[Arabidopsis thaliana]

Seq. No. 22866

Contig ID 101703\_1.R1040 5'-most EST dpv701098407.h1

Method BLASTX
NCBI GI g3695019
BLAST score 639
E value 1.0e-66
Match length 235
% identity 54

NCBI Description (AF055848) subtilisin-like protease [Arabidopsis thaliana]

Seq. No. 22867

Contig ID 101712 1.R1040 5'-most EST ssr700555379.h1

Seq. No. 22868

Contig ID 101728\_1.R1040



```
5'-most EST
                  rlr700901828.hl
                  BLASTX
Method
                  g3522937
NCBI GI
BLAST score
                  432
                  2.0e-42
E value
Match length
                  141
% identity
                  57
NCBI Description (AC004411) unknown protein [Arabidopsis thaliana]
```

Seq. No.

22869 101730 1.R1040 ssr700555409.hl

Seq. No. Contig ID 5'-most EST

Contig ID 5'-most EST

> 22870 101736\_1.R1040 g5676989

Seq. No. Contig ID 5'-most EST 22871 101738 1.R1040 ssr700555421.h1

Seq. No. Contig ID 5'-most EST 22872 101756 1.R1040 ssr700555446.hl

Seq. No. Contig ID 5'-most EST 22873 101774\_1.R1040 ssr700555480.hl

Seq. No. Contig ID 5'-most EST 22874 101789 1.R1040 zhf700963011.hl

Seq. No. Contig ID 5'-most EST

101790 1.R1040 ssr700555508.hl

22875

22876

Seq. No. Contig ID

5'-most EST

101810 1.R1040 hrw701060224.h1

Seq. No. Contig ID 5'-most EST 22877 101811 1.R1040 ssr700555532.hl BLASTN

Method NCBI GI BLAST score E value

Match length

g429103 154 4.0e-81 426

% identity

84 NCBI Description L.esculentum S-adenosyl-L-methionine synthetase mRNA, complete CDS

Seq. No. Contig ID 5'-most EST

22878 101830 1.R1040 ssr70055556.hl

3641



Seq. No. 22879

Contig ID 101832\_1.R1040 5'-most EST ssr700555558.h1

Seq. No. 22880

Contig ID 101833\_1.R1040 5'-most EST fC-gmle700557608f3

Method BLASTX
NCBI GI g2388574
BLAST score 522
E value 3.0e-53
Match length 153
% identity 71

NCBI Description (AC000098) Strong similarity to Phalaenopsis homeobox

protein (gb\_U34743). [Arabidopsis thaliana]

Seq. No. 22881

Contig ID 101835\_1.R1040 5'-most EST kl1701212811.h1

Seq. No. 22882

Contig ID 101856\_1.R1040 5'-most EST ssr700555583.h1

Seq. No. 22883

Contig ID 101898\_1.R1040 5'-most EST fC-gmle700555559f3

Method BLASTX
NCBI GI g1743354
BLAST score 647
E value 7.0e-68
Match length 154
% identity 76

NCBI Description (Y09876) aldehyde dehydrogenase (NAD+) [Nicotiana tabacum]

Seq. No. 22884

Contig ID 101905 1.R1040 5'-most EST gsv701055021.h1

Method BLASTX
NCBI GI g3643599
BLAST score 502
E value 2.0e-51
Match length 135
% identity 76

NCBI Description (AC005395) putative trytophanyl-tRNA synthetase

[Arabidopsis thaliana]

Seq. No. 22885

Contig ID 101906 1.R1040 5'-most EST kmv700740740.h1

Seq. No. 22886

Contig ID 101907\_1.R1040 5'-most EST ssr700555643.h1

Seq. No. 22887

Contig ID 101914\_1.R1040

Contig ID 5'-most EST

Method

NCBI GI



```
5'-most EST
                  kl1701213362.h1
Seq. No.
                  22888
                  101939 1.R1040
Contig ID
                  ssr700555681.hl
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2316016
                  216
BLAST score
                  1.0e-17
E value
Match length
                  88
                  49
% identity
NCBI Description (U92650) MRP-like ABC transporter [Arabidopsis thaliana]
                  22889
Seq. No.
Contig ID
                  101957 1.R1040
5'-most EST
                  ssr700555706.h1
Seq. No.
                  22890
Contig ID
                  101958 1.R1040
5'-most EST
                  epx701105793.h1
Method
                  BLASTX
                  g1209756
NCBI GI
BLAST score
                  322
                  6.0e-30
E value
Match length
                  81
% identity
                  77
                  (U43629) integral membrane protein [Beta vulgaris]
NCBI Description
Seq. No.
                  22891
Contig ID
                  101974 1.R1040
5'-most EST
                  zsg701123674.h1
Method
                  BLASTX
NCBI GI
                  g4115949
BLAST score
                  319
E value
                  2.0e-29
                  82
Match length
                  66
% identity
                  (AF118223) contains similarity to adenosine deaminases
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  22892
Contig ID
                  101990 1.R1040
5'-most EST
                   zhf700962978.h1
Method
                  BLASTX
NCBI GI
                  q3402690
BLAST score
                  197
                  4.0e-15
E value
Match length
                  86
% identity
                  45
                  (AC004697) hypothetical protein, 3' partial [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  22893
```

3643

101992 1.R1040

BLASTX

g2632252

ssr700555753.h1



```
BLAST score 280
E value 5.0e-25
Match length 113
% identity 50
```

NCBI Description (Y12464) serine/threonine kinase [Sorghum bicolor]

Seq. No. 22894

Contig ID 102001\_1.R1040 5'-most EST ssr700555764.h1

Seq. No. 22895

Contig ID 102015\_1.R1040 5'-most EST uC-gmropic030h08b1

Seq. No. 22896

Contig ID 102015\_2.R1040 5'-most EST asn701137224.h1

Seq. No. 22897

Contig ID 102031\_1.R1040 5'-most EST ssr700555808.h1

Method BLASTX
NCBI GI g4335735
BLAST score 646
E value 2.0e-67
Match length 162
% identity 73

NCBI Description (AC006248) hypothetical protein [Arabidopsis thaliana]

Seq. No. 22898

Contig ID 102036 1.R1040 5'-most EST ssr700555958.h1

Method BLASTX
NCBI GI g4454032
BLAST score 177
E value 4.0e-13
Match length 61
% identity 48

NCBI Description (AL035394) putative protein [Arabidopsis thaliana]

Seq. No. 22899

Contig ID 102040 1.R1040 5'-most EST jC-gmfl02220115e11a1

Method BLASTX
NCBI GI g1091678
BLAST score 230
E value 6.0e-19
Match length 143
% identity 32

NCBI Description activator-like transposable element [Pennisetum glaucum]

Seq. No. 22900

Contig ID 102042 1.R1040 5'-most EST epx701103995.h1

Method BLASTX
NCBI GI g3779218
BLAST score 202

E value 7.0e-16 Match length 55 % identity 67

NCBI Description (AF030879) protein kinase CPK1 [Solanum tuberosum]

Seq. No. 22901

Contig ID 102042\_2.R1040 5'-most EST ssr700556174.h1

Seq. No. 22902

Contig ID 102044\_1.R1040 5'-most EST ssr700555824.h1

Seq. No. 22903

Contig ID 102046\_1.R1040 5'-most EST fC-gmle700555454f3

Method BLASTX
NCBI GI g2632252
BLAST score 445
E value 3.0e-44
Match length 118
% identity 69

NCBI Description (Y12464) serine/threonine kinase [Sorghum bicolor]

Seq. No. 22904

Contig ID 102051 1.R1040

5'-most EST uC-gmflminsoy022a10b1

Method BLASTX
NCBI GI g4038042
BLAST score 722
E value 1.0e-76
Match length 151
% identity 87

NCBI Description (AC005936) putative DNA-binding protein [Arabidopsis

thaliana]

Seq. No. 22905

Contig ID 102057 1.R1040 5'-most EST gsv701053516.h1

Method BLASTX
NCBI GI g4510377
BLAST score 395
E value 2.0e-38
Match length 98
% identity 74

NCBI Description (AC007017) putative RNA helicase A [Arabidopsis thaliana]

Seq. No. 22906

Contig ID 102059\_1.R1040 5'-most EST bth700849890.h1

Method BLASTX
NCBI GI 94314363
BLAST score 384
E value 4.0e-38
Match length 179
% identity 51

NCBI Description (AC006340) hypothetical protein [Arabidopsis thaliana]

BLAST score

E value Match length 547 3.0e-56

156



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22907
Seq. No.
                  102068 1.R1040
Contig ID
                  txt700733245.hl
5'-most EST
                  BLASTX
Method
                  g3298502
NCBI GI
BLAST score
                  243
E value
                  3.0e-26
Match length
                  117
                  54
% identity
NCBI Description (AB015046) xylulokinase [Homo sapiens]
Seq. No.
                  22908
                  102074 1.R1040
Contig ID
                  uC-gmflminsoy070g11b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4262239
BLAST score
                  455
E value
                  4.0e-59
Match length
                  182
% identity
                  70
                 (AC006200) putative membrane transporter [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  22909
Contig ID
                  102080 1.R1040
5'-most EST
                  trc700562033.h1
                  BLASTN
Method
NCBI GI
                  q3873174
BLAST score
                  46
E value
                  8.0e-17
Match length
                  190
% identity
                  81
                  Genomic sequence for Arabidopsis thaliana BAC F14N23,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
                  22910
Seq. No.
                  102084 1.R1040
Contig ID
5'-most EST
                  fC-gmle700553993f3
                  BLASTX
Method
NCBI GI
                  g1170949
BLAST score
                  495
E value
                  3.0e-50
Match length
                  123
% identity
                  76
NCBI Description SERINE/THREONINE-PROTEIN KINASE MHK >gi 481207 pir S38327
                  protein kinase - Arabidopsis thaliana >gi 166811 (L07249)
                  protein kinase [Arabidopsis thaliana]
                  22911
Seq. No.
Contig ID
                  102093 1.R1040
5'-most EST
                  uC-gmrominsoy100a12b1
Method
                  BLASTX
NCBI GI
                  q3033392
```



% identity 68

NCBI Description (AC004238) putative translation initiation factor EIF-2B-epsilon subunit [Arabidopsis thaliana]

Seq. No. 22912

Contig ID 102099 1.R1040 5'-most EST ssr700555910.h1

Method BLASTX
NCBI GI g3461813
BLAST score 557
E value 2.0e-57
Match length 118
% identity 86

NCBI Description (AC004138) putative sucrose/H+ symporter [Arabidopsis

thaliana]

Seq. No. 22913

Contig ID 102103\_1.R1040 5'-most EST eep700868603.h1

Seq. No. 22914

Contig ID 102122\_1.R1040 5'-most EST kl1701213942.h1

Seq. No. 22915

Contig ID 102140 1.R1040 5'-most EST cf1700863673.h1

Method BLASTX
NCBI GI g1170149
BLAST score 429
E value 2.0e-42
Match length 115
% identity 70

NCBI Description HEAT SHOCK PROTEIN 101 >gi 537446 (U13949) AtHSP101

[Arabidopsis thaliana]

Seq. No. 22916

Contig ID 102140\_2.R1040 5'-most EST epx701106438.h1

Method BLASTX
NCBI GI g530207
BLAST score 191
E value 1.0e-14
Match length 46
% identity 76

NCBI Description (L35272) heat shock protein [Glycine max]

Seq. No. 22917

Contig ID 102147\_1.R1040 5'-most EST ssr700555965.h1

Seq. No. 22918

Contig ID 102151 1.R1040

5'-most EST uC-qmflminsoy063a07b1

Method BLASTX
NCBI GI g3927831
BLAST score 262

```
2.0e-22
E value
Match length
                  244
                  33
% identity
                 (AC005727) similar to mouse ankyrin 3 [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  22919
                  102151 2.R1040
Contig ID
5'-most EST
                  sat701010695.hl
Seq. No.
                  22920
Contig ID
                  102166 1.R1040
5'-most EST
                  uxk700668328.h1
Method
                  BLASTX
NCBI GI
                  g3647335
BLAST score
                  144
E value
                  7.0e-09
Match length
                  68
% identity
                  43
                  (AL031644) possible zinc-finger protein
NCBI Description
                  [Schizosaccharomyces pombe]
                  22921
Seq. No.
Contig ID
                  102179 1.R1040
5'-most EST
                  jC-gmst02400076a04a1
Method
                  BLASTX
                  q3702328
NCBI GI
BLAST score
                  1285
E value
                  1.0e-142
Match length
                  301
% identity
                  76
NCBI Description (AC005397) putative cytochrome b5 [Arabidopsis thaliana]
                  22922
Seq. No.
Contig ID
                  102183 1.R1040
5'-most EST
                  uC-gmrominsoy263g03b1
Method
                  BLASTX
NCBI GI
                  g2117624
BLAST score
                  1310
E value
                  1.0e-145
Match length
                  297
% identity
                  84
                  peroxidase (EC 1.11.1.7) 2 - alfalfa
NCBI Description
                  >gi 971564 emb CAA62228 (X90695) peroxidase2 [Medicago
                  sativa]
                  22923
Seq. No.
Contig ID
                  102183 2.R1040
```

5'-most EST ssr700556025.h1

Method BLASTX
NCBI GI g2117624
BLAST score 503
E value 5.0e-51
Match length 108
% identity 87

NCBI Description peroxidase (EC 1.11.1.7) 2 - alfalfa

>gi\_971564\_emb\_CAA62228\_ (X90695) peroxidase2 [Medicago



## sativa]

```
Seq. No. 22924
Contig ID 102196_1.R1040
5'-most EST g5677764
```

Seq. No. 22925

Contig ID 102222 1.R1040

5'-most EST uC-gmrominsoy201e02b1

Seq. No. 22926

Contig ID 102230 1.R1040

5'-most EST uC-gmrominsoy258f02b1

Method BLASTX
NCBI GI g4559334
BLAST score 286
E value 2.0e-50
Match length 247
% identity 41

NCBI Description (AC007087) unknown protein [Arabidopsis thaliana]

Seq. No. 22927

Contig ID 102235 1.R1040

5'-most EST jC-gmst02400032b02a1

Method BLASTX
NCBI GI g3281870
BLAST score 414
E value 2.0e-40
Match length 209
% identity 45

NCBI Description (AL031004) putative protein [Arabidopsis thaliana]

Seq. No. 22928

Contig ID 102237\_1.R1040 5'-most EST rca700998914.h1

Seq. No. 22929

Contig ID 102237 2.R1040 5'-most EST ncj700981901.h1

Seq. No. 22930

Contig ID 102246 1.R1040 5'-most EST ssr700556104.h1

Method BLASTX
NCBI GI g3047104
BLAST score 554
E value 9.0e-57
Match length 157
% identity 68

NCBI Description (AF058919) No definition line found [Arabidopsis thaliana]

Seq. No. 22931

Contig ID 102248\_1.R1040 5'-most EST leu701151551.h1

Method BLASTN NCBI GI 9758249 BLAST score 217



E value 1.0e-118
Match length 432
% identity 88

NCBI Description P.vulgaris mRNA for plasma membrane H+ ATPase

Seq. No. 22932

Contig ID 102262\_1.R1040 5'-most EST epx701105447.h1

Method BLASTX
NCBI GI g3915165
BLAST score 189
E value 3.0e-14
Match length 48
% identity 75

NCBI Description TRYPTOPHAN SYNTHASE BETA CHAIN 2 PRECURSOR >gi\_2792520

(AF042320) tryptophan synthase beta subunit [Camptotheca acuminata] >gi 2801771 (AF042321) tryptophan synthase beta

[Camptotheca acuminata]

Seq. No. 22933

Contig ID 102271 1.R1040 5'-most EST gsv701047301.h1

Seq. No. 22934

Contig ID 102271\_2.R1040 5'-most EST fde700872361.h1

Seq. No. 22935

Contig ID 102289\_1.R1040 5'-most EST ssr700556150.h1

Seq. No. 22936

Contig ID 102317\_1.R1040

5'-most EST uC-gmrominsoy058h04b1

Method BLASTX
NCBI GI g2832643
BLAST score 224
E value 7.0e-19
Match length 67
% identity 79

NCBI Description (AL021710) hypothetical protein [Arabidopsis thaliana]

Seq. No. 22937

Contig ID 102317\_2.R1040 5'-most EST pcp700993050.h1

Seq. No. 22938

Contig ID 102330 1.R1040 5'-most EST ssr700556204.h1

Method BLASTX
NCBI GI g2979559
BLAST score 151
E value 5.0e-10
Match length 38
% identity 76

NCBI Description (AC003680) putative DNA binding protein [Arabidopsis

thaliana]



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Seg. No. 22939
```

Contig ID 102340\_1.R1040 5'-most EST rlr700901293.h1

Method BLASTX
NCBI GI g4432840
BLAST score 196
E value 1.0e-21
Match length 95
% identity 52

NCBI Description (AC006283) unknown protein [Arabidopsis thaliana]

Seq. No. 22940

Contig ID 102342 1.R1040 5'-most EST ssr700556248.h1

Seq. No. 22941

Contig ID 102343\_1.R1040 5'-most EST ssr700556753.h1

Method BLASTX
NCBI GI g2829870
BLAST score 406
E value 1.0e-39
Match length 85
% identity 87

NCBI Description (AC002396) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 22942

Contig ID 102345 1.R1040

5'-most EST jC-gmfl02220060h08a1

Method BLASTX
NCBI GI g4006896
BLAST score 231
E value 9.0e-28
Match length 174
% identity 42

NCBI Description (Z99708) SCARECROW-like protein [Arabidopsis thaliana]

Seq. No. 22943

Contig ID 102370\_1.R1040 5'-most EST zhf700961010.h1

Method BLASTX
NCBI GI g2501102
BLAST score 153
E value 3.0e-10
Match length 74
% identity 54

NCBI Description SYNTAXIN-RELATED PROTEIN KNOLLE >gi\_1184165 (U39451) syntaxin-related [Arabidopsis thaliana] >gi\_1184167 (U39452) syntaxin-related [Arabidopsis thaliana]

>gi\_3063443 (AC003981) F22013.4 [Arabidopsis thaliana]
>gi\_1587182 prf 2206310A syntaxin-related protein

[Arabidopsis thaliana]

Seq. No. 22944

Contig ID 102377 1.R1040 5'-most EST zhf700955678.h1



```
22945
Seq. No.
                  102382 1.R1040
Contig ID
5'-most EST
                  taw700655373.hl
                  22946
Seq. No.
Contig ID
                  102391 1.R1040
5'-most EST
                  ssr700556296.hl
                  BLASTN
Method
NCBI GI
                  g2827644
BLAST score
                  55
                   4.0e-22
E value
Match length
                  55
                  100
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F18F4
                   (ESSAII project)
                  22947
Seq. No.
                  102410 1.R1040
Contig ID
                  ssr700556332.hl
5'-most EST
                  22948
Seq. No.
Contig ID
                  102418_1.R1040
5'-most EST
                  jC-gmro02910021c07d1
Seq. No.
                   22949
                   102420 1.R1040
Contig ID
5'-most EST
                   kmv700742404.hl
Method
                  BLASTX
```

Method BLASTX

NCBI GI g4105180

BLAST score 314

E value 8.0e-29

Match length 137

% identity 51

NCBI Description (AF043905) plastoglobule associated protein PG1 precursor [Pisum sativum]

 Seq. No.
 22950

 Contig ID
 102423\_1.R1040

 5'-most EST
 jC-gmfl02220062h12a1

 Method
 BLASTX

 NCBI GI
 g4432822

 BLAST score
 206

 E value
 4.0e-16

Match length 91 % identity 43

NCBI Description (AC006593) hypothetical protein [Arabidopsis thaliana]

22951 Seq. No. 102440\_1.R1040 Contig ID 5'-most EST leu701155347.hl BLASTX Method NCBI GI g2897875 BLAST score 264 E value 4.0e-23 Match length 123 % identity 46



NCBI Description (U90274) histone acetyltransferase HAT B [Zea mays]

Seq. No.

22952

Contig ID

102443 1.R1040

5'-most EST

uC-gmrominsoy232b05b1

Seq. No.

22953

Contig ID

102443 2.R1040

5'-most EST

uC-gmrominsoy109c09b1

Method NCBI GI BLASTX q1769901

BLAST score E value

762 5.0e-81

Match length

205 69

% identity

NCBI Description

(X95737) proline transporter 1 [Arabidopsis thaliana]

>gi 2088642 (AF002109) proline transporter 1 [Arabidopsis

thaliana]

Seq. No.

22954

Contig ID 5'-most EST 102450 1.R1040  $ssr700\overline{5}59373.h1$ 

Seq. No.

22955

Contig ID

102462 1.R1040

5'-most EST

`jC-gmst02400046e03a1

Seq. No.

22956

Contig ID

102475 1.R1040

5'-most EST

ssr700556429.h1

Seq. No.

22957

Contig ID

102479 1.R1040

5'-most EST Method

uC-gmropic018b08b1 BLASTX

NCBI GI

g3402718

BLAST score

148

E value

2.0e-09

Match length

48

% identity

56 NCBI Description (AC004261) hypothetical protein [Arabidopsis thaliana]

Seq. No.

22958

Contig ID 5'-most EST 102489 1.R1040 ncj700984172.h1

Method

BLASTX

NCBI GI

g2760326

BLAST score

172

E value

4.0e-12

Match length

125

% identity NCBI Description (AC002130) F1N21.11 [Arabidopsis thaliana]

35

Seq. No.

22959

Contig ID

102489 2.R1040

5'-most EST

dpv701102036.h1



```
22960
Seq. No.
Contig ID
                  102501 1.R1040
                  g5509120
5'-most EST
Method
                  BLASTX
NCBI GI
                  g4406792
BLAST score
                  221
E value
                  2.0e-17
Match length
                  167
% identity
                  29
                  (AC006304) putative reverse transcriptase [Arabidopsis
NCBI Description
                  thaliana]
                  22961
Seq. No.
Contig ID
                  102508 1.R1040
5'-most EST
                  ssr700556474.h1
Method
                  BLASTX
                  g3252794
NCBI GI
BLAST score
                  628
E value
                  9.0e-66
Match length
                  131
% identity
                  84
                  (AB015615) isoamylase [Oryza sativa]
NCBI Description
                  22962
Seq. No.
Contig ID
                  102517_1.R1040
5'-most EST
                  wvk700683794.h1
                  22963
Seq. No.
Contig ID
                  102529 1.R1040
5'-most EST
                  hyd700731231.h1
Method
                  BLASTX
                  g2104536
NCBI GI
BLAST score
                  548
E value
                  3.0e-56
Match length
                  155
                  70
% identity
                   (AF001308) predicted glycosyl transferase [Arabidopsis
NCBI Description
                  thaliana]
                  22964
Seq. No.
Contig ID
                  102540 1.R1040
                   awf700842594.hl
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4115916
BLAST score
                  169
E value
                   1.0e-11
Match length
                  117
% identity
                   42
                  (AF118222) F3H7.9 gene product [Arabidopsis thaliana]
NCBI Description
                  >gi 4539441 emb CAB40029.1 (AL049523) putative protein
                   [Arabidopsis thaliana]
```

Contig ID 102573 1.R1040 5'-most EST fC-gmse700675569f2

Method BLASTX NCBI GI g1497987



BLAST score 838
E value 4.0e-90
Match length 193
% identity 87

NCBI Description (U62798) SCARECROW [Arabidopsis thaliana]

Seq. No. 22966

Contig ID 102575\_1.R1040 5'-most EST gsv701055350.h1

Method BLASTX
NCBI GI g4415912
BLAST score 256
E value 7.0e-22
Match length 104
% identity 51

NCBI Description (AC006282) putative protease [Arabidopsis thaliana]

Seq. No. 22967

Contig ID 102595\_1.R1040 5'-most EST jsh701068284.h1

Method BLASTX
NCBI GI 94006877
BLAST score 469
E value 6.0e-70
Match length 215
% identity 32

NCBI Description (299707) RNA-binding like protein [Arabidopsis thaliana]

Seq. No. 22968

Contig ID 102601\_1.R1040 5'-most EST fde700873188.h1

Method BLASTX
NCBI GI g3413699
BLAST score 636
E value 3.0e-66
Match length 203
% identity 59

NCBI Description (AC004747) putative heat shock protein [Arabidopsis

thaliana]

Seq. No. 22969

Contig ID 102605\_1.R1040 5'-most EST ssr700556619.h1

Seq. No. 22970

Contig ID 102606\_1.R1040 5'-most EST ssr700556622.h1

Method BLASTX
NCBI GI g1946300
BLAST score 280
E value 8.0e-25
Match length 78
% identity 67

NCBI Description (Y12529) hypothetical protein [Silene latifolia]

Seq. No. 22971

Contig ID 102611\_1.R1040



```
ssr700556630.h1
5'-most EST
                  BLASTX
Method
                  g1685003
NCBI GI
BLAST score
                  148
E value
                  2.0e-09
Match length
                  76
% identity
                  49
                  (U32643) immediate-early salicylate-induced
NCBI Description
                  glucosyltransferase [Nicotiana tabacum]
Seq. No.
                  22972
                  102622 1.R1040
Contig ID
5'-most EST
                  fde700874961.hl
Method
                  BLASTX
NCBI GI
                  g2739360
BLAST score
                  167
E value
                  5.0e-19
Match length
                  104
% identity
                  (AC002505) unknown protein [Arabidopsis thaliana]
NCBI Description
                  >gi 3075385 (AC004484) unknown protein [Arabidopsis
                  thaliana]
Seq. No.
                  22973
Contig ID
                  102622 2.R1040
5'-most EST
                  jC-gmst02400073b09a1
                  BLASTX
Method
                  a2739360
NCBI GI
BLAST score
                  449
E value
                  2.0e-44
Match length
                  195
% identity
                  51
NCBI Description
                  (AC002505) unknown protein [Arabidopsis thaliana]
                  >gi 3075385 (AC004484) unknown protein [Arabidopsis
                  thaliana]
Seq. No.
                  22974
Contig ID
                  102637 1.R1040
5'-most EST
                  epx701110161.h1
Seq. No.
                  22975
Contig ID
                  102659 1.R1040
5'-most EST
                  ssr700556686.h1
                  22976
Seq. No.
                  102668 1.R1040
Contig ID
5'-most EST
                  ssr700556696.h1
                  BLASTX
Method
                  g4454050
NCBI GI
BLAST score
                  146
```

E value 5.0e-09 Match length 119 % identity 43

NCBI Description (AL035394) putative protein [Arabidopsis thaliana]

22977 Seq. No.

102675 1.R1040 Contig ID



```
5'-most EST
                   ssr700556708.h1
Seq. No.
                  22978
                  102676 1.R1040
Contig ID
5'-most EST
                  jC-gmle01810091g03a1
Seq. No.
                  22979
                  102690 1.R1040
Contig ID
5'-most EST
                  ssr700556724.h1
Seq. No.
                  22980
Contig ID
                  102692 1.R1040
5'-most EST
                  ssr700556826.h1
Method
                  BLASTX
NCBI GI
                  g2959781
BLAST score
                  587
                  2.0e-60
E value
                  225
Match length
% identity
                  51
NCBI Description (AJ223508) Zwille protein [Arabidopsis thaliana]
                  22981
Seq. No.
                  102703 1.R1040
Contig ID
5'-most EST
                  zhf700958249.h1
Method
                  BLASTX
                  q2809259
NCBI GI
BLAST score
                  299
E value
                  3.0e-27
Match length
                   68
                  79
% identity
NCBI Description (AC002560) F21B7.28 [Arabidopsis thaliana]
Seq. No.
                  22982
                  102723 1.R1040
Contig ID
5'-most EST
                  uC-gmflminsoy119g10b1
                   22983
Seq. No.
Contig ID
                  102723 2.R1040
5'-most EST
                  uC-gmropic104h06b1
Seq. No.
                  22984
Contig ID
                  102726 1.R1040
5'-most EST
                  ssr700556767.h1
Seq. No.
                  22985
                  102733_1.R1040
Contig ID
5'-most EST
                  ssr700556775.h1
Method
                  BLASTN
NCBI GI
                  g3695060
BLAST score
                  123
E value
                  1.0e-62
Match length
                  279
% identity
NCBI Description Lotus japonicus rac GTPase activating protein 2 mRNA,
```

partial cds

22986



Contig ID 102734\_1.R1040 5'-most EST ssr700556776.h1

Method BLASTX
NCBI GI g3287270
BLAST score 902
E value 1.0e-97
Match length 192
% identity 88

NCBI Description (Y09533) involved in starch metabalism [Solanum tuberosum]

Seq. No. 22987

Contig ID 102737\_1.R1040 5'-most EST wvk700681775.h1

Method BLASTX
NCBI GI g2342723
BLAST score 185
E value 4.0e-13
Match length 210
% identity 30

NCBI Description (AC002341) unknown protein [Arabidopsis thaliana]

Seq. No. 22988

Contig ID 102754\_1.R1040 5'-most EST jC-gmf102220060d12a1

Seq. No. 22989

Contig ID 102754\_2.R1040 5'-most EST ssr700556808.h1

Seq. No. 22990

Contig ID 102764 1.R1040 5'-most EST wvk700682142.h1

Method BLASTX
NCBI GI g4567273
BLAST score 224
E value 1.0e-18
Match length 48
% identity 83

NCBI Description (AC006841) putative vacuolar proton ATPase subunit

[Arabidopsis thaliana]

Seq. No. 22991

Contig ID 102767\_1.R1040 5'-most EST zsg701120323.h1

Seq. No. 22992

Contig ID 102787\_1.R1040 5'-most EST ssr700556845.h1

Seq. No. 22993

Contig ID 102802\_1.R1040 5'-most EST ssr700556862.h1

Seq. No. 22994

Contig ID 102810 1.R1040

5'-most EST uC-gmrominsoy106d04b1



22995

102810 2.R1040 Contig ID 5'-most EST uC-gmropic072g10b1

Seq. No.

22996

Contig ID 5'-most EST 102822 1.R1040 epx701105463.h1

Seq. No.

22997

Contig ID 5'-most EST 102836 1.R1040 sat701008295.hl

Method BLASTX NCBI GI g3860246 BLAST score 152 E value 1.0e-09 93

Match length % identity

NCBI Description

(AC005824) putative reverse-transcriptase protein [Arabidopsis thaliana] >gi 4510429 gb AAD21515.1

(AC006929) putative reverse transcriptase [Arabidopsis

thaliana]

Seq. No.

22998

43

Contig ID

102843 1.R1040

5'-most EST

uC-gmrominsoy117g03b1

Seq. No.

22999

Contig ID

102853 1.R1040

5'-most EST

jC-qmro02910061h08a1

Method BLASTX NCBI GI g3024362 BLAST score 328 E value 2.0e-30 83 Match length

% identity

NCBI Description

PHENYLALANINE AMMONIA-LYASE G2B >gi 2118317 pir S60042 phenylalanine ammonia-lyase (EC 4.3.1.5) 2b - Japanese

aspen x large-toothed aspen >gi 1109641 dbj BAA07860 (D43802) phenylalanine ammonia-lyase [Populus

kitakamiensis]

Seq. No.

23000

77

Contig ID 5'-most EST 102858 1.R1040 ssr700556933.h1

Method BLASTX NCBI GI q4508079 BLAST score 275 E value 1.0e-24

Match length 95 % identity 59

NCBI Description (AC005882) 66284 [Arabidopsis thaliana]

Seq. No.

23001

Contig ID 5'-most EST 102863 1.R1040 zhf700964602.h1

Method NCBI GI BLASTX g2760328



BLAST score E value 3.0e-09 59 Match length 49 % identity

NCBI Description (AC002130) F1N21.13 [Arabidopsis thaliana]

Seq. No. Contig ID 5'-most EST 23002 102875 1.R1040 jsh701064919.hl

Seq. No. Contig ID 23003 102878 1.R1040 ssr700556960.hl

5'-most EST Seq. No.

23004

Contig ID 5'-most EST

102884 1.R1040 uC-gmropic103h08b1

Seq. No.

23005

Contig ID 5'-most EST 102889 1.R1040 hrw701058004.h1

BLASTX Method g3776007 NCBI GI BLAST score 433 E value 1.0e-42 Match length 133 % identity 65

(AJ010467) RNA helicase [Arabidopsis thaliana] NCBI Description

Seq. No.

23006

Contig ID 5'-most EST 102906 1.R1040  $nsy700\overline{6}45638.h1$ 

Method BLASTX NCBI GI g2498291 BLAST score 195 E value 2.0e-20 172 Match length 43 % identity

NCBI Description DIHYDRODIPICOLINATE REDUCTASE >gi\_1651716 dbj BAA16644 (D90899) dihydrodipicolinate reductase [Synechocystis sp.]

Seq. No.

23007

Contig ID 5'-most EST 102913 1.R1040 ssr700557011.hl

Seq. No.

23008

Contig ID 5'-most EST 102925 1.R1040 ssr700557023.hl

Method BLASTX g3850583 NCBI GI BLAST score 653 2.0e-68 E value Match length 216 % identity 62

NCBI Description

(AC005278) Contains similarity to transcription initiation factor IIE, alpha subunit gb X63468 from Homo sapiens.

[Arabidopsis thaliana]



```
23009
Seq. No.
                  102926 1.R1040
Contig ID
                  kl1701209474.hl
5'-most EST
                  23010
Seq. No.
                  102932 1.R1040
Contig ID
                  kmv700742463.h1
5'-most EST
                  BLASTX
Method
                  g2129538
NCBI GI
                   344
BLAST score
                   2.0e-32
E value
Match length
                  72
                   90
% identity
                  AT103 protein - Arabidopsis thaliana >gi_1033195 (U38232)
NCBI Description
                  AT103 [Arabidopsis thaliana]
                   23011
Seq. No.
                   102948 1.R1040
Contig ID
                   pcp700994532.h2
5'-most EST
                   BLASTX
Method
                   g4115534
NCBI GI
                   202
BLAST score
                   4.0e-16
E value
                   80
Match length
                   45
% identity
                   (AB012114) UDP-glycose:flavonoid glycosyltransferase [Vigna
NCBI Description
                   mungo]
                   23012
Seq. No.
                   102959 1.R1040
Contig ID
                   ssr700559059.hl
5'-most EST
                   23013
Seq. No.
                   102969 1.R1040
Contig ID
                   ssr700557078.h1
5'-most EST
                   BLASTX
Method
                   q2145356
NCBI GI
                   461
BLAST score
                   3.0e-46
E value
                   124
Match length
                   78
 % identity
                   (Y11122) HD-Zip protein [Arabidopsis thaliana] >gi_3132474
 NCBI Description
                    (AC003096) homeobox protein, ATHB-14 [Arabidopsis thaliana]
                   23014
 Seq. No.
                   102982 1.R1040
 Contig ID
                   ssr700559040.h1
 5'-most EST
                   BLASTX
 Method
                   q4455334
 NCBI GI
 BLAST score
                    147
                    1.0e-09
 E value
                    50
 Match length
 % identity
                    80
                   (AL035525) myosin-like protein [Arabidopsis thaliana]
```

NCBI Description

3661



```
102998 1.R1040
Contig ID
                   zzp700830806.hl
5'-most EST
                   BLASTX
Method
                   g3269292
NCBI GI
                   179
BLAST score
                   4.0e-13
E value
                   71
Match length
                   48
% identity
                  (AL030978) putative protein [Arabidopsis thaliana]
NCBI Description
                   23016
Seq. No.
                   102998 2.R1040
Contig ID
                   pcp700993015.hl
5'-most EST
                   23017
Seq. No.
                   103004 1.R1040
Contig ID
                   uC-gmropic068f04b1
5'-most EST
                   23018
Seq. No.
                   103005 1.R1040
Contig ID
                   ssr700557140.hl
5'-most EST
                   23019
Seq. No.
                   103012 1.R1040
Contig ID
                   ssr700\overline{5}57163.h1
5'-most EST
                   23020
Seq. No.
                   103038 1.R1040
Contig ID
                   uC-gmropic110h02b1
5'-most EST
                   23021
Seq. No.
                   103040 1.R1040
Contig ID
                   leu701154094.h1
5'-most EST
                   23022
Seq. No.
                   103045 1.R1040
Contig ID
                    fC-qmle700555604f3
 5'-most EST
                    BLASTX
Method
                    q2465923
NCBI GI
                    221
BLAST score
                    1.0e-17
 E value
                    199
 Match length
                    28
 % identity
                   (AF024648) receptor-like serine/threonine kinase
 NCBI Description
                    [Arabidopsis thaliana]
                    23023
 Seq. No.
                    103050 1.R1040
 Contig ID
                    wrq700785984.h2
 5'-most EST
```

Seq. No. 23024 Contig ID 103055\_1.R1040

5'-most EST dpv701102717.h1
Method BLASTX
NCBI GI g4580523
BLAST score 769

E value

7.0e-82

3662



Match length 233 % identity 64

NCBI Description (AF036305) scarecrow-like 8 [Arabidopsis thaliana]

Seq. No. 23025

Contig ID 103062\_1.R1040 5'-most EST zzp700830240.h1

Seq. No. 23026

Contig ID 103071 1.R1040

5'-most EST uC-gmflminsoy074d08b1

Method BLASTX
NCBI GI g417328
BLAST score 209
E value 2.0e-16
Match length 143
% identity 33

NCBI Description UDP-N-ACETYLMURAMOYLALANYL-D-GLUTAMATE--2,

6-DIAMINOPIMELATE LIGASE (UDP-N-ACETYLMURAMYL-TRIPEPTIDE

SYNTHETASE) >gi 477729 pir B47691

UDP-N-acetylmuramoylalanyl-D-glutamate--2,

6-diaminopimelate ligase (EC 6.3.2.13) - Bacillus subtilis >gi\_40162\_emb\_CAA78767\_ (Z15056) murE [Bacillus subtilis]

 $>gi_2633889_{emb}_{CAB13391}_{C$ 

UDP-N-acetylmuramoylananine-D-glutamate-2,6diaminopimelate ligase [Bacillus subtilis]

Seq. No. 23027

Contig ID 103076\_1.R1040 5'-most EST uC-gmropic075g02b1

Seq. No. 23028

Contig ID 103082\_1.R1040 5'-most EST ssr700557290.h1

Method BLASTX
NCBI GI g3273196
BLAST score 149
E value 5.0e-12
Match length 58
% identity 64

NCBI Description (AB010915) responce regulator1 [Arabidopsis thaliana] >gi\_3323583 (AF057282) two-component response regulator homolog [Arabidopsis thaliana] >gi\_3953597\_dbj\_BAA34726\_

(AB008487) response regulator 4 [Arabidopsis thaliana]

Seq. No. 23029

Contig ID 103108\_1.R1040 5'-most EST fC-gmse700756809c1

Seq. No. 23030

Contig ID 103147\_1.R1040 5'-most EST hrw701062557.h1

Method BLASTX
NCBI GI g3831451
BLAST score 438
E value 1.0e-43
Match length 121



% identity

NCBI Description (AC005700) putative O-GlcNAc transferase [Arabidopsis thaliana]

Seq. No.

23031

Contig ID 5'-most EST 103158 1.R1040 ssr700557417.h1

Method NCBI GI BLASTX g1220453

BLAST score E value

414 1.0e-40

Match length % identity

125 54

NCBI Description (M79328) alpha-amylase [Solanum tuberosum]

Seq. No.

23032

Contig ID 5'-most EST 103170 1.R1040 sat701008540.h1

Method NCBI GI BLASTX g1362086 496

BLAST score E value Match length % identity

2.0e-50 122

76

NCBI Description 5-methyltetrahydropteroyltriglutamate--homocysteine

S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle

>gi\_2129919\_pir\_\_\$65957

5-methyltetrahydropteroyltriglutamate--homocysteine

S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi\_886471\_emb\_CAA58474\_ (X83499) methionine synthase

[Catharanthus roseus]

Seq. No.

23033

Contig ID 5'-most EST 103177 1.R1040 ssr700557439.h1

Method BLASTX NCBI GI q4539291 BLAST score 291 2.0e-26 E value

Match length % identity

NCBI Description (AL049480) putative protein [Arabidopsis thaliana]

Seq. No.

23034

105

52

Contig ID 5'-most EST 103193 1.R1040 pcp700990872.h1

Seq. No.

23035

Contig ID 5'-most EST 103196\_1.R1040 gsv701049095.hl

Seq. No.

23036

Contig ID

103203 1.R1040

5'-most EST

jC-gmf102220077e12a1

Seq. No.

23037

Contig ID

103204 1.R1040



5'-most EST ssr700557485.h1
Method BLASTX
NCBI GI g3184283
BLAST score 561
E value 6.0e-58
Match length 127
% identity 87

NCBI Description (AC004136) putative TBP-binding protein [Arabidopsis

thaliana]

Seq. No. 23038

Contig ID 103219\_1.R1040 5'-most EST fC-gmse700751156a2

Seq. No. 23039

Contig ID 103226\_1.R1040 5'-most EST ssr700557528.h1

Seq. No. 23040

Contig ID 103238\_1.R1040 5'-most EST wrg700786187.h2

Method BLASTN
NCBI GI g1052959
BLAST score 271
E value 1.0e-150
Match length 575
% identity 87

NCBI Description Ipomoea nil PNIL34 mRNA, complete cds

Seq. No. 23041

Contig ID 103247\_1.R1040 5'-most EST uC-gmronoir056h03b1

Method BLASTX
NCBI GI g4559380
BLAST score 1218
E value 1.0e-134
Match length 339
% identity 66

NCBI Description (AC006526) putative auxin-responsive GH3 protein

[Arabidopsis thaliana]

Seq. No. 23042

Contig ID 103250\_1.R1040 5'-most EST hyd700726225.h1

Method BLASTX
NCBI GI g2062164
BLAST score 315
E value 8.0e-29
Match length 110
% identity 29

NCBI Description (AC001645) jasmonate inducible protein isolog [Arabidopsis

thaliana]

Seq. No. 23043

Contig ID 103251\_1.R1040 5'-most EST fC-gmle700557575f2

Method BLASTX



NCBI GI g3056594
BLAST score 249
E value 2.0e-21
Match length 93
% identity 52

NCBI Description (AC004255) T1F9.15 [Arabidopsis thaliana]

Seq. No. 23044

Contig ID 103268\_1.R1040 5'-most EST jex700905675.h1

Seq. No. 23045

Contig ID 103279 1.R1040 5'-most EST seb700653059.h1

Method BLASTX
NCBI GI g3264757
BLAST score 365
E value 1.0e-34
Match length 137
% identity 61

NCBI Description (AF071888) zeaxanthin epoxidase [Prunus armeniaca]

Seq. No. 23046

Contig ID 103280\_1.R1040 5'-most EST uC-gmropic091b07b1

Method BLASTX
NCBI GI g3335336
BLAST score 170
E value 6.0e-12
Match length 42
% identity 79

NCBI Description (AC004512) Contains similarity to DnaJ gene YM8520.10 gb\_825566 from from S. cerevisiae cosmid gb\_Z49705. ESTs gb Z47720 and gb Z29879 come from this gene. [Arabidopsis

thaliana]

Seq. No. 23047

Contig ID 103291\_1.R1040 5'-most EST fC-gmle700557642f2

Method BLASTX
NCBI GI g4126403
BLAST score 180
E value 6.0e-17
Match length 92
% identity 51

NCBI Description (AB011796) flavonol synthase [Citrus unshiu]

Seq. No. 23048

Contig ID 103293\_1.R1040 5'-most EST asn701132075.h1

Method BLASTX
NCBI GI g4490310
BLAST score 346
E value 2.0e-32
Match length 175
% identity 42

NCBI Description (AL035678) somatic embryogenesis receptor-like kinase-like



## protein [Arabidopsis thaliana]

Seq. No. 23049 Contig ID 103300\_1.R1040 5'-most EST vwf700674658.h1

Seq. No. 23050

Contig ID 103302\_1.R1040 5'-most EST jex700908878.h1

Method BLASTX
NCBI GI g1742187
BLAST score 221
E value 1.0e-17
Match length 177
% identity 31

NCBI Description (D90771) ORF\_ID:o260#14; similar to [SwissProt Accession Number P11666] [Escherichia coli] >gi\_1742198\_dbj\_BAA14933\_ (D90772) ORF\_ID:o260#14; similar to [SwissProt Accession Number P11666] [Escherichia coli] >gi\_1787591 (AE000231)

orf, hypothetical protein [Escherichia coli]

Seq. No. 23051

Contig ID 103302\_2.R1040 5'-most EST fde700874255.h1

Seq. No. 23052

Contig ID 103314\_1.R1040 5'-most EST jex700908459.h1

Seq. No. 23053

Contig ID 103317\_1.R1040 5'-most EST ssr700557682.h1

Method BLASTX
NCBI GI g3426261
BLAST score 228
E value 4.0e-19
Match length 87

Match length 87 % identity 51

NCBI Description (U81378) disease resistance gene homolog Mi-copy1

[Lycopersicon esculentum]

Seq. No. 23054

Contig ID 103322\_1.R1040 5'-most EST ssr700557695.h1

Method BLASTX
NCBI GI g2832629
BLAST score 159
E value 6.0e-11
Match length 54
% identity 57

NCBI Description (AL021711) 4-coumarate-CoA ligase - like [Arabidopsis

thaliana]

Seq. No. 23055

Contig ID 103323 1.R1040 5'-most EST ssr700557701.h1



```
Seq. No.
                   23056
                   103328 1.R1040
Contig ID
5'-most EST
                   uC-qmrominsoy103c06b1
                   23057
Seq. No.
                  103338 1.R1040
Contig ID
5'-most EST
                  ssr700557720.h1
                   23058
Seq. No.
                  103338 2.R1040
Contig ID
5'-most EST
                   fC-gmro700843914f1
Method
                  BLASTX
NCBI GI
                   g4415932
BLAST score
                   164
                   4.0e-11
E value
Match length
                   122
% identity
NCBI Description (AC006418) unknown protein [Arabidopsis thaliana]
Seq. No.
                   23059
Contig ID
                  103343 1.R1040
5'-most EST
                  k11701\overline{2}02679.h1
                   23060
Seq. No.
Contig ID
                   103345 1.R1040
5'-most EST
                   g5058369
                   BLASTX
Method
NCBI GI
                   g3702342
BLAST score
                   178
E value
                   9.0e-13
Match length
                   70
% identity
                   44
NCBI Description (AC005397) hypothetical protein [Arabidopsis thaliana]
                   23061
Seq. No.
                  103368_1.R1040
Contig ID
                  zhf700956128.h1
5'-most EST
                   BLASTX
Method
                   g452593
NCBI GI
BLAST score
                   147
E value
                   3.0e-09
Match length
                   40
% identity
NCBI Description (D21814) ORF [Lilium longiflorum]
                   23062
Seq. No.
                   103374 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810062e12a1
Method
                   BLASTX
                   g404688
NCBI GI
BLAST score
                   194
E value
                   5.0e-15
Match length
                   58
% identity
                   59
NCBI Description (L19074) cytochrome P450 [Catharanthus roseus]
```

23063

Seq. No.

3668



Contig ID 103377\_1.R1040 5'-most EST zhf700962872.h1

Method BLASTX
NCBI GI g3360291
BLAST score 365
E value 1.0e-34
Match length 136
% identity 38

NCBI Description (AF023165) leucine-rich repeat transmembrane protein kinase

2 [Zea mays]

Seq. No. 23064

Contig ID 103379\_1.R1040 5'-most EST ssr700557772.h1

Seq. No. 23065

Contig ID 103386\_1.R1040 5'-most EST ssr700557779.h1

Method BLASTN
NCBI GI g4324494
BLAST score 159
E value 3.0e-84
Match length 270
% identity 91

NCBI Description Glycine max glutamyl-tRNA reductase precursor (gtr1) gene,

complete cds

Seq. No. 23066

Contig ID 103387\_1.R1040 5'-most EST leu701147117.h1

Method BLASTX
NCBI GI g3242702
BLAST score 184
E value 1.0e-13
Match length 47
% identity 68

NCBI Description (AC003040) hypothetical protein [Arabidopsis thaliana]

Seq. No. 23067

Contig ID 103387 2.R1040 5'-most EST jsh701069182.h1

Method BLASTX
NCBI GI g3242702
BLAST score 161
E value 3.0e-11
Match length 55
% identity 58

NCBI Description (AC003040) hypothetical protein [Arabidopsis thaliana]

Seq. No. 23068

Contig ID 103399 1.R1040 5'-most EST ssr700557802.h1

Seq. No. 23069

Contig ID 103402\_1.R1040 5'-most EST epx701109505.h1

Method BLASTX



g2623246 NCBI GI BLAST score 213 E value 4.0e-17 93 Match length 56 % identity

NCBI Description (AF030709) poly(A) polymerase [Pisum sativum]

23070 Seq. No.

103406 1.R1040 Contig ID 5'-most EST ssr700557816.hl

23071 Seq. No.

103410 1.R1040 Contig ID ssr700557821.h1 5'-most EST

Method BLASTX NCBI GI q2160756 BLAST score 602 2.0e-62 E value Match length 149 % identity 78

NCBI Description (U96879) CLV1 receptor kinase [Arabidopsis thaliana]

23072 Seq. No.

Contig ID 103416\_1.R1040

5'-most EST jC-gmle01810009c09a1

Method BLASTX q3582333 NCBI GI BLAST score 406 E value 3.0e-39 273 Match length % identity 32

NCBI Description (AC005496) hypothetical protein [Arabidopsis thaliana]

23073 Seq. No.

103421 1.R1040 Contig ID 5'-most EST fC-gmle700557833f2

BLASTX Method NCBI GI q3928862 BLAST score 151 E value 8.0e-10 Match length 139 % identity

NCBI Description (AF089710) disease resistance protein RPP8 [Arabidopsis

thaliana]

23074 Seq. No.

103427 1.R1040 Contig ID

5'-most EST  $jC-gmf\overline{1}02220070g12a1$ 

Seq. No. 23075

103429 1.R1040 Contig ID ssr700557846.h1 5'-most EST

Seq. No. 23076

103431 1.R1040 Contig ID 5'-most EST gsv701048816.h1

Method BLASTX

% identity

NCBI Description

thaliana]



```
NCBI GI
                   q4558591
BLAST score
                   407
E value
                   1.0e-39
                  142
Match length
                   59
% identity
NCBI Description
                  (AC006555) putative beta-1,3-glucanase [Arabidopsis
                  thaliana]
                  23077
Seq. No.
Contig ID
                  103431 2.R1040
5'-most EST
                  zhf700957726.h1
                  BLASTX
Method
NCBI GI
                  q4558591
BLAST score
                  222
E value
                   3.0e-18
Match length
                   54
                   80
% identity
                  (AC006555) putative beta-1,3-glucanase [Arabidopsis
NCBI Description
                   thaliana]
                   23078
Seq. No.
                   103433 1.R1040
Contig ID
5'-most EST
                   leu701153077.h1
Method
                  BLASTX
NCBI GI
                   g498038
BLAST score
                   581
                   4.0e-60
E value
                   166
Match length
% identity
NCBI Description (L33792) lipid transfer protein [Senecio odorus]
                   23079
Seq. No.
                   103462 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810040a08a1
Method
                   BLASTX
NCBI GI
                   g3970689
BLAST score
                   532
                   3.0e~54
E value
Match length
                   181
                   53
% identity
NCBI Description (Y18484) (+)-delta-cadinene synthase [Gossypium arboreum]
Seq. No.
                   23080
                   103466 1.R1040
Contig ID
5'-most EST
                   wrg700787508.h1
                   23081
Seq. No.
                   103471 1.R1040
Contig ID
5'-most EST
                   ssr700\overline{5}58306.h1
Method
                   BLASTX
NCBI GI
                   g3065835
                   292
BLAST score
                   3.0e-26
E value
Match length
                   76
```

(AF058800) putative methyltransferase [Arabidopsis



Contig ID 103474\_1.R1040 5'-most EST ssr700558309.h1

Method BLASTX
NCBI GI g4206209
BLAST score 238
E value 3.0e-20
Match length 93
% identity 54

NCBI Description (AF071527) putative glucan synthase component [Arabidopsis

thaliana] >gi\_4263042\_gb\_AAD15311\_ (AC005142) putative

glucan synthase component [Arabidopsis thaliana]

Seq. No. 23083

Contig ID 103479\_1.R1040 5'-most EST leu701154548.h1

Seq. No. 23084

Contig ID 103481\_1.R1040 5'-most EST pmv700894348.h1

Method BLASTX
NCBI GI g2501011
BLAST score 157
E value 1.0e-10
Match length 76
% identity 49

NCBI Description ISOLEUCYL-TRNA SYNTHETASE (ISOLEUCINE--TRNA LIGASE) (ILERS)

>gi\_1652625\_dbj\_BAA17545\_ (D90907) isoleucyl-tRNA

synthetase [Synechocystis sp.]

Seq. No. 23085

Contig ID 103484\_1.R1040 5'-most EST gsv701049113.h1

Method BLASTX
NCBI GI g3702966
BLAST score 435
E value 4.0e-43
Match length 86
% identity 94

NCBI Description (AF079486) rac GTP binding protein Arac8 [Arabidopsis

thaliana]

Seq. No. 23086

Contig ID 103500\_1.R1040 5'-most EST ssr700558340.h1

Method BLASTX
NCBI GI g4262148
BLAST score 233
E value 2.0e-19
Match length 118
% identity 43

NCBI Description (AC005275) predicted protein of unknown function

[Arabidopsis thaliana]

Seq. No. 23087

Contig ID 103523\_1.R1040



```
ssr700558368.hl
5'-most EST
                  23088
Seq. No.
                  103541 1.R1040
Contig ID
                  epx701106572.h1
5'-most EST
                  BLASTN
Method
NCBI GI
                  q2598578
                  133
BLAST score
                  2.0e-68
E value
                   316
Match length
% identity
NCBI Description Medicago truncatula mRNA for L-ascorbate oxidase
                   23089
Seq. No.
                   103548 1.R1040
Contig ID
                   leu701152225.h1
5'-most EST
                   23090
Seq. No.
                   103548 2.R1040
Contig ID
                   zsg701124870.h1
5'-most EST
                   23091
Seq. No.
                   103551 1.R1040
Contig ID
5'-most EST
                   wvk700685344.hl
                   BLASTX
Method
                   q3668080
NCBI GI
                   148
BLAST score
                   2.0e-18
E value
Match length
                   67
                   70
% identity
                  (AC004667) unknown protein [Arabidopsis thaliana]
NCBI Description
                   23092
Seq. No.
                   103560 1.R1040
Contig ID
5'-most EST
                   zvj700605249.h2
                   23093
Seq. No.
                   103586 1.R1040
Contig ID
5'-most EST
                   ssr700558451.hl
                   BLASTX
Method
                   q4049401
NCBI GI
                   138
BLAST score
                   1.0e-08
E value
Match length
                   83
                   42
% identity
                   (AJ131580) glutathione transferase AtGST 10 [Arabidopsis
NCBI Description
                   thaliana]
                   23094
Seq. No.
                   103596 1.R1040
Contig ID
                   zhf700959722.hl
5'-most EST
                   BLASTX
Method
                   g3335366
NCBI GI
                   187
BLAST score
```

8.0e-14

64

55

E value

Match length

% identity



```
NCBI Description
                  (AC003028) unknown protein [Arabidopsis thaliana]
                   23095
Seq. No.
Contig ID
                   103628 1.R1040
5'-most EST
                  uC-gmronoir042c04b1
Method
                  BLASTX
NCBI GI
                  g1707012
BLAST score
                  806
E value
                   1.0e-133
Match length
                   279
% identity
                  82
                  (U78721) tyrosyl-tRNA synthetase isolog [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  23096
                  103628 2.R1040
Contig ID
5'-most EST
                  zzp700835745.h1
Method
                  BLASTX
                  g1841468
NCBI GI
BLAST score
                  156
E value
                  1.0e-10
Match length
                   64
% identity
                  55
NCBI Description (Y10990) Tyrosyl-tRNA synthetase [Nicotiana tabacum]
                   23097
Seq. No.
                  103650 1.R1040
Contig ID
5'-most EST
                  ssr700558541.h1
Method
                  BLASTX
NCBI GI
                  g4469021
BLAST score
                   309
E value
                   4.0e-28
                  83
Match length
% identity
                  72
NCBI Description (AL035602) hypothetical protein [Arabidopsis thaliana]
                  23098
Seq. No.
Contig ID
                   103657 1.R1040
5'-most EST
                   ssr700\overline{5}58554.h1
Seq. No.
                   23099
Contig ID
                  103662 1.R1040
5'-most EST
                  uC-gmronoir071d07b1
Seq. No.
                  23100
                  103669 1.R1040
Contig ID
5'-most EST
                  gsv701053424.h1
Method
                  BLASTX
NCBI GI
                  q1076386
BLAST score
                  1446
E value
                   1.0e-161
Match length
                  297
% identity
                   90
```

23101

3674

(U48779) dual specificity kinase 1 [Arabidopsis thaliana]

NCBI Description protein kinase ADK1 - Arabidopsis thaliana >qi 1216484



103677 1.R1040 Contig ID ssr700558670.hl 5'-most EST

23102 Seq. No.

103690 1.R1040 Contig ID  $ssr700\overline{5}58609.h1$ 5'-most EST

BLASTX Method g1943945 NCBI GI 251 BLAST score 1.0e-21 E value 90 Match length 53 % identity

(U85780) Spinacia oleracea Spinach choline monooxygenase NCBI Description TRANSLATE of cmoll17.gcg from: 57 to: 1376 [Spinacia

oleracea]

23103 Seq. No.

103697 1.R1040 Contig ID

uC-gmrominsoy126e08b1 5'-most EST

BLASTX Method g4263707 NCBI GI 1179 BLAST score 1.0e-130 E value 272 Match length 83 % identity

(AC006223) putative 70kD heat shock protein [Arabidopsis NCBI Description

thaliana]

23104 Seq. No.

103705 2.R1040 Contig ID ssr700558629.h1 5'-most EST

23105 Seq. No.

103725 1.R1040 Contig ID  $k11701\overline{2}09784.h1$ 5'-most EST

BLASTX Method q3287696 NCBI GI 777 BLAST score 5.0e-83 E value 173 Match length % identity

(AC003979) Strong similarity to phosphoribosylanthranilate NCBI Description

transferase gb\_D86180 from Pisum sativum. This ORF may be part of a larger gene that lies in the overlapping region.

[Arabidopsis thaliana]

23106 Seq. No.

103726 1.R1040 Contig ID  $ssr700\overline{5}58657.h1$ 5'-most EST

Seq. No. 23107

103731 1.R1040 Contig ID

uC-gmrominsoy154g11b1 5'-most EST

BLASTX Method g4567197 NCBI GI 465 BLAST score 2.0e-46 E value

```
Match length
% identity
                    62
NCBI Description
                    (AC007168) unknown protein [Arabidopsis thaliana]
Seq. No.
                    23108
                    103738 1.R1040
Contig ID
5'-most EST
                    hyd700729964.h1
Method
                    BLASTX
NCBI GI
                    g4490733
BLAST score
                    355
E value
                    7.0e - 34
Match length
                    112
% identity
                    62
                    (AL035709) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                    23109
                    103743 1.R1040
Contig ID
5'-most EST
                    uC-gmflminsoy028a12b1
Seq. No.
                    23110
Contig ID
                    103755 1.R1040
5'-most EST
                    kmv700738076.h1
Method
                    BLASTX
NCBI GI
                    g4512678
BLAST score
                    463
E value
                    3.0e-46
Match length
                    145
% identity
                    66
NCBI Description
                    (AC006931) unknown protein [Arabidopsis thaliana]
Seq. No.
                    23111
Contig ID
                    103756 1.R1040
5'-most EST
                    sat701014551.h1
Method
                    BLASTX
NCBI GI
                    g2829689
BLAST score
                    156
E value
                    4.0e-10
Match length
                    169
% identity
                    22
NCBI Description
                   TRIGGER FACTOR (TF) (VEGETATIVE PROTEIN 2) (VEG2)
                   >gi_1770074_emb_CAA99536_ (Z75208) trigger factor [Bacillus
subtilis] >gi_2635288_emb_CAB14783_ (Z99118) trigger factor
                    (prolyl isomerase) [Bacillus subtilis]
Seq. No.
                    23112
Contig ID
                   103760 1.R1040
                   trc700566870.h1
Method
                   BLASTX
NCBI GI
                   q1076318
```

5'-most EST

BLAST score 513 E value 1.0e-104 Match length 313 % identity

NCBI Description dihydrolipoamide S-acetyltransferase (EC 2.3.1.12)

precursor - Arabidopsis thaliana (fragment)

>gi\_559395\_emb\_CAA86300\_ (Z46230) dihydrolipoamide acetyltransferase (E2) subunit of PDC [Arabidopsis



## thaliana]

Seq. No. 23113 Contig ID 103760 2.R1040 5'-most EST fC-gmse700836661g1 Method BLASTX NCBI GI g1076318

BLAST score 487 E value 2.0e-88 Match length 268 % identity 66

NCBI Description dihydrolipoamide S-acetyltransferase (EC 2.3.1.12)

precursor - Arabidopsis thaliana (fragment)
>gi\_559395\_emb\_CAA86300\_ (Z46230) dihydrolipoamide acetyltransferase (E2) subunit of PDC [Arabidopsis

thaliana]

Seq. No. 23114

103773 1.R1040 Contig ID 5'-most EST  $gsv701\overline{0}55278.h1$ Method

BLASTX NCBI GI g1723242 BLAST score 171 E value 5.0e-12 Match length 83 % identity 34

NCBI Description HYPOTHETICAL 36.8 KD PROTEIN C26A3.16 IN CHROMOSOME I >gi\_1177363 emb\_CAA93239\_ (Z69240) yeast dsk2 homolog,

ubiquitin-like protein [Schizosaccharomyces pombe]

Seq. No. 23115

103777 1.R1040 Contig ID 5'-most EST ssr700558738.h1

Method BLASTX NCBI GI g2117355 BLAST score 665 E value 7.0e-70 Match length 196 % identity

NCBI Description mitochondrial processing peptidase (EC 3.4.99.41) alpha-II

chain precursor - potato >gi\_587562\_emb\_CAA56520\_ (X80236)

mitochondrial processing peptidase [Solanum tuberosum]

Seq. No. 23116

103782 1.R1040 Contig ID 5'-most EST ssr700558743.h1

Method BLASTX NCBI GI g2262178 BLAST score 231 E value 6.0e-19 Match length 168 % identity 39

NCBI Description (AC002329) putative Mlo-like protein [Arabidopsis thaliana]

Seq. No. 23117

Contig ID 103787 1.R1040 5'-most EST pcp700991139.h1



```
Seq. No.
                   23118
Contig ID
                   103805 1.R1040
5'-most EST
                   ssr700558770.h1
Seq. No.
                   23119
                   103806 1.R1040
Contig ID
5'-most EST
                   ssr700558773.h1
Seq. No.
                   23120
                   103812 1.R1040
Contig ID
5'-most EST
                   jsh701064710.h1
Seq. No.
                   23121
Contig ID
                   103818 1.R1040
5'-most EST
                   ssr700\overline{5}58788.h1
Method
                   BLASTX
NCBI GI
                   g2344894
BLAST score
                   464
E value
                   2.0e-46
Match length
                   142
% identity
                   21
NCBI Description
                  (AC002388) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   23122
Contig ID
                   103828 2.R1040
5'-most EST
                   dpv701102138.h1
Method
                   BLASTX
NCBI GI
                   g2367392
BLAST score
                   162
E value
                   6.0e-20
Match length
                   94
% identity
                   59
NCBI Description
                   (U82513) random slug cDNA25 protein [Dictyostelium
                   discoideum]
Seq. No.
                   23123
Contig ID
                   103831 1.R1040
5'-most EST
                   uC-gmrominsoy287f07b1
Method
                   BLASTN
NCBI GI
                   g3116019
BLAST score
                   115
E value
                   8.0e-58
Match length
                   246
% identity
NCBI Description Pisum sativum mRNA for ftsZ gene
Seq. No.
                   23124
Contig ID
                   103833 1.R1040
5'-most EST
                  zhf700956579.h1
Method
                  BLASTX
NCBI GI
                  q4522007
```

NCBI GI g4522007
BLAST score 268
E value 1.0e-23
Match length 80
% identity 65

NCBI Description (AC007069) unknown protein [Arabidopsis thaliana]



Seq. No. 23126

Contig ID 103876 1.R1040

5'-most EST uC-gmflminsoy028e06b1

Method BLASTX
NCBI GI g1616918
BLAST score 155
E value 6.0e-10
Match length 214
% identity 25

NCBI Description (D82060) membrane protein with histidine rich charge

clusters [Homo sapiens] >gi 4219088 (AF117221) KE4 protein

[Homo sapiens]

Seq. No. 23127

Contig ID 103882 1.R1040 5'-most EST rlr700895518.h1

Seq. No. 23128

Contig ID 103888\_1.R1040 5'-most EST uC-gmronoir037g06b1

Seq. No. 23129

Contig ID 103895\_1.R1040 5'-most EST ssr700558912.h1

Seq. No. 23130

Contig ID 103897\_1.R1040 5'-most EST uxk700672771.h1

Seq. No. 23131

Contig ID 103914\_1.R1040 5'-most EST ssr700558943.h1

Seq. No. 23132

Contig ID 103925\_1.R1040 5'-most EST fC-gmle700558959a1

Method BLASTX
NCBI GI g2459435
BLAST score 990
E value 1.0e-107
Match length 294
% identity 62

NCBI Description (AC002332) putative serine carboxypeptidase [Arabidopsis

thaliana]

Seq. No. 23133

Contig ID 103928 1.R1040

5'-most EST jC-gmle01810029c08d1

Seq. No. 23134

Contig ID 103930 1.R1040

5'-most EST jC-gmle01810020c12a1



```
23135
Seq. No.
                  103934 1.R1040
Contig ID
                  pxt700946265.hl
5'-most EST
Method
                  BLASTX
                  q4415912
NCBI GI
                  295
BLAST score
                  1.0e-26
E value
                  138
Match length
% identity
                   41
                  (AC006282) putative protease [Arabidopsis thaliana]
NCBI Description
                   23136
Seq. No.
                   103939 1.R1040
Contig ID
5'-most EST
                  uC-gmflminsoy018d06b1
                   23137
Seq. No.
                   103949 1.R1040
Contig ID
                   ssr700558995.hl
5'-most EST
                   BLASTX
Method
                   g3377810
NCBI GI
                   169
BLAST score
                   3.0e-12
E value
                   46
Match length
                   70
% identity
                   (AF076275) contains similarity to glutaredoxins
NCBI Description
                   [Arabidopsis thaliana]
                   23138
Seq. No.
                   103949 2.R1040
Contig ID
                   ncj700\overline{9}87304.h1
5'-most EST
                   BLASTX
Method
                   g3377810
NCBI GI
BLAST score
                   253
                   6.0e-22
E value
                   70
Match length
                   69
% identity
                   (AF076275) contains similarity to glutaredoxins
NCBI Description
                   [Arabidopsis thaliana]
                   23139
Seq. No.
                   103971 1.R1040
Contig ID
5'-most EST
                   gsv701044933.h1
Seq. No.
                   23140
                   103979 1.R1040
Contig ID
5'-most EST
                   bth700845740.h1
                   BLASTX
Method
NCBI GI
                   q4415940
BLAST score
                   422
E value
                   3.0e-41
Match length
                   108
% identity
```

NCBI Description

Contig ID 103979\_2.R1040

(AC006418) hypothetical protein [Arabidopsis thaliana]



```
pmv700888775.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4415940
BLAST score
                   219
E value
                   5.0e-18
Match length
                   57
                   74
% identity
                  (AC006418) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   23142
Seq. No.
                   103979 3.R1040
Contig ID
5'-most EST
                  bth700849403.h1
Method
                  BLASTX
                   g4415940
NCBI GI
BLAST score
                   224
                   2.0e-18
E value
Match length
                   77
                   61
% identity
NCBI Description
                  (AC006418) hypothetical protein [Arabidopsis thaliana]
                   23143
Seq. No.
Contig ID
                   103983 1.R1040
5'-most EST
                   leu701151558.hl
Method
                  BLASTX
NCBI GI
                   g3785996
BLAST score
                   478
E value
                   7.0e-48
Match length
                   180
% identity
                   40
                  (AC005499) putative annexin [Arabidopsis thaliana]
NCBI Description
                   23144
Seq. No.
                   104001 1.R1040
Contig ID
5'-most EST
                   ssr700559081.h1
Method
                   BLASTX
NCBI GI
                   g3236240
BLAST score
                   415
E value
                   8.0e-41
Match length
                   120
% identity
                   71
                  (AC004684) unknown protein [Arabidopsis thaliana]
NCBI Description
                   23145
Seq. No.
                   104003 2.R1040
Contig ID
5'-most EST
                   ssr700559083.h1
Seq. No.
                   23146
                   104010 1.R1040
Contig ID
5'-most EST
                   seb700650701.hl
                   BLASTX
Method
NCBI GI
                   g3047065
                   271
BLAST score
```

E value 1.0e-23 88 Match length % identity 56

(AF058825) contains similarity to human OS-9 precurosor NCBI Description

(GB:U41635) [Arabidopsis thaliana]



Contig ID 104015\_1.R1040 5'-most EST ssr700559104.h1

Seq. No. 23148

Contig ID 104016\_1.R1040 5'-most EST zsg701129102.h1

Method BLASTN
NCBI GI g297171
BLAST score 226
E value 1.0e-124
Match length 270
% identity 96

NCBI Description R.rattus mRNA for ribosomal protein S7

Seq. No. 23149

Contig ID 104023\_1.R1040 5'-most EST ssr700559117.h1

Method BLASTN
NCBI GI g206744
BLAST score 283
E value 1.0e-158
Match length 287
% identity 100

NCBI Description Rat ribosomal protein S17 mRNA, complete cds

Seq. No. 23150

Contig ID 104030\_1.R1040 5'-most EST ssr700559128.h1

Method BLASTN
NCBI GI g38422
BLAST score 351
E value 0.0e+00
Match length 415
% identity 96

NCBI Description H.sapiens mRNA for ribosomal protein S18

Seq. No. 23151

Contig ID 104031\_1.R1040 5'-most EST fC-qmle700559131f2

Method BLASTN
NCBI GI g57703
BLAST score 208
E value 1.0e-113
Match length 280
% identity 94

NCBI Description R.rattus mRNA for ribosomal protein L8

Seq. No. 23152

Contig ID 104037\_1.R1040 5'-most EST ssr700559491.h1

Method BLASTN
NCBI GI g55822
BLAST score 298
E value 1.0e-167
Match length 302

3682



% identity 100
NCBI Description Rat mRNA for beta-globin

Seq. No. 23153
Contig ID 104040\_1.R1040
5'-most EST ssr700559145.h1

Seq. No. 23154

Contig ID 104049\_1.R1040 5'-most EST ssr700559157.h1

Method BLASTN
NCBI GI g57112
BLAST score 360
E value 0.0e+00
Match length 391
% identity 98

NCBI Description Rat mRNA for ribosomal protein L28

Seq. No. 23155

Contig ID 104050\_1.R1040 5'-most EST ssr700559196.h1

Method BLASTN
NCBI GI g57128
BLAST score 259
E value 1.0e-144
Match length 275
% identity 99

NCBI Description Rat mRNA for ribosomal protein S14

Seq. No. 23156

Contig ID 104068\_1.R1040 5'-most EST ssr700559234.h1

Method BLASTN
NCBI GI g3128488
BLAST score 101
E value 1.0e-49
Match length 231
% identity 89

NCBI Description Mus musculus ficolin B mRNA, partial cds

Seq. No. 23157

Contig ID 104071\_1.R1040 5'-most EST seb700652495.h1

Method BLASTX
NCBI GI g3142290
BLAST score 438
E value 2.0e-43
Match length 122
% identity 75

NCBI Description (AC002411) Contains similarity to gb Z69902 from C.

elegans. [Arabidopsis thaliana]

Seq. No. 23158

Contig ID 104082 1.R1040 5'-most EST ssr700559231.h1

Method BLASTN NCBI GI g204558



BLAST score 293 E value 1.0e-164 Match length 293 % identity 100

NCBI Description Rat major alpha-globin mRNA, complete cds

Seq. No. 23159

Contig ID 104088\_1.R1040 5'-most EST ssr700559328.h1

Seq. No. 23160

Contig ID 104101\_1.R1040 5'-most EST ssr700559246.h1

Method BLASTN
NCBI GI g515864
BLAST score 342
E value 0.0e+00
Match length 369
% identity 99

NCBI Description R.norvegicus (Sprague Dawley) ribosomal protein L15 mRNA

Seq. No. 23161

Contig ID 104102\_1.R1040 5'-most EST ssr700559248.h1

Method BLASTN
NCBI GI g575383
BLAST score 300
E value 1.0e-168
Match length 312
% identity 99

NCBI Description R.norvegicus mRNA for ribosomal protein L41

Seq. No. 23162

Contig ID 104112\_1.R1040 5'-most EST hyd700729527.h1

Method BLASTX
NCBI GI g1731078
BLAST score 240
E value 7.0e-20
Match length 166
% identity 36

NCBI Description HYPOTHETICAL OXIDOREDUCTASE IN ANSR-BMRU INTERGENIC REGION

>gi\_1303968\_dbj\_BAA12623\_ (D84432) YqjQ [Bacillus subtilis]
>gi\_2634813\_emb\_CAB14310\_ (Z99116) similar to ketoacyl

reductase [Bacillus subtilis]

Seq. No. 23163

Contig ID 104113\_1.R1040 5'-most EST fC-gmle700559288f2

Method BLASTN
NCBI GI g1055227
BLAST score 379
E value 0.0e+00
Match length 387
% identity 100

NCBI Description Rattus norvegicus prostaglandin F2a receptor mRNA, complete

cds



104118 1.R1040 Contig ID

uC-qmflminsoy056c04b1 5'-most EST

BLASTX Method q2498490 NCBI GI BLAST score 414 3.0e-40 E value 159 Match length 51 % identity

NCBI Description

VIRAL INTEGRATION SITE PROTEIN INT-6 >gi\_1854579 (L35556)
Int-6 [Mus musculus] >gi\_2114363 (U62962) similar to mouse
Int-6 [Homo sapiens] >gi\_2351382 (U54562) eIF3-p48 [Homo

sapiens] >gi 2688818 (U8 $\overline{5}$ 947) Int-6 [Homo sapiens]

>gi 2695701 (U94175) mammary tumor-associated protein INT6 [Homo sapiens] >gi 4503521\_ref\_NP\_001559.1\_pEIF3S6\_ murine

mammary tumor integration site 6 (oncogene homolog)

23165 Seq. No.

104121 1.R1040 Contig ID ssr700559295.h1 5'-most EST

BLASTN Method g194030 NCBI GI BLAST score 124 E value 2.0e-63 211 Match length % identity 92

NCBI Description Mouse heat shock protein 86 mRNA, complete cds, and 28S

ribosomal RNA, partial sequence

23166 Seq. No.

104123 1.R1040 Contig ID ssr700559389.hl 5'-most EST

Seq. No. 23167

104125 1.R1040 Contig ID 5'-most EST ssr700559294.hl

23168 Seq. No.

104127 1.R1040 Contig ID 5'-most EST ssr700559490.h1

BLASTN Method NCBI GI g1050757 BLAST score 251 E value 1.0e-139 259 Match length 100 % identity

R.norvegicus mRNA for a fusion protein of ubiquitin and NCBI Description

ribosomal protein L40

23169 Seq. No.

104132 1.R1040 Contig ID fC-gmle700559311f2 5'-most EST

BLASTN Method g984651 NCBI GI 1448 BLAST score 0.0e + 00E value



Match length 1603 % identity 97

NCBI Description Rattus norvegicus gene for Ad4BP, exon 7 and complete cds

Seq. No. 23170

Contig ID 104138\_1.R1040 5'-most EST ssr700559317.h1

Method BLASTN
NCBI GI g710365
BLAST score 294
E value 1.0e-165
Match length 342
% identity 96

NCBI Description Human ribosomal protein L9 mRNA, complete cds

Seq. No. 23171

Contig ID 104166\_1.R1040 5'-most EST wrg700789555.h2

Method BLASTX
NCBI GI g3822403
BLAST score 498
E value 4.0e-50
Match length 209
% identity 46

NCBI Description (AF087932) hydroperoxide lyase [Arabidopsis thaliana]

Seq. No. 23172

Contig ID 104167\_1.R1040 5'-most EST sat701014803.h1

Seq. No. 23173

Contig ID 104195\_1.R1040 5'-most EST tku700646491.h1

Method BLASTN
NCBI GI g337732
BLAST score 282
E value 1.0e-157
Match length 306
% identity 98

NCBI Description H.sapiens S19 ribosomal protein mRNA, complete cds.

>gi 4506694 ref NM 001022.1 RPS19 Homo sapiens ribosomal

protein S19 (RPS19) mRNA

Seq. No. 23174

Contig ID 104202 1.R1040

5'-most EST jC-gmro02910031c03d1

Method BLASTX
NCBI GI g3426064
BLAST score 237
E value 6.0e-20
Match length 91
% identity 54

NCBI Description (AJ007588) monooxygenase [Arabidopsis thaliana]

>gi\_4467141\_emb\_CAB37510\_ (AL035540) monooxygenase 2 (MO2)

[Arabidopsis thaliana]

Seq. No. 23175



Contig ID 104211\_1.R1040 5'-most EST zzp700833580.h1

Method BLASTX
NCBI GI g3367587
BLAST score 249
E value 3.0e-21
Match length 119
% identity 43

NCBI Description (AL031135) putative protein [Arabidopsis thaliana]

Seq. No. 23176

Contig ID 104236\_1.R1040 5'-most EST gsv701055474.h1

Seq. No. 23177

Contig ID 104273\_1.R1040

 5'-most EST
 g4396140

 Method
 BLASTX

 NCBI GI
 g2739046

 BLAST score
 288

 E value
 2.0e-25

 Match length
 150

 % identity
 41

NCBI Description (AF024652) polyphosphoinositide binding protein Ssh2p

[Glycine max]

Seq. No. 23178

Contig ID 104273\_2.R1040 5'-most EST fde700871322.h1

Method BLASTX
NCBI GI g2739046
BLAST score 199
E value 3.0e-15
Match length 120
% identity 35

NCBI Description (AF024652) polyphosphoinositide binding protein Ssh2p

[Glycine max]

Seq. No. 23179

Contig ID 104287 1.R1040 5'-most EST fde700872108.h1

Seq. No. 23180

Contig ID 104308\_1.R1040 5'-most EST vzy700753219.h1

Seq. No. 23181

Contig ID 104312\_1.R1040 5'-most EST fC-gmro700844032d3

Seq. No. 23182

Contig ID 104316\_1.R1040 5'-most EST ssr700559591.h1

Method BLASTX
NCBI GI g4522012
BLAST score 781
E value 3.0e-83



Match length 248 % identity 64

NCBI Description (AC007069) hypothetical protein [Arabidopsis thaliana]

Seq. No. 23183

Contig ID 104328\_1.R1040 5'-most EST ssr700559609.h1

Seq. No. 23184

Contig ID 104333\_1.R1040 5'-most EST zsg701122530.h1

Method BLASTX
NCBI GI g3047065
BLAST score 409
E value 1.0e-39
Match length 155
% identity 52

NCBI Description (AF058825) contains similarity to human OS-9 precurosor

(GB:U41635) [Arabidopsis thaliana]

Seq. No. 23185

Contig ID 104340\_1.R1040 5'-most EST jC-gmle01810030b02a2

Method BLASTX
NCBI GI g3894389
BLAST score 167
E value 9.0e-12
Match length 120
% identity 5

NCBI Description (AF053996) Hcr2-2A [Lycopersicon pimpinellifolium]

Seq. No. 23186

Contig ID 104344 1.R1040 5'-most EST ssr700559628.h1

Seq. No. 23187

Contig ID 104351\_1.R1040 5'-most EST fC-qmle700559636f2

Method BLASTX
NCBI GI g1174718
BLAST score 635
E value 2.0e-66
Match length 144
% identity 81

NCBI Description PUTATIVE RECEPTOR PROTEIN KINASE TMK1 PRECURSOR

>gi\_322579\_pir\_\_JQ1674 receptor protein kinase TMK1 (EC
2.7.1.-) precursor - Arabidopsis thaliana >gi\_166888

(L00670) protein kinase [Arabidopsis thaliana]

Seq. No. 23188

Contig ID 104370\_1.R1040 5'-most EST uxk700673389.h1

Method BLASTX
NCBI GI g3859570
BLAST score 175
E value 9.0e-13
Match length 49



% identity 63
NCBI Description (AF098753) unknown [Oryza sativa]

Seq. No. 23189

Contig ID 104374\_1.R1040 5'-most EST jsh701069071.h1

Method BLASTX
NCBI GI g2980772
BLAST score 160
E value 5.0e-11
Match length 63
% identity 56

NCBI Description (AL022198) putative protein [Arabidopsis thaliana]

Seq. No. 23190

Contig ID 104377 1.R1040 5'-most EST gsv701043810.h1

Seq. No. 23191

Contig ID 104384 1.R1040 5'-most EST sat701005269.h1

Seq. No. 23192

Contig ID 104387\_1.R1040 5'-most EST ssr700559685.h1

Seq. No. 23193

Contig ID 104400\_1.R1040 5'-most EST jsh701064704.h1

Method BLASTX
NCBI GI g3142292
BLAST score 301
E value 2.0e-27
Match length 80
% identity 79

NCBI Description (AC002411) Contains similarity to tetratricopeptide repeat protein gb U46571 from home sapiens. EST gb Z47802 and

gb Z48402 come from this gene. [Arabidopsis thaliana]

Seq. No. 23194

Contig ID 104420\_1.R1040 5'-most EST jC-gmle01810088h01a1

Method BLASTN
NCBI GI g2618602
BLAST score 40
E value 7.0e-13
Match length 92
% identity 86

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MSJ1, complete sequence [Arabidopsis thaliana]

Seq. No. 23195

Contig ID 104436\_1.R1040 5'-most EST dpv701102752.h1

Method BLASTX NCBI GI g2760321 BLAST score 282



E value Match length 53 % identity 89

(AC002130) F1N21.6 [Arabidopsis thaliana] NCBI Description

23196 Seq. No.

104436 2.R1040 Contig ID 5'-most EST g5752886 Method BLASTX

g2760321 NCBI GI 213 BLAST score 5.0e-17 E value 39 Match length % identity 90

NCBI Description (AC002130) F1N21.6 [Arabidopsis thaliana]

23197 Seq. No.

104458 1.R1040 Contig ID 5'-most EST  $ssr700\overline{5}59780.h1$ 

BLASTN Method g3402671 NCBI GI 47 BLAST score 4.0e-17 E value Match length 162 % identity 85

Arabidopsis thaliana chromosome II BAC T16B24 genomic NCBI Description

sequence, complete sequence [Arabidopsis thaliana]

23198 Seq. No.

104468 1.R1040 Contig ID qsv701045227.h1 5'-most EST

BLASTN Method g2618602 NCBI GI BLAST score 36 2.0e-10 E value Match length 76 % identity

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MSJ1, complete sequence [Arabidopsis thaliana]

23199 Seq. No.

104471 1.R1040 Contig ID ssr700559806.hl 5'-most EST

Seq. No.

23200 104475 1.R1040 Contig ID 5'-most EST ejt700606117.h2

Seq. No.

23201

104487 1.R1040 Contig ID fC-gmle700559825a1 5'-most EST

23202 Seq. No.

104509 1.R1040 Contig ID  $epx701\overline{1}08151.h1$ 5'-most EST

Seq. No.



Contig ID 104513\_1.R1040 5'-most EST uC-gmflminsoy080d10b1 Method BLASTX

NCBI GI g4510375
BLAST score 166
E value 3.0e-11
Match length 114
% identity 40

NCBI Description (AC007017) putative homeotic protein BEL1 [Arabidopsis

thaliana]

Seq. No. 23204

Contig ID 104515\_1.R1040 5'-most EST ssr700559860.h1

Method BLASTX
NCBI GI g4160300
BLAST score 216
E value 9.0e-35
Match length 116
% identity 60

NCBI Description (AJ011893) cyclin D3.1 protein [Nicotiana tabacum]

Seq. No. 23205

Contig ID 104521\_1.R1040 5'-most EST uC-gmropic036h10b1

Seq. No. 23206

Contig ID 104528\_1.R1040

5'-most EST jC-gmf\(\bar{1}\)02220102h10a1

Method BLASTX
NCBI GI g4239765
BLAST score 596
E value 1.0e-61
Match length 173
% identity 67

NCBI Description (AJ006233) putative thaumatin-like protein precursor

[Nicotiana tabacum]

Seq. No. 23207

Contig ID 104536\_1.R1040 5'-most EST zhf700955682.h1

Method BLASTX
NCBI GI g3298542
BLAST score 474
E value 3.0e-47
Match length 237
% identity 43

NCBI Description (AC004681) putative cellulose synthase [Arabidopsis

thaliana]

Seq. No. 23208

Contig ID 104543\_1.R1040 5'-most EST ssr700559892.h1

Seq. No. 23209

Contig ID 104566\_1.R1040 5'-most EST fC-gmle700559932a1



```
Method
                   BLASTX
NCBI GI
                   q2586083
BLAST score
                   420
                   3.0e-41
E value
                   169
Match length
                   53
% identity
                   (U72725) receptor kinase-like protein [Oryza
NCBI Description
                   longistaminata]
                   23210
Seq. No.
                   104569 1.R1040
Contig ID
5'-most EST
                   ssr700\overline{5}59937.h1
Seq. No.
                   23211
                   104578_1.R1040
Contig ID
                   uC-gmropic074c12b1
5'-most EST
                   BLASTN
Method
NCBI GI
                   g3668068
BLAST score
                   43
                   9.0e-15
E value
                   98
Match length
                   86
% identity
                   Lycopersicon esculentum Pto kinase interactor 1 (Pti1)
NCBI Description
                   mRNA, complete cds
                   23212
Seq. No.
                   104618 1.R1040
Contig ID
                   epx701105537.h1
5'-most EST
                   BLASTN
Method
                   g4210834
NCBI GI
BLAST score
                   258
                   1.0e-143
E value
Match length
                   537
                   87
% identity
NCBI Description Pisum sativum mRNA for ketol-acid reductoisomerase
Seq. No.
                   23213
                   104619 1.R1040
Contia ID
5'-most EST
                   ssr700\overline{5}60011.h1
Method
                   BLASTX
NCBI GI
                    q2245127
BLAST score
                    397
E value
                    4.0e-38
Match length
                    184
% identity
                    47
                   (Z97344) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                    23214
                    104631 1.R1040
Contig ID
                    ssr700\overline{5}60026.h1
5'-most EST
                    23215
Seq. No.
```

Contig ID 104639\_1.R1040 5'-most EST ssr700560039.h1

Seq. No. 23216

Contig ID 104658\_1.R1040



```
bth700845560.h1
5'-most EST
                  23217
Seq. No.
                  104660 1.R1040
Contig ID
                  zhf700963134.hl
5'-most EST
                  BLASTX
Method
NCBI GI
                  g4406808
                  235
BLAST score
                  2.0e-26
E value
Match length
                  100
% identity
                  62
NCBI Description (AC006201) unknown protein [Arabidopsis thaliana]
Seq. No.
                  23218
                  104661 1.R1040
Contig ID
                  vzy700755612.h1
5'-most EST
                  23219
Seq. No.
                  104661 2.R1040
Contig ID
5'-most EST
                  ncj700982416.hl
                  23220
Seq. No.
                  104667 1.R1040
Contig ID
5'-most EST
                  ssr700560083.hl
Seq. No.
                  23221
                  104668 1.R1040
Contig ID
                  fC-qmse700842377f1
5'-most EST
Method
                  BLASTX
                  q2833378
NCBI GI
                  604
BLAST score
                  2.0e-62
E value
                  281
Match length
% identity
                  HEXOKINASE >gi 619928 (U18754) hexokinase [Arabidopsis
NCBI Description
                  thaliana] >gi 1582383 prf 2118367A hexokinase [Arabidopsis
                  thaliana]
                   23222
Seq. No.
                   104674 1.R1040
Contig ID
                   ssr700560101.hl
5'-most EST
Method
                  BLASTX
                   g1463123
NCBI GI
BLAST score
                   560
                   7.0e-62
E value
                   132
Match length
% identity
                   84
                  (U34817) violaxanthin de-epoxidase precursor [Nicotiana
NCBI Description
                   tabacum]
                   23223
Seq. No.
                   104675 1.R1040
Contig ID
```

5'-most EST vwf700678402.h1
Method BLASTX

Method BLASTX
NCBI GI g3236259
BLAST score 619
E value 1.0e-113



Match length 283 % identity 71

NCBI Description (AC004684) putative alcohol dehydrogenase [Arabidopsis

thaliana]

Seq. No. 23224

Contig ID 104703\_1.R1040

5'-most EST uC-gmflminsoy057h09b1

Method BLASTX
NCBI GI g3135269
BLAST score 234
E value 2.0e-19
Match length 161
% identity 29

NCBI Description (AC003058) unknown protein [Arabidopsis thaliana]

Seq. No. 23225

Contig ID 104751 1.R1040

5'-most EST jC-gmro02910032a02a1

Method BLASTX
NCBI GI g3738324
BLAST score 352
E value 3.0e-33
Match length 117
% identity 55

NCBI Description (AC005170) GMP synthase-like protein [Arabidopsis thaliana]

Seq. No. 23226

Contig ID 104801\_1.R1040 5'-most EST ssr700560790.h1

Seq. No. 23227

Contig ID 104803 2.R1040 5'-most EST gsv701048714.h1

Seq. No. 23228

Contig ID 104808\_1.R1040 5'-most EST ssr700560316.h1

Method BLASTX
NCBI GI g2924777
BLAST score 343
E value 3.0e-32
Match length 131
% identity 50

NCBI Description (AC002334) putative receptor protein kinase [Arabidopsis

thaliana]

Seq. No. 23229

Contig ID 104817\_1.R1040 5'-most EST seb700649812.h1

Seq. No. 23230

Contig ID 104822\_1.R1040 5'-most EST ssr700560332.h1

Method BLASTX
NCBI GI g2492678
BLAST score 221



E value 6.0e-18 Match length 133 % identity 36

NCBI Description

ACTIN-LIKE PROTEIN ARP8 >gi\_2132896\_pir\_\_S67026 probable membrane protein YOR141c - yeast (Saccharomyces cerevisiae) >gi\_1262142\_emb\_CAA64058\_ (X94335) YOR3348c [Saccharomyces cerevisiae] >gi\_1420356\_emb\_CAA99341\_ (Z75049) ORF YOR141c [Saccharomyces cerevisiae]

Seq. No. 23231

Contig ID 104823\_1.R1040 5'-most EST sat701003815.h1

Seq. No. 23232

Contig ID 104824 2.R1040 5'-most EST wvk700685082.h1

Seq. No. 23233

Contig ID 104882 1.R1040 5'-most EST ssr700560418.h1 Method BLASTX

Method BLASTX
NCBI GI g4539389
BLAST score 1243
E value 1.0e-137
Match length 264
% identity 87

NCBI Description (AL035526) putative protein kinase [Arabidopsis thaliana]

Seq. No. 23234

Contig ID 104889\_1.R1040 5'-most EST ssr700560428.h1

Method BLASTX
NCBI GI g1418331
BLAST score 369
E value 5.0e-35
Match length 197
% identity 40

NCBI Description (X95909) receptor like protein kinase [Arabidopsis

thaliana]

23236

23237

Seq. No. 23235

Contig ID 104899\_1.R1040 5'-most EST ssr700560452.h1

Seq. No.

Contig ID 104903\_1.R1040 5'-most EST ssr700560457.h1

Seq. No.

Contig ID 104906\_1.R1040 5'-most EST trc700563528.h1

Seq. No. 23238

Contig ID 104917\_1.R1040 5'-most EST pcp700991229.h1

Method BLASTX NCBI GI g4559334



BLAST score 372 E value 1.0e-35 Match length 92 % identity 68

NCBI Description (AC007087) unknown protein [Arabidopsis thaliana]

Seq. No. 23239

Contig ID 104938\_1.R1040 5'-most EST ssr700560531.h1

Seq. No. 23240

Contig ID 104939 1.R1040 5'-most EST leu701155807.h1

Method BLASTX
NCBI GI g2651310
BLAST score 401
E value 6.0e-39
Match length 178
% identity 48

NCBI Description (AC002336) putative PTR2-B peptide transporter [Arabidopsis

thaliana]

Seq. No. 23241

Contig ID 104942\_1.R1040 5'-most EST jC-gmle01810060d12a1

Method BLASTX
NCBI GI g2262114
BLAST score 278
E value 2.0e-27
Match length 189
% identity 40

NCBI Description (AC002343) cellulose synthase isolog [Arabidopsis thaliana]

Seq. No. 23242

Contig ID 104959\_1.R1040 5'-most EST ssr700560563.h1

Seq. No. 23243

Contig ID 104964\_1.R1040 5'-most EST fua701042649.h1

Method BLASTX
NCBI GI g4204265
BLAST score 216
E value 3.0e-17
Match length 124
% identity 41

NCBI Description (AC005223) 45643 [Arabidopsis thaliana]

Seq. No. 23244

Contig ID 104966\_1.R1040

5'-most EST jC-gmle01810059e08a1

Seq. No. 23245

Contig ID 104987\_1.R1040 5'-most EST jsh701066491.h1

Method BLASTX NCBI GI g2642450



BLAST score 1285 E value 1.0e-142 Match length 307

Match length 30° % identity 81

NCBI Description (AC002391) putative metal ion transporter (Nramp)
[Arabidopsis thaliana] >gi\_3169188 (AC004401) putative
metal ion transporter (Nramp) [Arabidopsis thaliana]

Seq. No. 23246

Contig ID 104998\_1.R1040 5'-most EST zhf700959433.h1

Method BLASTX
NCBI GI g4432870
BLAST score 345
E value 2.0e-32
Match length 190
% identity 43

NCBI Description (AC006300) putative selenium-binding protein, 3' partial

[Arabidopsis thaliana]

Seq. No. 23247

Contig ID 105004\_1.R1040 5'-most EST ssr700560635.h1

Seq. No. 23248

Contig ID 105011\_1.R1040 5'-most EST fC-gmle700557881r2

Seq. No. 23249

Contig ID 105012\_1.R1040 5'-most EST ncj700975593.h1

Seq. No. 23250

Contig ID 105018\_1.R1040

5'-most EST uC-gmflminsoy071f02b2

Seq. No. 23251

Contig ID 105018 2.R1040 5'-most EST rca701002575.h1

Seq. No.

23252

Contig ID 105030\_1.R1040 5'-most EST pxt700944161.h1

Method BLASTX
NCBI GI g2842490
BLAST score 240
E value 2.0e-20
Match length 102
% identity 52

NCBI Description (AL021749) heat-shock protein [Arabidopsis thaliana]

Seq. No. 23253

Contig ID 105034\_1.R1040 5'-most EST kl1701214786.h1

Seq. No. 23254

Contig ID 105041\_1.R1040



```
uC-gmflminsoy014b08b1
5'-most EST
                  BLASTX
Method
                  g2565436
NCBI GI
                  796
BLAST score
                  3.0e-85
E value
                  165
Match length
                  95
% identity
                  (AF028842) DegP protease precursor [Arabidopsis thaliana]
NCBI Description
                  23255
Seq. No.
                  105053 2.R1040
Contig ID
                  kl1701208345.h1
5'-most EST
                  BLASTX
Method
                  g2809237
NCBI GI
BLAST score
                  261
                  4.0e-23
E value
Match length
                  77
                  66
% identity
NCBI Description (AC002560) F21B7.6 [Arabidopsis thaliana]
                  23256
Seq. No.
                  105060 1.R1040
Contig ID
                  xpa700796733.h1
5'-most EST
                  23257
Seq. No.
                  105100 1.R1040
Contig ID
                  zzp700831796.hl
5'-most EST
                   23258
Seq. No.
                   105116 1.R1040
Contig ID
                   kmv700738716.hl
5'-most EST
                   23259
Seq. No.
                   105116 2.R1040
Contig ID
                   pcp700995216.hl
5'-most EST
                   23260
Seq. No.
                   105125 1.R1040
Contig ID
                   vzy700756230.h1
5'-most EST
                   23261
Seq. No.
                   105132 1.R1040
Contig ID
                   ssr700560840.hl
5'-most EST
                   23262
Seq. No.
                   105150 1.R1040
Contig ID
                   ssr700560875.h1
5'-most EST
                   BLASTN
Method
NCBI GI
                   q1853969
                   66
BLAST score
                   8.0e-29
E value
Match length
                   254
% identity
NCBI Description Vigna unguiculata mRNA for CPRD46 protein, complete cds
```

Seq. No. 23263

Contig ID 105155\_1.R1040



5'-most EST tku700646396.h1

Method BLASTX
NCBI GI g2499115
BLAST score 587
E value 6.0e-61
Match length 138
% identity 78

NCBI Description VACUOLAR ASSEMBLY PROTEIN VPS41 HOMOLOG >gi\_1835788

(U86662) VPS41 [Lycopersicon esculentum]

Seq. No. 23264

Contig ID 105170\_1.R1040 5'-most EST hrw701058908.h1

Method BLASTX
NCBI GI g1903034
BLAST score 1817
E value 0.0e+00
Match length 541
% identity 64

NCBI Description (X94625) amp-binding protein [Brassica napus]

Seq. No. 23265

Contig ID 105186\_1.R1040 5'-most EST uaw700662791.h1

Method BLASTX
NCBI GI g4455221
BLAST score 180
E value 5.0e-13
Match length 100
% identity 38

NCBI Description (AL035440) putative protein [Arabidopsis thaliana]

Seq. No. 23266

Contig ID 105206\_1.R1040 5'-most EST epx701107663.h1

Seq. No. 23267

Contig ID 105219\_1.R1040 5'-most EST zhf700961282.h1

Method BLASTX
NCBI GI g3461828
BLAST score 204
E value 5.0e-16
Match length 79
% identity 52

NCBI Description (AC004138) unknown protein [Arabidopsis thaliana]

Seq. No. 23268

Contig ID 105229\_1.R1040 5'-most EST ssr700561017.h1

Seq. No. 23269

Contig ID 105244\_1.R1040 5'-most EST sat701010629.h1

Seq. No. 23270

Contig ID 105244\_2.R1040



5'-most EST uC-gmropic022h04b1

Seq. No. 23271

Contig ID 105261\_1.R1040 5'-most EST fua701042502.h1

Seq. No. 23272

Contig ID 105265 1.R1040

5'-most EST uC-gmrominsoy286d06b1

Seq. No. 23273

Contig ID 105265\_2.R1040 5'-most EST uC-gmropic058g08b1

Seq. No. 23274

Contig ID 105276\_1.R1040 5'-most EST vwf700675747.h1

Method BLASTN
NCBI GI g166411
BLAST score 265
E value 1.0e-147
Match length 493
% identity 88

NCBI Description Medicago sativa NADH-glutamate synthase mRNA, comlete cds

Seq. No. 23275

Contig ID 105281\_1.R1040 5'-most EST jC-gmro02910032d11a1

Method BLASTX
NCBI GI g3695019
BLAST score 430
E value 2.0e-42
Match length 143
% identity 55

NCBI Description (AF055848) subtilisin-like protease [Arabidopsis thaliana]

Seq. No. 23276

Contig ID 105282\_1.R1040 5'-most EST pmv700888848.h1

Method BLASTX
NCBI GI g4049341
BLAST score 146
E value 2.0e-09
Match length 87
% identity 39

NCBI Description (AL034567) putative protein [Arabidopsis thaliana]

Seq. No. 23277

Contig ID 105292 1.R1040

5'-most EST g5753107
Method BLASTX
NCBI GI g3892057
BLAST score 462
E value 4.0e-46
Match length 142
% identity 63

NCBI Description (AC002330) hypothetical protein [Arabidopsis thaliana]



Seq. No. 23278

Contig ID 105297\_1.R1040 5'-most EST jC-gmle01810070f02a1

Method BLASTN
NCBI GI g169127
BLAST score 237
E value 1.0e-130
Match length 475
% identity 88

NCBI Description Pisum sativum (clone pCLp) nuclear encoded precursor to

chloroplast protein mRNA, complete cds

Seq. No. 23279

Contig ID 105312\_1.R1040 5'-most EST has700548176.h1

Seq. No. 23280

Contig ID 105314\_1.R1040 5'-most EST pmv700892185.h1

Method BLASTX
NCBI GI g3451060
BLAST score 117
E value 1.0e-09
Match length 88
% identity 40

NCBI Description (AL031326) putative protein [Arabidopsis thaliana]

Seq. No. 23281

Contig ID 105333\_1.R1040 5'-most EST has700548214.h1

Method BLASTX
NCBI GI g3044214
BLAST score 502
E value 9.0e-51
Match length 115
% identity 80

NCBI Description (AF057044) acyl-CoA oxidase [Arabidopsis thaliana]

Seq. No. 23282

Contig ID 105333\_2.R1040 5'-most EST jC-qmf102220090c03d1

Method BLASTX
NCBI GI g3044214
BLAST score 336
E value 2.0e-31
Match length 74
% identity 81

NCBI Description (AF057044) acyl-CoA oxidase [Arabidopsis thaliana]

Seq. No. 23283

Contig ID 105335\_1.R1040 5'-most EST dpv701099013.h1

Method BLASTX
NCBI GI g4406820
BLAST score 862
E value 6.0e-93



Match length 208 % identity

NCBI Description (AC006201) putative ras superfamily member [Arabidopsis

thaliana]

Seq. No. Contig ID 23284

5'-most EST

105336 1.R1040  $has700\overline{5}48217.h1$ 

BLASTX Method NCBI GI g3549626 BLAST score 153 E value 5.0e-10 Match length 114 % identity 36

NCBI Description (AJ009696) wall-associated kinase 1 [Arabidopsis thaliana]

Seq. No.

23285

Contig ID 5'-most EST

105353 1.R1040 gsv701048201.h1

Seq. No.

23286

Contig ID 5'-most EST

105355 1.R1040  $has700\overline{5}48239.h1$ 

Seq. No.

23287

Contig ID 5'-most EST

105365 1.R1040 rlr700897165.h1

Seq. No.

23288

Contig ID 5'-most EST 105372 1.R1040 has700548259.h1

Seq. No.

23289

Contiq ID 5'-most EST

105373 1.R1040 zsg701121035.h1

Seq. No.

23290

Contig ID 5'-most EST 105379 1.R1040 wvk700681131.h2

Seq. No.

23291

Contig ID 5'-most EST

105380 1.R1040  $has700\overline{5}48268.h1$ 

Seq. No.

23292

Contig ID 5'-most EST

105384 1.R1040 ncj700986774.h1

Seq. No.

23293

Contig ID 5'-most EST 105385 1.R1040  $k11701\overline{2}13433.h1$ 

Seq. No.

23294

Contig ID 5'-most EST

105387 1.R1040 has700548275.h1

Seq. No.

23295



Contig ID 105390\_1.R1040 5'-most EST has700548278.h1

Seq. No. 23296

Contig ID 105393\_1.R1040 5'-most EST has700548281.h1

Seq. No. 23297

Contig ID 105398\_1.R1040 5'-most EST pmv700890363.h1

Method BLASTX
NCBI GI g2529677
BLAST score 456
E value 2.0e-45
Match length 137
% identity 66

NCBI Description (AC002535) kinesin-like protein, heavy chain [Arabidopsis

thaliana]

Seq. No. 23298

Contig ID 105400\_1.R1040 5'-most EST sat701014979.h1

Method BLASTX
NCBI GI g3941289
BLAST score 400
E value 4.0e-39
Match length 100
% identity 72

NCBI Description (AF018093) similarity to SCAMP37 [Pisum sativum]

Seq. No.

Contig ID 105401 1.R1040

23299

5'-most EST g4437105

Seq. No. 23300

Contig ID 105405\_1.R1040 5'-most EST fC-gmse700672216y1

Method BLASTX
NCBI GI g1350783
BLAST score 364
E value 1.0e-34
Match length 140
% identity 54

NCBI Description RECEPTOR-LIKE PROTEIN KINASE 5 PRECURSOR

>gi\_282883\_pir\_\_S27756 receptor-like protein kinase
precursor - Arabidopsis thaliana >gi\_166850 (M84660)
receptor-like protein kinase [Arabidopsis thaliana]

>gi 2842492 emb CAA16889 (AL021749) receptor-like protein

kinase 5 precursor (RLK5) [Arabidopsis thaliana]

Seq. No. 23301

Contig ID 105411\_1.R1040 5'-most EST zhf700952313.h1

Method BLASTX
NCBI GI g3913425
BLAST score 408
E value 8.0e-40



Match length 134 % identity 62

NCBI Description PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE >gi 2275203 (AC002337) RNA helicase isolog

[Arabidopsis thaliana]

Seq. No. 23302

Contig ID 105416\_1.R1040 5'-most EST trc700561116.h1

Seq. No. 23303

Contig ID 105430\_1.R1040 5'-most EST zsq701118678.h1

Method BLASTX
NCBI GI g3668089
BLAST score 651
E value 5.0e-68
Match length 197
% identity 64

NCBI Description (AC004667) unknown protein [Arabidopsis thaliana]

Seq. No. 23304

Contig ID 105436\_1.R1040 5'-most EST trc700561141.h1

Method BLASTX
NCBI GI g3953603
BLAST score 150
E value 7.0e-10
Match length 51
% identity 67

NCBI Description (AB008490) response regulator 7 [Arabidopsis thaliana]

Seq. No. 23305

Contig ID 105437\_1.R1040 5'-most EST trc700561142.h1

Seq. No. 23306

Contig ID 105438\_1.R1040 5'-most EST vzy700752065.h1

Seq. No. 23307

Contig ID 105447\_1.R1040 5'-most EST trc700561158.h1

Method BLASTX
NCBI GI g3885344
BLAST score 149
E value 7.0e-10
Match length 74
% identity 45

NCBI Description (AC005623) unknown protein [Arabidopsis thaliana]

>gi\_4557057\_gb\_AAD22497.1\_AC007154\_1 (AC007154) unknown

protein [Arabidopsis thaliana]

Seq. No. 23308

Contig ID 105452\_1.R1040 5'-most EST trc700561164.h1

Method BLASTX



NCBI GI q3786016 BLAST score 230 E value 7.0e-19 Match length 117 % identity

NCBI Description (AC005499) putative elongation factor [Arabidopsis

thaliana]

Seq. No. Contig ID

23309 105453 1.R1040

5'-most EST Method

fC-gmro700561167a1

BLASTX NCBI GI g4097522 BLAST score 498 E value 3.0e-50 Match length 168 % identity 56

NCBI Description (U63534) cinnamyl alcohol dehydrogenase [Fragaria x

ananassa]

Seq. No.

23310

23311

Contig ID 5'-most EST 105465\_1.R1040 wvk700684224.h1

Method BLASTX NCBI GI q3924613 BLAST score 366 E value 1.0e-34 Match length 308

% identity 35

(AF069442) hypothetical protein [Arabidopsis thaliana] NCBI Description

>gi\_4263512\_gb\_AAD15338\_ (AC004044) hypothetical protein

[Arabidopsis thaliana]

Seq. No.

Contig ID 5'-most EST

105476 1.R1040 pcp700993617.h1

Seq. No. 23312

Contig ID 5'-most EST

105484 1.R1040 trc700561209.h1

23313 Seq. No.

Contig ID 5'-most EST

105488 1.R1040 trc700561214.h1

Seq. No. 23314

105490 1.R1040 Contig ID 5'-most EST trc700564676.h1

Seq. No. 23315

105492 1.R1040 Contig ID 5'-most EST trc700561223.h1

Method BLASTX NCBI GI g2894607 BLAST score 302 E value 2.0e-27 Match length 90



Method BLASTX
NCBI GI g2275211
BLAST score 184
E value 2.0e-13
Match length 125
% identity 39

NCBI Description (AC002337) RNA helicase isolog [Arabidopsis thaliana]

Seq. No. 23317

Contig ID 105514\_1.R1040 5'-most EST jC-gmro02800040f06a1

Method BLASTX
NCBI GI g3695023
BLAST score 219
E value 3.0e-17
Match length 164
% identity 35

NCBI Description (AF055850) unknown [Arabidopsis thaliana]

Seq. No. 23318

Contig ID 105524 1.R1040

5'-most EST uC-gmrominsoy103e02b1

Method BLASTX
NCBI GI g2462832
BLAST score 494
E value 5.0e-50
Match length 132
% identity 70

NCBI Description (AF000657) similar to Bacillus CotA [Arabidopsis thaliana]

Seq. No. 23319

Contig ID 105540\_1.R1040 5'-most EST jC-gmro02910013d03a1

Method BLASTX
NCBI GI g2245020
BLAST score 902
E value 1.0e-97
Match length 222
% identity 77

NCBI Description (Z97341) growth regulator homolog [Arabidopsis thaliana]

Seq. No. 23320

Contig ID 105551\_1.R1040 5'-most EST ncj700986355.h1

Method BLASTX
NCBI GI g1351722
BLAST score 281
E value 7.0e-25
Match length 142
% identity 40



HYPOTHETICAL 29.7 KD PROTEIN C18G6.06 IN CHROMOSOME I NCBI Description >gi 1122371\_emb\_CAA92386\_ (Z68198) hypothetical protein [Schizosaccharomyces pombe]

23321 Seq. No.

105555 1.R1040 Contig ID vzy700752235.hl 5'-most EST

BLASTN Method g727263 NCBI GI 40 BLAST score 3.0e-13E value 193 Match length 16 % identity

NCBI Description Phaseolus vulgaris hydroxyproline-rich glycoprotein precursor gene, complete cds and promoter region

23322 Seq. No.

105566 1.R1040 Contig ID

uC-gmflminsoy046a02b1 5'-most EST

BLASTX Method g2961390 NCBI GI 659 BLAST score 3.0e-69 E value 163 Match length

% identity (AL022141) beta-galactosidase like protein [Arabidopsis NCBI Description

thaliana]

23323 Seq. No.

105571 1.R1040 Contig ID uC-gmronoir045h08b1 5'-most EST

BLASTX Method q1103318 NCBI GI 436 BLAST score 1.0e-42 E value Match length 194 49 % identity

(X78818) casein kinase I [Arabidopsis thaliana] NCBI Description >qi 2244791 emb CAB10213.1\_ (Z97336) casein kinase I

[Arabidopsis thaliana]

23324 Seq. No.

105575 1.R1040 Contig ID smc700747934.h1 5'-most EST

Method BLASTX g2129473 NCBI GI BLAST score 350 1.0e-32 E value 141 Match length 50 % identity

arabinogalactan-like protein - loblolly pine >gi\_607774 NCBI Description

(U09556) arabinogalactan-like protein [Pinus taeda]

23325 Seq. No.

105575 2.R1040 Contig ID

jC-gmst02400023b09a1 5'-most EST



```
23326
Seq. No.
                  105578 1.R1040
Contig ID
5'-most EST
                  fua701041596.h1
                  BLASTX
Method
NCBI GI
                  g4056506
BLAST score
                  339
                  1.0e-31
E value
                  143
Match length
% identity
NCBI Description (AC005896) nodulin-like protein [Arabidopsis thaliana]
Seq. No.
                  23327
                  105582 1.R1040
Contig ID
                  vwf700679270.h1
5'-most EST
Seq. No.
                  23328
                  105597 1.R1040
Contig ID
5'-most EST
                  trc700561373.h1
                  23329
Seq. No.
                  105608 1.R1040
Contig ID
5'-most EST
                  trc700561386.h1
Seq. No.
                  23330
                  105612 1.R1040
Contig ID
5'-most EST
                  uC-gmropic068d01b1
Method
                  BLASTX
NCBI GI
                  q417148
BLAST score
                  432
                  2.0e-42
E value
                  195
Match length
% identity
                  47
NCBI Description PROBABLE GLUTATHIONE S-TRANSFERASE (HEAT SHOCK PROTEIN 26A)
                  (G2-4) >gi_99912_pir__A33654 heat shock protein 26A -
                  soybean >gi 169981 (M20363) Gmhsp26-A [Glycine max]
                  23331
Seq. No.
                  105627 1.R1040
Contig ID
                  trc700561416.h1
5'-most EST
Method
                  BLASTX
                  g3763933
NCBI GI
BLAST score
                  274
                  3.0e-24
E value
Match length
                  121
% identity
                  42
NCBI Description (AC004450) unknown protein [Arabidopsis thaliana]
Seq. No.
                  23332
                  105630 1.R1040
Contig ID
5'-most EST
                  pcp700990540.h1
Method
                  BLASTX
```

NCBI GI g2781345
BLAST score 926
E value 1.0e-100
Match length 288
% identity 66

NCBI Description (AC003113) F2401.2 [Arabidopsis thaliana]

Match length

% identity

169



```
Seq. No.
                  23333
                  105633 1.R1040
Contig ID
5'-most EST
                  trc700561424.h1
Seq. No.
                  23334
                  105638 1.R1040
Contig ID
                  fC-qmle700553960a4
5'-most EST
                  BLASTX
Method
NCBI GI
                  q1086263
BLAST score
                  214
E value
                  4.0e-17
Match length
                  135
% identity
                  39
NCBI Description TMV resistance protein N - tobacco (Nicotiana glutinosa)
                  >gi 558887 (U15605) N [Nicotiana glutinosa]
Seq. No.
                  23335
Contig ID
                  105677 1.R1040
                  trc700561480.h1
5'-most EST
                  23336
Seq. No.
Contig ID
                  105679 1.R1040
5'-most EST
                  fua701042080.h1
                  BLASTX
Method
NCBI GI
                  q3451147
BLAST score
                  361
E value
                  4.0e-34
Match length
                  104
% identity
                  61
NCBI Description (AJ010397) chitinase [Hevea brasiliensis]
                  23337
Seq. No.
                  105695 1.R1040
Contig ID
5'-most EST
                  trc700561562.h1
Seq. No.
                  23338
                  105697 1.R1040
Contig ID
5'-most EST
                  fC-gmse700754533c1
Method
                  BLASTX
NCBI GI
                  g3367568
BLAST score
                  340
E value
                  1.0e-31
Match length
                  93
% identity
                  61
NCBI Description (AL031135) protein kinase - like protein [Arabidopsis
                  thaliana]
Seq. No.
                  23339
                  105733 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy261d10b1
Method
                  BLASTX
NCBI GI
                  g4510406
BLAST score
                  537
E value
                  7.0e-55
```



NCBI Description (AC006587) putative protein kinase [Arabidopsis thaliana]

Seq. No. 23340

Contig ID 105758 1.R1040 5'-most EST trc700563916.h1

Seq. No. 23341

Contig ID 105760\_1.R1040 5'-most EST pxt700946478.h1

Method BLASTX
NCBI GI g3135277
BLAST score 181
E value 6.0e-13
Match length 103
% identity 42

NCBI Description (AC003058) hypothetical protein [Arabidopsis thaliana]

>gi 4191776 (AC005917) hypothetical protein [Arabidopsis

thalianal

Seq. No. 23342

Contig ID 105761\_1.R1040 5'-most EST sat701013353.h1

Seq. No. 23343

Contig ID 105767\_1.R1040 5'-most EST jC-gmst02400011g01a1

Method BLASTX
NCBI GI g2760839
BLAST score 457
E value 1.0e-45
Match length 152
% identity 61

NCBI Description (AC003105) putative receptor kinase [Arabidopsis thaliana]

Seq. No. 23344

Contig ID 105768\_1.R1040 5'-most EST trc700561702.h1

Seq. No. 23345

Contig ID 105770\_1.R1040 5'-most EST ncj700978095.h1

Method BLASTX
NCBI GI 94530126
BLAST score 253
E value 2.0e-21
Match length 108
% identity 49

NCBI Description (AF078082) receptor-like protein kinase homolog RK20-1

[Phaseolus vulgaris]

Seq. No. 23346

Contig ID 105784\_1.R1040 5'-most EST djj700605919.h2

Seq. No. 23347

Contig ID 105792 1.R1040 5'-most EST trc700561744.h1



Method BLASTX
NCBI GI g3080435
BLAST score 203
E value 3.0e-16
Match length 44
% identity 82

NCBI Description (AL022605) putative protein [Arabidopsis thaliana]

Seq. No. 23348

Contig ID 105812\_1.R1040 5'-most EST hrw701057721.h1

Method BLASTX
NCBI GI g2864625
BLAST score 418
E value 1.0e-40
Match length 172
% identity 51

NCBI Description (AL021811) putative protein [Arabidopsis thaliana]

Seq. No. 23349

Contig ID 105813\_1.R1040 5'-most EST pxt700945355.h1

Method BLASTX
NCBI GI g3540207
BLAST score 1223
E value 1.0e-135
Match length 365
% identity 69

NCBI Description (AC004260) Putative protein kinase [Arabidopsis thaliana]

Seq. No. 23350

Contig ID 105834\_1.R1040 5'-most EST zhf700962779.h1

Method BLASTX
NCBI GI g4262226
BLAST score 184
E value 3.0e-13
Match length 83
% identity 49

NCBI Description (AC006200) putative protein kinase [Arabidopsis thaliana]

Seq. No. 23351

Contig ID 105834 2.R1040 5'-most EST dpv701098026.h1

Method BLASTX
NCBI GI g3033400
BLAST score 133
E value 2.0e-09
Match length 61
% identity 48

NCBI Description (AC004238) putative Ser/Thr protein kinase [Arabidopsis

thaliana]

Seq. No. 23352

Contig ID 105844\_1.R1040 5'-most EST trc700561823.h1



```
23353
Seq. No.
                  105869 1.R1040
Contig ID
                  sat701\overline{0}11317.h1
5'-most EST
                  BLASTX
Method
                  g4469019
NCBI GI
                   351
BLAST score
                   3.0e-33
E value
                   81
Match length
                   83
% identity
                  (AL035602) putative protein [Arabidopsis thaliana]
NCBI Description
                   23354
Seq. No.
                   105886 1.R1040
Contig ID
                   trc700561888.hl
5'-most EST
                   BLASTX
Method
                   g3004556
NCBI GI
                   267
BLAST score
                   1.0e-23
E value
                   105
Match length
                   48
% identity
                  (AC003673) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   23355
Seq. No.
                   105887 1.R1040
Contig ID
                   wrg700788135.h1
5'-most EST
                   BLASTX
Method
                   g1841355
NCBI GI
                   374
BLAST score
                   8.0e-36
E value
                   135
Match length
                   56
% identity
                   (D85381) cytochrome c oxidase subunit Vb precursor [Oryza
NCBI Description
                   sativa]
                   23356
Seq. No.
                   105904 1.R1040
Contig ID
                   wrq700785990.h2
5'-most EST
                   BLASTX
Method
                   q3859598
NCBI GI
BLAST score
                   255
                    4.0e-22
E value
                    45
Match length
                    98
 % identity
                    (AF104919) contains similarity to Myb DNA-binding domains
NCBI Description
                    (Pfam: PF00249, E=3.7e-27 N=3) [Arabidopsis thaliana]
 Seq. No.
                    23357
                    105906 1.R1040
 Contig ID
                    fC-gmro700561916a1
 5'-most EST
 Method
                    BLASTX
                    q3024360
 NCBI GI
                    1228
 BLAST score
                    1.0e-135
 E value
```

Match length 261 % identity 90

NCBI Description PHENYLALANINE AMMONIA-LYASE >gi\_1276903 (U43338) phenylalanine ammonia-lyase [Citrus limon]



Seq. No. 23358

Contig ID 105917\_1.R1040 5'-most EST trc700561931.h1

Method BLASTN
NCBI GI g310562
BLAST score 144
E value 2.0e-75
Match length 275
% identity 89

NCBI Description Glycine max calmodulin (SCaM-5) mRNA, complete cds

Seq. No. 23359

Contig ID 105922\_1.R1040 5'-most EST jC-gmro02910014h10a1

Method BLASTX
NCBI GI g3341693
BLAST score 399
E value 3.0e-38
Match length 280
% identity 42

NCBI Description (AC003672) unknown protein [Arabidopsis thaliana]

Seq. No. 23360

Contig ID 105922\_2.R1040 5'-most EST jC-gmle01810005c07a1

Method BLASTX
NCBI GI g3341693
BLAST score 380
E value 2.0e-36
Match length 93
% identity 74

NCBI Description (AC003672) unknown protein [Arabidopsis thaliana]

Seq. No. 23361

Contig ID 105927\_1.R1040 5'-most EST trc700561942.h1

Method BLASTX
NCBI GI g2462927
BLAST score 494
E value 5.0e-50
Match length 126
% identity 71

NCBI Description (Y10342) putative amidase [Arabidopsis thaliana]

Seq. No. 23362

Contig ID 105941\_1.R1040 5'-most EST uC-gmropic019f04b1

Method BLASTX
NCBI GI g3927830
BLAST score 450
E value 1.0e-44
Match length 175
% identity 36

NCBI Description (AC005727) hypothetical protein [Arabidopsis thaliana]

Seq. No. 23363



```
105942 1.R1040
Contig ID
                  trc700561965.hl
5'-most EST
                  BLASTX
Method
NCBI GI
                  g2463509
BLAST score
                  799
E value
                  2.0e-85
                  198
Match length
                  74
% identity
NCBI Description (Y09541) pectate lyase [Zinnia elegans]
Seq. No.
                  23364
Contig ID
                  105946 1.R1040
5'-most EST
                  q5175408
Method
                  BLASTX
NCBI GI
                  g3935187
BLAST score
                  274
E value
                  5.0e-24
Match length
                  71
% identity
                  72
NCBI Description (AC004557) F17L21.30 [Arabidopsis thaliana]
                  23365
Seq. No.
Contig ID
                  105965 1.R1040
5'-most EST
                  trc700561993.h1
Seq. No.
                  23366
Contig ID
                  105971 1.R1040
5'-most EST
                  uC-gmrominsoy105a06b1
Seq. No.
                  23367
                  105987_1.R1040
Contig ID
5'-most EST
                  rca701001533.hl
Method
                  BLASTX
                  g4138209
NCBI GI
BLAST score
                  161
E value
                   4.0e-11
Match length
                  92
% identity
                  35
NCBI Description
                  (AJ223071) serine/threonine kinase protein MSTK2L, long-form
                   [Mus musculus]
                  23368
Seq. No.
                  105988 1.R1040
Contig ID
5'-most EST
                  txt700736110.h1
                  23369
Seq. No.
                  105988 2.R1040
Contig ID
5'-most EST
                  trc700562025.h1
```

Seq. No. 23370

105991 1.R1040 Contig ID

5'-most EST g4397088

Seq. No. 23371

Contig ID 106005 1.R1040 5'-most EST trc700562044.h1

Method BLASTX



NCBI GI g3426036 BLAST score 190 E value 1.0e-14 Match length 100 % identity 45

NCBI Description (AC005168) unknown protein [Arabidopsis thaliana]

Seq. No. 23372

Contig ID 106018\_1.R1040 5'-most EST zzp700834039.h1

Seq. No. 23373

Contig ID 106018\_2.R1040 5'-most EST asn701140756.h1

Seq. No. 23374

Contig ID 106020\_1.R1040 5'-most EST jC-gmst02400065e08d1

Seq. No. 23375

Contig ID 106041\_1.R1040 5'-most EST hrw701063558.h1

Method BLASTX
NCBI GI g3894387
BLAST score 331
E value 1.0e-30
Match length 203
% identity 3

NCBI Description (AF053995) Hcr2-0B [Lycopersicon esculentum]

Seq. No. 23376

Contig ID 106051\_1.R1040 5'-most EST trc700562103.h1

Method BLASTX
NCBI GI g1905924
BLAST score 267
E value 4.0e-23
Match length 112
% identity 43

NCBI Description (L77890) DNA repair protein [Homo sapiens]

Seq. No. 23377

Contig ID 106060\_1.R1040 5'-most EST jC-gmfl02220086c05a1

Seq. No. 23378

Contig ID 106061\_1.R1040 5'-most EST trc700562119.h1

Seq. No. 23379

Contig ID 106066 1.R1040 5'-most EST trc700562174.h1

Method BLASTX
NCBI GI g3805962
BLAST score 208
E value 8.0e-17
Match length 85



% identity 56

NCBI Description (Y13772) laccase [Populus balsamifera subsp. trichocarpa]

Seq. No. 23380

Contig ID 106069 1.R1040 5'-most EST ncj700977134.h1

Method BLASTX
NCBI GI g3850108
BLAST score 409
E value 5.0e-43
Match length 168
% identity 54

NCBI Description (AL033388) putative calcium-transporting atpase

[Schizosaccharomyces pombe]

Seq. No. 23381

Contig ID 106083\_1.R1040 5'-most EST kl1701214047.h1

Method BLASTX
NCBI GI g2244781
BLAST score 289
E value 8.0e-26
Match length 93
% identity 30

NCBI Description (Z97335) hypothetical protein [Arabidopsis thaliana]

Seq. No. 23382

Contig ID 106086\_1.R1040 5'-most EST wrg700786908.h2

Seq. No. 23383

Contig ID 106097\_1.R1040 5'-most EST rrt700646012.h1

Method BLASTX
NCBI GI g3249064
BLAST score 377
E value 8.0e-42
Match length 131
% identity 71

NCBI Description (AC004473) Strong similarity to trehalose-6-phosphate

synthase homolog  $gb_2245136$  from A. thaliana chromosome 4

contig gb Z97344. [Arabidopsis thaliana]

Seq. No. 23384

Contig ID 106130\_1.R1040 5'-most EST uC-gmropic072h11b1

Method BLASTX
NCBI GI g3548802
BLAST score 378
E value 3.0e-36
Match length 178
% identity 45

NCBI Description (AC005313) axi 1-like protein [Arabidopsis thaliana]

>gi\_4335769\_gb\_AAD17446\_ (AC006284) putative axi1 protein

[Nicotiana tabacum] [Arabidopsis thaliana]

Seq. No. 23385



Contig ID 106140 1.R1040 5'-most EST hrw701060269.h1 Method BLASTX

Method BLASTX
NCBI GI g3319884
BLAST score 244
E value 6.0e-21
Match length 65
% identity 32

NCBI Description (AJ224306) PRT1 [Arabidopsis thaliana]

>gi 3319886 emb CAA11892 (AJ224307) PRT1 [Arabidopsis

thaliana]

Seq. No. 23386

Contig ID 106156\_1.R1040 5'-most EST trc700562244.h1

Method BLASTX
NCBI GI g3249064
BLAST score 172
E value 4.0e-12
Match length 53
% identity 64

NCBI Description (AC004473) Strong similarity to trehalose-6-phosphate

synthase homolog gb\_2245136 from A. thaliana chromosome 4

contig gb\_Z97344. [Arabidopsis thaliana]

Seq. No. 23387

Contig ID 106169\_1.R1040 5'-most EST trc700562262.h1

Method BLASTX
NCBI GI g3249070
BLAST score 228
E value 5.0e-19
Match length 102
% identity 59

NCBI Description (AC004473) Contains similarity to siah binding protein 1

(SiahBP1) gb\_U51586 from Homo sapiens. ESTs gb\_T43314, gb\_T43315 and gb\_R90521, gb\_T75905 [Arabidopsis thaliana]

Seq. No. 23388

Contig ID 106170\_1.R1040 5'-most EST trc700562268.h1

Seq. No. 23389

Contig ID 106173\_1.R1040 5'-most EST bth700846064.h1

Method BLASTX
NCBI GI g4263791
BLAST score 197
E value 6.0e-15
Match length 65
% identity 55

NCBI Description (AC006068) putative receptor protein kinase [Arabidopsis

thaliana]

Seq. No. 23390

Contig ID 106173\_2.R1040 5'-most EST xzm700763885.h1



Seq. No. 23391

Contig ID 106193\_1.R1040 5'-most EST trc700562290.h1

Method BLASTX
NCBI GI g3169059
BLAST score 477
E value 5.0e-48
Match length 146
% identity 66

NCBI Description (AL023704) weak similarity to B.subtilis spore outgrowth

factor B [Schizosaccharomyces pombe]

Seq. No. 23392

Contig ID 106230\_1.R1040 5'-most EST leu701153172.h1

Seq. No. 23393

Contig ID 106245\_1.R1040

5'-most EST  $g56769\overline{0}0$ 

Seq. No. 23394

Contig ID 106257\_2.R1040 5'-most EST hrw701059688.h1

Method BLASTX
NCBI GI g3924597
BLAST score 143
E value 5.0e-09
Match length 61

% identity 46

NCBI Description (AF069442) putative oxidoreductase [Arabidopsis thaliana]

Seq. No. 23395

Contig ID 106266\_1.R1040 5'-most EST trc700562644.h1

Seq. No. 23396

Contig ID 106270\_1.R1040 5'-most EST trc700562426.h1

Seq. No. 23397

Contig ID 106276\_1.R1040

5'-most EST jC-gmf102220073c09a1

Method BLASTX
NCBI GI g4510395
BLAST score 168
E value 2.0e-11
Match length 56
% identity 61

NCBI Description (AC006587) putative beta-galactosidase precursor

[Arabidopsis thaliana]

Seq. No. 23398

Contig ID 106280\_1.R1040 5'-most EST rlr700898360.h1

Method BLASTX NCBI GI g2623199



```
765
BLAST score
                   2.0e-81
E value
Match length
                   153
% identity
                   91
```

(AF030290) protein phosphatase X isoform 2 [Arabidopsis NCBI Description

thaliana]

23399 Seq. No.

Contig ID 106283 1.R1040

5'-most EST g5342400 Method BLASTX NCBI GI g3559816 BLAST score 642 E value 4.0e-67 Match length 194 % identity 62

NCBI Description (Y15782) transketolase 2 [Capsicum annuum]

Seq. No.

23400

Contig ID 106289 1.R1040 5'-most EST jC-gmle01810033d01d1

Seq. No. 23401

Contig ID 106291 1.R1040 5'-most EST jex700909815.hl

Method BLASTN NCBI GI g22379 BLAST score 48 E value 5.0e-18 Match length 133 % identity 88

NCBI Description Z.mays mRNA for CAAT-box DNA binding protein subunit B

(NF-YB)

Seq. No.

23402

106306 1.R1040 Contig ID

5'-most EST g4405724 Method BLASTX NCBI GI g3513727 BLAST score 508 E value 1.0e-51 Match length 163 % identity 61

NCBI Description (AF080118) contains similarity to TPR domains (Pfam:

TPR.hmm: score: 11.15) and kinesin motor domains (Pfam: kinesin2.hmm, score: 17.49, 20.52 and 10.94) [Arabidopsis thaliana] >gi\_4539358 emb\_CAB40052.1\_ (AL049525) putative

protein [Arabidopsis thaliana]

Seq. No. 23403

Contig ID 106317 1.R1040 5'-most EST wrg700787054.h2

Method BLASTX NCBI GI g1871187 BLAST score 189 E value 7.0e-14 Match length 74



% identity 61

NCBI Description (U90439) unknown protein [Arabidopsis thaliana]

Seq. No.

23404

Contig ID 5'-most EST

106319\_1.R1040 vzy700754560.h1

Seq. No.

23405

Contig ID 5'-most EST

106324\_1.R1040 trc700562575.h1

Seq. No.

23406

Contig ID 5'-most EST

106327\_1.R1040 trc700562580.h1

Method NCBI GI BLASTX g535454

BLAST score E value 453 5.0e-45

Match length % identity

123 65

NCBI Description

(U13940) cysteine proteinase [Alnus glutinosa]

Seq. No.

23407

Contig ID 5'-most EST

106329\_1.R1040 trc700562583.h1

Method

BLASTX

NCBI GI

g3927830

BLAST score

327 1.0e-30

E value Match length

1.0e-30

Match length % identity 112 28

% identity

NCBI Description (AC005727) hypothetical protein [Arabidopsis thaliana]

Seq. No.

23408

Contig ID

106342 1.R1040

5'-most EST

trc700562608.hl

Seq. No.

23409

Contig ID

106348\_1.R1040

5'-most EST

ncj700975290.h1

Method

BLASTX

NCBI GI

g3128210

BLAST score

279

E value

2.0e-28

Match length

126

% identity
NCBI Description

62 (AC004077) putative cytochrome P450 protein [Arabidopsis

thaliana] >gi\_3337378 (AC004481) putative cytochrome P450 protein [Arabidopsis thaliana]

Seq. No.

23410

Contig ID 5'-most EST

106351\_1.R1040

Method

leu701153538.h1

NCBI GI

BLASTX

BLAST score

g2146732

730

E value

2.0e-77



Match length 192 % identity 31

NCBI Description FK506-binding protein - Arabidopsis thaliana >gi\_1373396

(U57838) rof1 [Arabidopsis thaliana]

Seq. No. 23411

Contig ID 106404\_1.R1040 5'-most EST sat701008864.h1

Seq. No. 23412

Contig ID 106405\_1.R1040 5'-most EST trc700562744.h1

Seq. No. 23413

Contig ID 106411\_1.R1040 5'-most EST hrw701062918.h1

Method BLASTX
NCBI GI 94204285
BLAST score 348
E value 8.0e-33
Match length 142
% identity 54

NCBI Description (AC003027) lcl prt seq No definition line found

[Arabidopsis thaliana]

Seq. No. 23414

Contig ID 106414 1.R1040 5'-most EST seb700651545.h1

Method BLASTX
NCBI GI g3236238
BLAST score 521
E value 1.0e-52
Match length 248
% identity 52

NCBI Description (AC004684) putative ARF1 GTPase activating protein

[Arabidopsis thaliana] >gi 4519792 dbj BAA75744.1

(AB017876) Asp1 [Arabidopsis thaliana]

Seg. No. 23415

Contig ID 106414\_4.R1040 5'-most EST zsg701130171.h1

Seq. No. 23416

Contig ID 106423 1.R1040

5'-most EST uC-gmrominsoy079f03b1

Method BLASTX
NCBI GI g3894168
BLAST score 259
E value 4.0e-22
Match length 139
% identity 40

NCBI Description (AC005312) similar to phloem-specific lectin [Arabidopsis

thaliana]

Seq. No. 23417

Contig ID 106429 1.R1040 5'-most EST xpa700795217.h1



Seq. No. 23418 Contig ID 106429\_2.R1040

5'-most EST uC-gmrominsoy127f04b1

Seq. No. 23419

Contig ID 106435\_1.R1040 5'-most EST jC-gmro02910013c11d1

Seq. No. 23420

Contig ID 106437 1.R1040

5'-most EST uC-gmrominsoy276h02b1

Method BLASTX
NCBI GI g576509
BLAST score 441
E value 2.0e-43
Match length 240
% identity 40

NCBI Description (L36857) GTP-binding protein [Pisum sativum]

Seq. No. 23421

Contig ID 106444\_1.R1040 5'-most EST pxt700943655.h1

Method BLASTN
NCBI GI g310577
BLAST score 183
E value 3.0e-98
Match length 395
% identity 87

NCBI Description Glycine max nodulin-26 mRNA, complete cds

Seq. No. 23422

Contig ID 106458 1.R1040 5'-most EST trc700562826.h1

Method BLASTX
NCBI GI g4063744
BLAST score 141
E value 6.0e-09
Match length 62
% identity 47

NCBI Description (AC005851) hypothetical protein [Arabidopsis thaliana]

Seq. No. 23423

Contig ID 106472 1.R1040 5'-most EST trc700562848.h1

Seq. No. 23424

Contig ID 106490\_1.R1040 5'-most EST sat701003446.h1

Method BLASTX
NCBI GI 94309730
BLAST score 280
E value 8.0e-25
Match length 90
% identity 58

NCBI Description (AC006439) putative lipid transfer protein [Arabidopsis

thaliana]



```
Seq. No.
                  23425
Contig ID
                  106496 1.R1040
5'-most EST
                  zzp700832018.h1
Seq. No.
                  23426
                  106500 1.R1040
Contig ID
5'-most EST
                  trc700562884.h1
                  23427
Seq. No.
Contig ID
                  106501 1.R1040
```

5'-most EST sat701002748.h2
Method BLASTX
NCBI GI g2832660
BLAST score 286
E value 1.0e-30
Match length 132

% identity 58
NCBI Description (AL021710) lipase-like protein [Arabidopsis thaliana]

 Seq. No.
 23428

 Contig ID
 106512\_1.R1040

 5'-most EST
 trc700562909.h1

 Method
 BLASTX

 NCBI GI
 g3250675

NCBI GI g3250675 BLAST score 519 E value 1.0e-52 Match length 197 % identity 54

NCBI Description (AL024486) putative protein [Arabidopsis thaliana]

Seq. No. 23429

Contig ID 106522\_1.R1040 5'-most EST g5509495

Seq. No. 23430

Contig ID 106522 2.R1040 5'-most EST g4277022

Seq. No. 23431

Contig ID 106522\_3.R1040 5'-most EST g5607169

Seq. No. 23432

Contig ID 106522\_4.R1040 5'-most EST sat701012252.h1 Method BLASTX

NCBI GI g4249384
BLAST score 335
E value 2.0e-31
Match length 126
% identity 47

NCBI Description (AC005966) Similar to gi\_4056506 F3G5.25 nodulin-like

protein from Arabidopsis thaliana BAC gb\_AC005896.

[Arabidopsis thaliana]

Seq. No. 23433



```
106530 1.R1040
Contig ID
5'-most EST
                  uC-gmflminsoy057e10b1
Method
                  BLASTX
NCBI GI
                  g2618698
BLAST score
                  375
E value
                  1.0e-36
Match length
                  143
                  57
% identity
                  (AC002510) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  23434
Contig ID
                  106537 1.R1040
5'-most EST
                  trc700562942.hl
Method
                  BLASTX
NCBI GI
                  g1737490
BLAST score
                  275
E value
                  2.0e-24
Match length
                  102
% identity
                  46
NCBI Description
                  (U81006) p76 [Homo sapiens]
                  23435
Seq. No.
Contig ID
                  106572 1.R1040
5'-most EST
                  bth700848328.hl
                  23436
Seq. No.
Contig ID
                  106581 1.R1040
5'-most EST
                  uC-gmrominsoy071a11b1
Method
                  BLASTX
                  g4580464
NCBI GI
BLAST score
                  167
E value
                  2.0e-11
Match length
                  144
                  45
% identity
NCBI Description
                  (AC006081) unknown protein [Arabidopsis thaliana]
                  23437
Seq. No.
Contig ID
                  106585 1.R1040
5'-most EST
                  leu701156439.h1
Seq. No.
                  23438
Contig ID
                  106592 1.R1040
5'-most EST
                  trc700563022.h1
Method
                  BLASTX
                  g3805964
NCBI GI
BLAST score
                  505
E value
                  5.0e-51
Match length
                  106
% identity
```

NCBI Description (Y13773) laccase [Populus balsamifera subsp. trichocarpa]

Seq. No. 23439

106594 1.R1040 Contig ID 5'-most EST zhf700959895.hl Method

BLASTN NCBI GI g2330650 BLAST score 108



E value 1.0e-53 Match length 459 % identity 59

NCBI Description Pisum sativum mRNA for topoisomerase II

Seq. No. 23440

Contig ID 106595\_1.R1040 5'-most EST trc700563026.h1

Method BLASTX
NCBI GI g2213601
BLAST score 168
E value 9.0e-12
Match length 127
% identity 36

NCBI Description (AC000348) T7N9.21 [Arabidopsis thaliana]

Seq. No. 23441

Contig ID 106608\_1.R1040 5'-most EST trc700563046.h1

Seq. No. 23442

Contig ID 106610 1.R1040 5'-most EST gsv701054916.h1

Seq. No. 23443

Contig ID 106614\_1.R1040 5'-most EST dpv701099569.h1

Method BLASTX
NCBI GI g4455287
BLAST score 404
E value 5.0e-39
Match length 140
% identity 56

NCBI Description (AL035527) putative protein [Arabidopsis thaliana]

Seq. No. 23444

Contig ID 106619\_1.R1040 5'~most EST trc700563063.h1

Method BLASTN
NCBI GI g1885382
BLAST score 117
E value 4.0e-59
Match length 349
% identity 83

NCBI Description Arabidopsis thaliana phospholipase D (PLDbeta) mRNA,

complete cds

Seq. No. 23445

Contig ID 106626\_1.R1040 5'-most EST trc700563074.h1

Method BLASTX
NCBI GI g4454050
BLAST score 396
E value 4.0e-38
Match length 188
% identity 44

NCBI Description (AL035394) putative protein [Arabidopsis thaliana]

E value

Match length

NCBI Description

% identity

6.0e-27

(U43082) RF2 [Zea mays]

95

58

```
23446
Seq. No.
                  106626_2.R1040
Contig ID
                  xpa700794665.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4454050
BLAST score
                  120
E value
                  3.0e-12
Match length
                  50
                  74
% identity
                  (AL035394) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  23447
                  106641 1.R1040
Contig ID
5'-most EST
                  trc700563094.h1
Method
                  BLASTX
                  q4490756
NCBI GI
BLAST score
                   406
E value
                  2.0e-39
                  156
Match length
% identity
                  54
                  (AL035708) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   23448
                  106660 1.R1040
Contig ID
5'-most EST
                   trc700563124.h1
Method
                  BLASTX
NCBI GI
                   g2911080
BLAST score
                   164
E value
                   3.0e-11
                   138
Match length
                   26
% identity
NCBI Description
                   (AL021960) receptor kinase - like protein [Arabidopsis
                  thaliana]
Seq. No.
                   23449
                   106665 1.R1040
Contig ID
5'-most EST
                   sat701012474.h1
Method
                   BLASTX
NCBI GI
                   g1166450
BLAST score
                   366
E value
                   6.0e-35
Match length
                   81
                   80
% identity
NCBI Description
                   (X95262) Tfm5 [Lycopersicon esculentum]
Seq. No.
                   23450
                   106667 1.R1040
Contig ID
5'-most EST
                  leu701151261.h1
Method
                  BLASTX
NCBI GI
                   g1421730
BLAST score
                   298
```



Seq. No. 23451 106667 2.R1040 Contig ID trc700564801.hl 5'-most EST Method BLASTX NCBI GI g1743354 BLAST score 163 2.0e-11 E value 52 Match length 62 % identity NCBI Description (Y09876) aldehyde dehydrogenase (NAD+) [Nicotiana tabacum] 23452 Seq. No. 106682 1.R1040 Contig ID art700605355.h2 5'-most EST Seq. No. 23453 106685 1.R1040 Contig ID crh700851695.h15'-most EST Method BLASTN g3402278 NCBI GI BLAST score 49 E value 2.0e-18 Match length 101 % identity 87 Solanum tuberosum mRNA for putative beta-subunit of K+ NCBI Description channel Seq. No. 23454 106685 2.R1040 Contig ID 5'-most EST trc700563359.hl Seq. No. 23455 106688 1.R1040 Contig ID 5'-most EST uC-gmropic061a11b1 Method BLASTX NCBI GI q3721540 BLAST score 446 E value 4.0e-44 Match length 155 % identity 63 (D83583) Sulfite Reductase [Nicotiana tabacum] NCBI Description >gi 3738234 dbj BAA33796 (AB010717) sulfite reductase [Nicotiana tabacum] 23456 Seq. No. 106688 2.R1040 Contig ID

5'-most EST rry700808444.hl

Seq. No. 23457

106695 1.R1040 Contig ID 5'-most EST crh700851773.hl

Method BLASTX NCBI GI g1723761 BLAST score 250 E value 1.0e-21 Match length 97 % identity 48



NCBI Description HYPOTHETICAL 86.6 KD PROTEIN IN PFK1-TDS4 INTERGENIC REGION >gi\_2132628\_pir\_\_S64571 probable membrane protein YGR245c -

yeast (Saccharomyces cerevisiae) >gi\_1323444\_emb\_CAA97274\_

(Z73030) ORF YGR245c [Saccharomyces cerevisiae] >gi\_1702955\_emb\_CAA68967\_ (Y07703) unknown ORF

[Saccharomyces cerevisiae]

Seq. No. 23458

Contig ID 106714\_1.R1040 5'-most EST pxt700943072.h1

Seq. No. 23459

Contig ID 106738\_1.R1040 5'-most EST trc700567566.h1

Method BLASTX
NCBI GI g1184075
BLAST score 268
E value 1.0e-23
Match length 125
% identity 2

NCBI Description (U42444) Cf-2.1 [Lycopersicon pimpinellifolium]

>gi\_1587673\_prf\_\_2207203A Cf-2 gene [Lycopersicon

esculentum]

Seq. No. 23460

Contig ID 106739\_1.R1040

5'-most EST uC-gmrominsoy030h10b1

Method BLASTX
NCBI GI g2245005
BLAST score 665
E value 1.0e-69
Match length 191
% identity 34

NCBI Description (Z97341) hypothetical protein [Arabidopsis thaliana]

Seq. No. 23461

Contig ID 106752 1.R1040 5'-most EST trc700563287.h1

Seq. No. 23462

Contig ID 106757 1.R1040

5'-most EST jC-gmst02400051c08d1

Seq. No. 23463

Contig ID 106757\_2.R1040

5'-most EST jC-gmst02400061b12d1

Seq. No. 23464

Contig ID 106808\_1.R1040 5'-most EST trc700563375.h1

Method BLASTN
NCBI GI g4388705
BLAST score 33
E value 4.0e-09
Match length 37
% identity 97

NCBI Description Arabidopsis thaliana chromosome I BAC F20D21 genomic



## sequence, complete sequence [Arabidopsis thaliana]

23465 Seq. No. Contig ID 106809 1.R1040 5'-most EST asn701136011.hl Method BLASTX NCBI GI q2367431 BLAST score 128 E value 2.0e-16 Match length 57 79 % identity NCBI Description (AF000403) putative cytochrome P450 [Lotus japonicus] Seq. No. 23466 106810 1.R1040 Contig ID 5'-most EST zvj700605184.h2 Method BLASTX NCBI GI q3850568 BLAST score 456 E value 9.0e-46 Match length 106 % identity 83 (AC005278) Similar to hypothetical protein SPAC2F7.14c NCBI Description gi 1052797 from Schizosaccharomyces pombe cosmid gb Z50142. [Arabidopsis thaliana] Seq. No. 23467 Contig ID 106819 1.R1040 5'-most EST trc700563391.h1 Method BLASTX NCBI GI g1705765 BLAST score 161 E value 5.0e-11 87 Match length 43 % identity NCBI Description CFXQ PROTEIN HOMOLOG >qi 2147549 pir S73149 hypothetical protein 301 - Porphyra purpurea chloroplast >gi 1276694 (U38804) ORF301 [Porphyra purpurea] Seq. No. 23468 106838 1.R1040 Contig ID 5'-most EST trc700563433.h1 Method BLASTX

Method BLASTX
NCBI GI 94538905
BLAST score 464
E value 1.0e-46
Match length 101
% identity 82

NCBI Description (AL049482) putative protein [Arabidopsis thaliana]

Seq. No. 23469

Contig ID 106853\_1.R1040 5'-most EST kl1701206721.h1

Method BLASTX
NCBI GI g2935525
BLAST score 482
E value 1.0e-48



Match length 134 % identity 66

NCBI Description (AF049067) cytochrome P450 [Pinus radiata]

Seq. No.

23470

Contig ID 5'-most EST 106866\_1.R1040 trc700563485.h1

Seq. No.

23471

Contig ID 5'-most EST

106873\_1.R1040 trc700563502.h1

Method NCBI GI BLAST score BLASTX g3249072 166

E value Match length 1.0e-11 75

% identity

44

NCBI Description

(AC004473) Contains similarity to hypothetical 43.1 KD protein in NDK-GCPE intergenic region gb 493519 from E.

coli sequence gb U02965. [Arabidopsis thaliana]

Seq. No.

23472

Contig ID 5'-most EST 106884\_1.R1040 sat701008501.h1

Method NCBI GI BLASTX g4220461 158

BLAST score E value Match length

2.0e-10 95

% identity
NCBI Description

41 (AC006216) ESTs gb\_T75642 and gb\_AA650997 come from this gene. [Arabidopsis thaliana]

Seq. No. 23473

Contig ID 5'-most EST

106889\_1.R1040 trc700563521.h1

Seq. No.

23474

Contig ID 5'-most EST

106894\_1.R1040 trc700563526.h1

Seq. No.

23475

Contig ID

106898 1.R1040

5'-most EST

jC-gmf102220112g09d1

Method NCBI GI BLASTX g4510395

NCBI GI BLAST score g4510395 663

E value

1.0e-86

Match length % identity

190 80

NCBI Description

(AC006587) putative beta-galactosidase precursor

[Arabidopsis thaliana]

Seq. No.

23476

Contig ID 5'-most EST

106903\_1.R1040 hyd700728730.h1

Method

BLASTX



NCBI GI g584862 BLAST score 157 E value 1.0e-10 Match length 55 % identity 53

NCBI Description CYTOCHROME P450 71A3 (CYPLXXIA3) (P-450EG3)

>gi\_480397\_pir\_\_S36807 cytochrome P450 71A3 - eggplant

(fragment) >gi 408142 emb CAA50313 (X70982) P450

hydroxylase [Solanum melongena]

Seq. No. 23477

Contig ID 106921\_1.R1040 5'-most EST trc700563566.h1

Seq. No. 23478

Contig ID 106924\_1.R1040 5'-most EST xpa700793071.h1

Seq. No. 23479

Contig ID 106925 1.R1040 5'-most EST trc700563571.h1

Seq. No. 23480

Contig ID 106931\_1.R1040 5'-most EST epx701105435.h1

Seq. No. 23481

Contig ID 106936\_1.R1040

5'-most EST jC-gmf\(\bar{1}\)02220103c05d1

Seq. No. 23482

Contig ID 106953 1.R1040 5'-most EST rca700999864.h1

Method BLASTX
NCBI GI g1669593
BLAST score 152
E value 9.0e-10
Match length 86
% identity 42

NCBI Description (D88743) AR781 [Arabidopsis thaliana]

Seq. No. 23483

Contig ID 106961 1.R1040 5'-most EST pxt700942721.h1

Method BLASTX
NCBI GI g4580396
BLAST score 247
E value 1.0e-20
Match length 71
% identity 63

NCBI Description (AC007171) hypothetical protein [Arabidopsis thaliana]

Seq. No. 23484

Contig ID 106961 2.R1040 5'-most EST leu701157342.h1

Seq. No. 23485

3731

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Contig ID
                  106964 1.R1040
5'-most EST
                  trc700563624.h1
Method
                  BLASTX
NCBI GI
                  g2443357
BLAST score
                  401
                  4.0e-39
E value
Match length
                  98
                  76
% identity
                  (AB004293) SigB [Arabidopsis thaliana]
NCBI Description
                  >gi 2597831 emb CAA75584 (Y15362) sigma factor
                  [Arabidopsis thaliana] >gi 2879922 dbj BAA24825 (AB004820)
                  plastid RNA polymerase sigma-subunit [Arabidopsis thaliana]
                  >gi 3063440 (AC003981) F22013.2 [Arabidopsis thaliana]
```

Contig ID 106982\_1.R1040 5'-most EST trc700563646.h1

Seq. No. 23487

Contig ID 106994 1.R1040 5'-most EST trc700563662.h1

Method BLASTX
NCBI GI g2980641
BLAST score 587
E value 1.0e-60
Match length 132
% identity 50

NCBI Description (Y11250) multi resistance protein [Arabidopsis thaliana]

Seq. No. 23488

Contig ID 107019 1.R1040 5'-most EST jC-gmfl02220081e07a1

Seq. No. 23489

Contig ID 107024 1.R1040 5'-most EST dpv701096940.h1

Method BLASTX
NCBI GI g1786134
BLAST score 152
E value 3.0e-10
Match length 68
% identity 54

NCBI Description (AB000451) PEThy; ZPT2-5 [Petunia x hybrida]

Seq. No. 23490

Contig ID 107025\_1.R1040 5'-most EST trc700567190.h1

Seq. No. 23491

Contig ID 107030\_1.R1040 5'-most EST trc700563716.h1

Method BLASTX
NCBI GI g3582333
BLAST score 332
E value 1.0e-30
Match length 203
% identity 34



NCBI Description (AC005496) hypothetical protein [Arabidopsis thaliana]

Seq. No. 23492

Contig ID 107035\_1.R1040 5'-most EST gsv701054350.h1

Method BLASTX
NCBI GI g2465923
BLAST score 230
E value 2.0e-19
Match length 72
% identity 61

NCBI Description (AF024648) receptor-like serine/threonine kinase

[Arabidopsis thaliana]

Seq. No. 23493

Contig ID 107039\_1.R1040 5'-most EST fua701037449.h1

Seq. No. 23494

Contig ID 107040\_1.R1040 5'-most EST trc700565059.h1

Method BLASTX
NCBI GI g2842493
BLAST score 299
E value 4.0e-32
Match length 89
% identity 79

NCBI Description (AL021749) predicted protein [Arabidopsis thaliana]

Seq. No. 23495

Contig ID 107046 1.R1040 5'-most EST rca700999589.h1

Seq. No. 23496

Contig ID 107046\_3.R1040 5'-most EST dpv701102788.h1

Seq. No. 23497

Contig ID 107048\_1.R1040 5'-most EST zzp700832249.h1

Method BLASTX
NCBI GI g1001252
BLAST score 316
E value 1.0e-28
Match length 285
% identity 31

NCBI Description (D64003) cytochrome P450 [Synechocystis sp.]

Seq. No. 23498

Contig ID 107055\_1.R1040 5'-most EST trc700563760.h1

Method BLASTX
NCBI GI g3024362
BLAST score 573
E value 4.0e-59
Match length 128
% identity 85

3733

NCBI Description PHENYLALANINE AMMONIA-LYASE G2B >gi\_2118317\_pir\_\_S60042 phenylalanine ammonia-lyase (EC 4.3.1.5) 2b - Japanese aspen x large-toothed aspen >gi\_1109641 dbj\_BAA07860

(D43802) phenylalanine ammonia-lyase [Populus

kitakamiensis]

Seq. No. 23499

Contig ID 107065\_1.R1040 5'-most EST trc700563779.h1

Seq. No. 23500

Contig ID 107070\_1.R1040 5'-most EST gsv701050605.h1

Method BLASTX
NCBI GI g2213922
BLAST score 167
E value 2.0e-11
Match length 80
% identity 44

NCBI Description (AF005043) poly(ADP-ribose) glycohydrolase [Homo sapiens]

>gi\_4505609\_ref\_NP\_003622.1\_pPARG\_ poly (ADP-ribose)

glycohydrolase

Seq. No. 23501

Contig ID 107078\_1.R1040 5'-most EST trc700563802.h1

Seq. No. 23502

Contig ID 107085\_1.R1040 5'-most EST fua701039428.h1

Method BLASTX
NCBI GI g3249068
BLAST score 208
E value 4.0e-21
Match length 152
% identity 43

NCBI Description (AC004473) Contains similarity to zinc-binding protein

(PWA33) gb\_L04190 from Pleurodeles waltlii. [Arabidopsis

thaliana]

Seq. No. 23503

Contig ID 107097\_1.R1040 5'-most EST jsh701065258.h1

Seq. No. 23504

Contig ID 107106 1.R1040

5'-most EST uC-gmrominsoy055a05b1

Method BLASTX
NCBI GI 9728905
BLAST score 244
E value 7.0e-21
Match length 80
% identity 57

NCBI Description PROBABLE CALCIUM-TRANSPORTING ATPASE 3 (ENDOPLASMIC

RETICULUM CA2+-ATPASE) >gi\_1078206\_pir\_\_S51995 probable ATPase (EC 3.6.1.-) DRS2 - yeast (Saccharomyces cerevisiae)

>gi 171114 (L01795) ATPase [Saccharomyces cerevisiae]



>gi 595560 (U12980) Drs2p: Membrane spanning Ca-ATPase(P-type), member of the cation transport(E1-E2) ATPase [Saccharomyces cerevisiae]

23505 Seq. No. 107107 1.R1040 Contig ID 5'-most EST fC-gmro700563838f2 Method BLASTX NCBI GI g4262167 BLAST score 371 E value 2.0e-39 Match length 140 % identity 62 NCBI Description (AC005275) putative LRR receptor-linked protein kinase [Arabidopsis thaliana]

23506 Seq. No. 107113 1.R1040 Contig ID 5'-most EST uC-gmropic068g01b1 Method BLASTX

g4539389 NCBI GI 446 BLAST score E value 7.0e-44 Match length 125 % identity 71

NCBI Description (AL035526) putative protein kinase [Arabidopsis thaliana]

Seq. No. 23507 Contig ID

107166 1.R1040 5'-most EST hrw701058009.h1

Seq. No. 23508

107168 1.R1040 Contig ID 5'-most EST rca700999741.hl

Method BLASTX NCBI GI g2842490 BLAST score 589 9.0e-61 E value Match length 199 47 % identity

NCBI Description (AL021749) heat-shock protein [Arabidopsis thaliana]

Seq. No. 23509

Contig ID 107174 1.R1040 5'-most EST trc700563948.hl

Method BLASTX NCBI GI q4539335 BLAST score 530 E value 5.0e-54152 Match length % identity

NCBI Description (AL035539) putative protein [Arabidopsis thaliana]

Seq. No. 23510

Contig ID 107177 1.R1040 fC-gmf1700904718f4 5'-most EST



Seq. No. 23512

Contig ID 107195 1.R1040 5'-most EST trc700563989.h1

Method BLASTX
NCBI GI g2909781
BLAST score 372
E value 6.0e-36
Match length 98
% identity 78

NCBI Description (AF020288) MgATP-energized glutathione S-conjugate pump

[Arabidopsis thaliana]

Seq. No. 23513

Contig ID 107197 1.R1040 5'-most EST trc700563994.h1

Method BLASTX
NCBI GI g1946361
BLAST score 254
E value 9.0e-22
Match length 80
% identity 61

NCBI Description (U93215) C3HC4 zinc finger protein isolog [Arabidopsis

thaliana]

Seq. No. 23514

Contig ID 107198 1.R1040 5'-most EST trc700563995.h1

Method BLASTX
NCBI GI g2245020
BLAST score 361
E value 2.0e-34
Match length 86
% identity 83

NCBI Description (Z97341) growth regulator homolog [Arabidopsis thaliana]

Seq. No. 23515

Contig ID 107202\_1.R1040 5'-most EST jC-gmle01810092f09d1

Seq. No. 23516

Contig ID 107208\_1.R1040 5'-most EST pmv700890185.h1

Method BLASTX
NCBI GI g3738297
BLAST score 231
E value 1.0e-38
Match length 145
% identity 42

NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]

Seq. No. 23517

Contig ID 107214 1.R1040 5'-most EST smc700745982.h1



Method BLASTX
NCBI GI g100226
BLAST score 298
E value 5.0e-27
Match length 145
% identity 42

NCBI Description hypothetical protein - tomato >gi\_19275\_emb\_CAA78112\_ (Z12127) protein of unknown function [Lycopersicon esculentum] >gi 445619 prf 1909366A Leu zipper protein

[Lycopersicon esculentum]

Seq. No. 23518

Contig ID 107218\_1.R1040 5'-most EST fC-gmse700832291d1

Seq. No. 23519

Contig ID 107227 1.R1040

5'-most EST jC-gmle01810084e06a1

Seq. No. 23520

Contig ID 107231\_1.R1040 5'-most EST trc700566250.h1

Method BLASTX
NCBI GI g3746060
BLAST score 147
E value 1.0e-09
Match length 30
% identity 83

NCBI Description (AC005311) unknown protein [Arabidopsis thaliana]

Seq. No. 23521

Contig ID 107231 2.R1040 5'-most EST gsv701056479.h1

Method BLASTX
NCBI GI g3746060
BLAST score 210
E value 6.0e-17
Match length 50
% identity 78

NCBI Description (AC005311) unknown protein [Arabidopsis thaliana]

Seq. No. 23522

Contig ID 107240\_1.R1040 5'-most EST leu701147445.h1

Seq. No. 23523

Contig ID 107240\_2.R1040 5'-most EST trc700564071.h1

Seq. No. 23524

Contig ID 107243 1.R1040 5'-most EST trc700564076.h1

Seq. No. 23525

Contig ID 107244\_1.R1040 5'-most EST zsg701122126.h1

Method BLASTX

```
NCBI GI g3600036
BLAST score 308
E value 1.0e-27
Match length 142
% identity 53
```

NCBI Description (AF080119) contains similarity to protein kinase domains (Pfam: pkinase.hmm, score: 227.04) [Arabidopsis thaliana]

Seq. No. 23526

Contig ID 107245\_1.R1040 5'-most EST trc700564079.h1

Seq. No. 23527

Contig ID 107256\_1.R1040 5'-most EST eep700865724.h1

Seq. No. 23528

Contig ID 107256\_2.R1040

5'-most EST uC-gmrominsoy048a08b1

Seq. No. 23529

Contig ID 107284 1.R1040 5'-most EST trc700564160.h1

Seq. No. 23530

Contig ID 107293\_1.R1040 5'-most EST trc700564896.h1

Method BLASTX
NCBI GI g3193296
BLAST score 318
E value 1.0e-29
Match length 98
% identity 62

NCBI Description (AF069298) similar to pectinesterase [Arabidopsis thaliana]

Seq. No. 23531

Contig ID 107319\_1.R1040 5'-most EST trc700564230.h1

Seq. No. 23532

Contig ID 107334\_1.R1040 5'-most EST jC-gmst02400027c09a1

Method BLASTX
NCBI GI g1168217
BLAST score 202
E value 1.0e-15

Match length 98 % identity 43

NCBI Description DNA-3-METHYLADENINE GLYCOSIDASE (3-METHYLADENINE-DNA

GLYCOSYLASE) (TAG) >gi\_1074039\_pir\_\_G64084

DNA-3-methyladenine glycosidase I (tagI) homolog - Haemophilus influenzae (strain Rd KW20) >gi\_1573653 (U32748) DNA-3-methyladenine glycosidase I (tagI)

[Haemophilus influenzae Rd]

Seq. No. 23533

Contig ID 107347\_1.R1040



5'-most EST pcp700993884.h1 Method BLASTX g98837 NCBI GI BLAST score 108 E value 7.0e-09 Match length 90 % identity 41 NCBI Description enantiomer-selective amidase - Rhodococcus sp >gi\_152052 (M74531) enantiomerase-selective amidase [Rhodococcus sp.] Seq. No. 23534 Contig ID 107377 2.R1040 5'-most EST trc700564401.h1 Seq. No. 23535 Contig ID 107391 1.R1040 5'-most EST trc700564472.h1 Method BLASTX NCBI GI g2982458 BLAST score 492 2.0e-49 E value Match length 110 86 % identity NCBI Description (AL022223) putative protein [Arabidopsis thaliana] Seq. No. 23536 107392 1.R1040 Contig ID 5'-most EST pxt700943624.h1 Seq. No. 23537 107402 1.R1040 Contig ID 5'-most EST rlr700901302.h1 Seq. No. 23538 107417 1.R1040 Contig ID 5'-most EST gsv701049292.h1 Method BLASTX NCBI GI g2204236 BLAST score 463 E value 5.0e-46 Match length 158 % identity 61 (Y13861) enoyl-ACP reductase [Nicotiana tabacum] NCBI Description Seq. No. 23539

107417 2.R1040 Contig ID 5'-most EST fua701038793.h1

Seq. No. 23540

Contig ID 107435 1.R1040 5'-most EST trc700564633.h1

Seq. No. 23541 107467 1.R1040 Contig ID 5'-most EST ncj700980474.h1 Method BLASTX NCBI GI g4160300



BLAST score 3.0e-25 E value Match length 91 % identity 55

NCBI Description (AJ011893) cyclin D3.1 protein [Nicotiana tabacum]

Seq. No. Contig ID 23542 107475 1.R1040

5'-most EST

uC-gmrominsoy173e12b1

Seq. No.

23543

Contig ID

107475 2.R1040

5'-most EST

uC-gmrominsoy241a02b1

Seq. No.

23544

Contig ID

107497 1.R1040

5'-most EST jC-gmf102220143b07a1

Seq. No.

23545

Contig ID 5'-most EST 107497 2.R1040 gsv701053604.h1

Seq. No.

23546

Contig ID 5'-most EST 107498\_1.R1040 trc700564773.h1

BLASTX Method NCBI GI q2832408 BLAST score 400 E value 3.0e-39 Match length 74 95

% identity

NCBI Description (Y14209) R2R3-MYB transcription factor [Arabidopsis

thaliana]

Seq. No.

23547

Contig ID 5'-most EST 107509 1.R1040 rlr700902295.h1

Seq. No.

23548

Contig ID 5'-most EST 107510 1.R1040 crh700853065.h1

Method NCBI GI BLAST score BLASTX g3820531 465

E value Match length

2.0e-46 149

% identity NCBI Description

(AF072736) beta-glucosidase [Pinus contorta]

Seq. No.

23549

58

Contig ID 5'-most EST 107514\_1.R1040 zhf700963410.h1

Method BLASTX NCBI GI q4263722 BLAST score 403 E value 4.0e-52 Match length 127



% identity 79 NCBI Description (AC006223) putative glucan synthase [Arabidopsis thaliana]

Seq. No. 23550

Contig ID 107516\_1.R1040 5'-most EST trc700564810.h1

Method BLASTX
NCBI GI g1174470
BLAST score 592
E value 3.0e-61
Match length 211
% identity 55

NCBI Description OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5)

(INTEGRAL MEMBRANE PROTEIN 1) >gi\_508543 (L34260) integral membrane protein 1 [Mus musculus] >gi\_1588285\_prf\_\_2208301A

integral membrane protein [Mus musculus]

Seq. No. 23551

Contig ID 107517\_1.R1040 5'-most EST trc700564996.h1

Seq. No. 23552

Contig ID 107532\_1.R1040 5'-most EST trc700564857.h1

Seq. No. 23553

Contig ID 107534\_1.R1040 5'-most EST trc700564836.h1

Method BLASTX
NCBI GI g4510398
BLAST score 315
E value 6.0e-29
Match length 64
% identity 92

NCBI Description (AC006587) hypothetical protein [Arabidopsis thaliana]

Seq. No. 23554

Contig ID 107535\_1.R1040

5'-most EST g4304291

Method BLASTX

NCBI GI g4006882

BLAST score 310

E value 2.0e-58

Match length 145
% identity 73

NCBI Description (Z99707) UDP-glucuronyltransferase-like protein

[Arabidopsis thaliana]

Seq. No. 23555

Contig ID 107558\_1.R1040

5'-most EST uC-gmflminsoy080d09b1

Method BLASTX
NCBI GI g4371296
BLAST score 335
E value 2.0e-31
Match length 132
% identity 57



NCBI Description (AC006260) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No. 23556

Contig ID 107566 1.R1040 5'-most EST fua701039635.h1

Method BLASTX
NCBI GI g123178
BLAST score 1822
E value 0.0e+00
Match length 436
% identity 79

NCBI Description HISTIDINOL DEHYDROGENASE, CHLOROPLAST PRECURSOR (HDH) >gi 99844 pir A39358 histidinol dehydrogenase (EC

1.1.1.23) precursor, chloroplast - cabbage >gi 167142 (M60466) histidinol dehydrogenase [Brassica oleracea]

Seq. No. 23557

Contig ID 107571\_1.R1040 5'-most EST trc700564904.h1

Method BLASTX
NCBI GI g1935019
BLAST score 533
E value 2.0e-73
Match length 180
% identity 77

NCBI Description (Z93774) sucrose transport protein [Vicia faba]

Seq. No. 23558

Contig ID 107573\_1.R1040 5'-most EST uC-gmropic014g04b1

Method BLASTX
NCBI GI g3046694
BLAST score 469
E value 1.0e-46
Match length 131
% identity 67

NCBI Description (AL022224) vacuolar sorting receptor-like protein

[Arabidopsis thaliana]

Seq. No. 23559

Contig ID 107573\_2.R1040 5'-most EST trc700564907.h1

Method BLASTX
NCBI GI g2827665
BLAST score 131
E value 1.0e-10
Match length 55
% identity 55

NCBI Description (AL021637) vacuolar sorting receptor-like protein

[Arabidopsis thaliana]

Seq. No. 23560

Contig ID 107577\_1.R1040 5'-most EST trc700564912.h1

Seq. No. 23561



```
Contig ID
                  107580 1.R1040
5'-most EST
                  zhf700959330.h1
                  BLASTX
Method
                  q4539422
NCBI GI
                  157
BLAST score
                  9.0e-11
E value
                  76
Match length
                  43
% identity
NCBI Description (AL049171) putative protein [Arabidopsis thaliana]
                  23562
Seq. No.
                  107584 1.R1040
Contig ID
5'-most EST
                  trc700564921.hl
                  23563
Seq. No.
                  107587 1.R1040
Contig ID
                  trc700564924.h1
5'-most EST
Seq. No.
                  23564
                  107593 1.R1040
Contig ID
                  uC-gmropic039a10b1
5'-most EST
                  23565
Seq. No.
Contig ID
                  107596 1.R1040
                  trc700565555.hl
5'-most EST
                  BLASTX
Method
                  a3047103
NCBI GI
                  215
BLAST score
                  1.0e-17
E value
                   96
Match length
                   53
% identity
NCBI Description (AF058919) regions of weak similarity to 1-asparaginase
                   [Arabidopsis thaliana]
                   23566
Seq. No.
                   107605 1.R1040
Contig ID
5'-most EST
                   zsq701123625.h1
                   23567
Seq. No.
                   107621 1.R1040
Contig ID
                   pmv700889964.h1
5'-most EST
Seq. No.
                   23568
                   107633 1.R1040
Contig ID
                   gsv701046518.hl
5'-most EST
Seq. No.
                   23569
                   107633 2.R1040
 Contig ID
```

fde700873464.h1 5'-most EST

23570 Seq. No.

107638 1.R1040 Contig ID trc700565002.h1 5'-most EST

BLASTX Method g4204284 NCBI GI 361 BLAST score 2.0e-34 E value



Match length 154 % identity 47

NCBI Description (AC003027) lcl\_prt\_seq No definition line found

[Arabidopsis thaliana]

Seq. No. 23571

Contig ID 107649\_1.R1040 5'-most EST trc700565015.h1

Seq. No. 23572

Contig ID 107654\_1.R1040 5'-most EST zhf700959489.h1

Method BLASTX
NCBI GI g3068717
BLAST score 557
E value 7.0e-74
Match length 206
% identity 68

NCBI Description (AF049236) unknown [Arabidopsis thaliana]

Seq. No. 23573

Contig ID 107662\_1.R1040

5'-most EST jC-gmro02910067a07d1

Method BLASTX
NCBI GI g2118017
BLAST score 393
E value 5.0e-38
Match length 100
% identity 70

NCBI Description non-S-RNase (EC 3.1.-.-) - Japanese pear

>gi\_1526417\_dbj\_BAA08475\_ (D49529) ribonuclease [Pyrus

pyrifolia]

Seq. No. 23574

Contig ID 107668\_1.R1040 5'-most EST vzy700755749.h1

Method BLASTX
NCBI GI g1808656
BLAST score 471
E value 2.0e-47
Match length 102
% identity 59

NCBI Description (Y10804) Ubiquitin activating enzyme El [Nicotiana tabacum]

Seq. No. 23575

Contig ID 107675 1.R1040 5'-most EST uxk700667102.h1

Seq. No. 23576

Contig ID 107704\_1.R1040 5'-most EST gsv701047364.h1

Seq. No. 23577

Contig ID 107719\_1.R1040 5'-most EST smc700749093.h1

Method BLASTX NCBI GI g3236241



BLAST score 205 E value 4.0e-16 Match length 51 % identity 76

NCBI Description (AC004684) putative zinc finger protein [Arabidopsis

thaliana]

Seq. No. 23578

Contig ID 107724 1.R1040 5'-most EST trc700565148.h1

Seq. No. 23579

Contig ID 107729\_1.R1040 5'-most EST leu701146972.h1

Seq. No. 23580

Contig ID 107735\_1.R1040 5'-most EST uC-gmronoir026c05b1

Method BLASTX
NCBI GI g3269289
BLAST score 332
E value 5.0e-31
Match length 104
% identity 62

NCBI Description (AL030978) putative protein [Arabidopsis thaliana]

Seq. No. 23581

Contig ID 107741\_1.R1040 5'-most EST uC-gmronoir042b12b1

Seq. No. 23582

Contig ID 107745 1.R1040 5'-most EST trc700565426.h1

Seq. No. 23583

Contig ID 107751\_1.R1040

5'-most EST g5510161

Method BLASTX

NCBI GI g3341684

BLAST score 151

E value 2.0e-11

Match length 93
% identity 46

NCBI Description (AC003672) hypothetical protein [Arabidopsis thaliana]

Seq. No. 23584

Contig ID 107787 1.R1040 5'-most EST ncj700978387.h1

Seq. No. 23585

Contig ID 107793\_1.R1040 5'-most EST trc700565265.h1

Method BLASTX
NCBI GI g3420008
BLAST score 291
E value 4.0e-26
Match length 109



% identity 53
NCBI Description (AF000307) steroid sulfotransferase 3 [Brassica napus]

Seq. No. 23586

Contig ID 107804 1.R1040 5'-most EST trc700565492.h1

Seq. No. 23587

Contig ID 107806\_1.R1040 5'-most EST sat701008756.h1

Seq. No. 23588

Contig ID 107813\_1.R1040 5'-most EST epx701105582.h1

Method BLASTX
NCBI GI g2894558
BLAST score 615
E value 3.0e-64
Match length 142
% identity 87

NCBI Description (AL021890) putative protein [Arabidopsis thaliana]

Seq. No. 23589

Contig ID 107814 2.R1040

5'-most EST uC-gmflminsoy058c10b1

Seq. No. 23590

Contig ID 107816\_1.R1040 5'-most EST trc700565312.h1

Seq. No. 23591

Contig ID 107820\_1.R1040 5'-most EST trc700565316.h1

Seq. No. 23592

Contig ID 107828 1.R1040 5'-most EST trc700565328.h1

Method BLASTX
NCBI GI g3157941
BLAST score 370
E value 3.0e-35
Match length 106
% identity 62

NCBI Description (AC002131) Contains similarity to hypothetical protein

gb\_U95973 from A. thaliana. [Arabidopsis thaliana]

Seq. No. 23593

Contig ID 107848\_1.R1040 5'-most EST eep700864856.h1

Seq. No. 23594

Contig ID 107873\_1.R1040 5'-most EST trc700565413.h1

Seq. No. 23595

Contig ID 107904\_1.R1040

5'-most EST uC-gmflminsoy075a08b1

```
Method
NCBI GI
                  q4262154
BLAST score
                  568
E value
                  3.0e-58
Match length
                  207
% identity
                  58
                  (AC005275) putative protein phosphatase regulatory subunit
NCBI Description
                  [Arabidopsis thaliana]
                  23596
Seq. No.
                  107907 1.R1040
Contig ID
5'-most EST
                  trc700565472.h1
Seq. No.
                  23597
                  107943 1.R1040
Contig ID
5'-most EST
                  sat701014543.h1
                  BLASTN
Method
NCBI GI
                  g1944151
BLAST score
                  327
                  0.0e+00
E value
Match length
                  929
% identity
                  88
NCBI Description Vigna angularis mRNA for ACC-oxidase, complete cds
Seq. No.
                  107946 1.R1040
Contig ID
                  trc700565531.hl
5'-most EST
                  23599
Seq. No.
                  107947 1.R1040
Contig ID
5'-most EST
                  trc700565532.h1
                  23600
Seq. No.
                  107952 1.R1040
Contig ID
5'-most EST
                  zhf700958089.h1
                  23601
Seq. No.
Contig ID
                  107989 1.R1040
5'-most EST
                  awf700839193.hl
Method
                  BLASTX
NCBI GI
                  q4510362
```

 NCBI GI
 g4510362

 BLAST score
 334

 E value
 5.0e-31

 Match length
 144

 % identity
 51

NCBI Description (AC007017) hypothetical protein [Arabidopsis thaliana]

Seq. No. 23602

Contig ID 107997 1.R1040 5'-most EST trc700565605.h1 Method BLASTX

NCBI GI g129749
BLAST score 167
E value 9.0e-12
Match length 90
% identity 39

NCBI Description EXO-POLY-ALPHA-D-GALACTURONOSIDASE PRECURSOR (EXO-PG)



23603

>gi 95579 pir\_ A36715 exo-poly-alpha-galacturonosidase (EC 3.2.1.82) precursor - Erwinia chrysanthemi >gi\_148447 (M31308) exo-poly-alpha-D-galacturonosidase [Erwinia chrysanthemi]

107998 1.R1040 Contig ID uC-gmflminsoy075h09b1 5'-most EST BLASTX Method q4220480 NCBI GI 336 BLAST score 2.0e-31 E value 160 Match length 30 % identity

Seq. No.

(AC006069) unknown protein [Arabidopsis thaliana] NCBI Description

23604 Seq. No.

108011 1.R1040 Contig ID fC-gmro700565822f2 5'-most EST BLASTX

Method g1754522 NCBI GI 193 BLAST score 1.0e-14 E value Match length 60 % identity

(D89984) ornithine decarboxylase [Nicotiana tabacum] NCBI Description

23605 Seq. No.

108016 1.R1040 Contig ID hrw701063258.hl 5'-most EST

23606 Seq. No.

108018 1.R1040 Contig ID 5'-most EST ncj700984571.h1

BLASTX Method NCBI GI g951453 450 BLAST score 9.0e-45E value 153 Match length % identity 58

(M95746) initiation factor (iso)4f p82 subunit [Triticum NCBI Description

aestivum]

23607 Seq. No.

108020 1.R1040 Contig ID jC-gmr002910030a09a1 5'-most EST

BLASTX Method g3122389 NCBI GI 381 BLAST score 1.0e-36 E value 133 Match length 53 % identity

WD-40 REPEAT PROTEIN MSI3 >gi\_2394233 (AF016848) WD-40 NCBI Description

repeat protein [Arabidopsis thaliana]

23608 Seq. No.

108030 1.R1040 Contig ID



```
jC-qmfl02220141a05d1
5'-most EST
Method
                  BLASTX
                  q2736147
NCBI GI
                   164
BLAST score
                   2.0e-11
E value
                   41
Match length
% identity
                   (AF021804) fatty acid hydroxylase Fahlp [Arabidopsis
NCBI Description
                   thaliana] >gi_3132481 (AC003096) fatty acid hydroxylase,
                   FAH1 [Arabidopsis thaliana]
                   23609
Seq. No.
                   108039 1.R1040
Contig ID
                   trc700565665.h1
5'-most EST
Seq. No.
                   23610
                   108040 1.R1040
Contig ID
5'-most EST
                   trc700565662.h1
                   23611
Seq. No.
                   108090 1.R1040
Contig ID
                   uC-gmronoir037f11b1
5'-most EST
                   BLASTN
Method
NCBI GI
                   q18376
BLAST score
                   420
                   0.0e + 00
E value
                   499
Match length
                   98
% identity
                   Glycine max PAL1 gene for phenylalanine ammonia lyase (EC
NCBI Description
                   4.3.1.5)
                   23612
Seq. No.
                   108090 2.R1040
Contig ID
                   pxt700942832.h1
5'-most EST
Method
                   BLASTN
                   g18376
NCBI GI
BLAST score
                   138
                   1.0e-71
E value
                   208
Match length
% identity
                   94
                   Glycine max PAL1 gene for phenylalanine ammonia lyase (EC
NCBI Description
                   4.3.1.5)
                   23613
Seq. No.
                   108090 3.R1040
Contig ID
                   trc700565755.hl
 5'-most EST
Method
                   BLASTN
                   g18376
NCBI GI
BLAST score
                   78
                   4.0e-36
E value
                   145
Match length
                   89
 % identity
                   Glycine max PAL1 gene for phenylalanine ammonia lyase (EC
NCBI Description
```

Contig ID 108096\_1.R1040

4.3.1.5)

Contig ID

5'-most EST

```
uC-qmropic112h05b1
5'-most EST
                  BLASTX
Method
                  g2739369
NCBI GI
                  197
BLAST score
                   3.0e-15
E value
                  128
Match length
                   38
% identity
                  (AC002505) putative pectinesterase [Arabidopsis thaliana]
NCBI Description
                   23615
Seq. No.
                   108115 1.R1040
Contig ID
                   trc700565789.hl
5'-most EST
                  BLASTX
Method
                   g2245081
NCBI GI
                   373
BLAST score
                   4.0e-36
E value
                   96
Match length
                   74
% identity
                   (Z97343) myosin II heavy chain homolog [Arabidopsis
NCBI Description
                   thaliana]
                   23616
Seq. No.
                   108136 1.R1040
Contig ID
                   trc700565820.h1
5'-most EST
                   23617
Seq. No.
                   108146 1.R1040
Contig ID
                   fC-gmro700565834f3
5'-most EST
                   BLASTX
Method
                   g3450842
NCBI GI
                   629
BLAST score
                   3.0e-65
E value
                   299
Match length
                   56
% identity
                   (AF080436) mitogen activated protein kinase kinase [Oryza
NCBI Description
                   sativa]
                   23618
Seq. No.
                   108174 1.R1040
Contig ID
5'-most EST
                   trc700565890.hl
                   BLASTX
Method
                   g2924781
NCBI GI
                   257
BLAST score
                   2.0e-22
E value
Match length
                   85
                   56
 % identity
                    (AC002334) putative cellulose synthase [Arabidopsis
NCBI Description
                   thaliana]
                    23619
 Seq. No.
                    108188 1.R1040
 Contig ID
                    trc700565918.hl
 5'-most EST
                    23620
```

108192 1.R1040

jC-gms\(\overline{t}\)02400037e04d2



108193 1.R1040 Contig ID  $trc700\overline{5}65929.h1$ 5'-most EST

BLASTN Method NCBI GI q2351069 BLAST score 42 4.0e-14 E value 168 Match length

86 % identity Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MSH12, complete sequence [Arabidopsis thaliana]

23622 Seq. No.

108219 2.R1040 Contig ID trc700565972.h1 5'-most EST

BLASTX Method NCBI GI q3399767 BLAST score 322 2.0e-29 E value 169 Match length 44 % identity

(U76298) uclacyanin I [Arabidopsis thaliana] >gi\_3831466 NCBI Description

(AC005700) uclacyanin I [Arabidopsis thaliana]

23623 Seq. No.

108225 1.R1040 Contig ID

jC-gmle01810066d05d15'-most EST

BLASTX Method g4262154 NCBI GI 595 BLAST score 3.0e-61 E value Match length 346 42 % identity

(AC005275) putative protein phosphatase regulatory subunit NCBI Description

[Arabidopsis thaliana]

23624 Seq. No.

108255 1.R1040 Contig ID sat701007992.h1 5'-most EST

BLASTX Method g4539369 NCBI GI BLAST score 262 2.0e-22 E value 189 Match length 33 % identity

(AL049525) putative protein [Arabidopsis thaliana] NCBI Description

23625 Seq. No.

108258 1.R1040 Contig ID trc700566037.h1 5'-most EST

23626 Seq. No.

108264 1.R1040 Contig ID wrg700790882.hl 5'-most EST

23627 Seq. No.

108267\_1.R1040 Contig ID



```
trc700566051.hl
5'-most EST
                  23628
Seq. No.
                  108269 1.R1040
Contig ID
                  uC-gmrominsoy315c07b1
5'-most EST
                  23629
Seq. No.
                  108281 1.R1040
Contig ID
                  trc700566068.hl
5'-most EST
                  BLASTX
Method
                  g3355465
NCBI GI
                  225
BLAST score
                  2.0e-18
E value
                  153
Match length
% identity
NCBI Description (AC004218) putative Ser/Thr protein kinase [Arabidopsis
                  thaliana]
                   23630
Seq. No.
Contig ID
                   108285 1.R1040
                  uC-gmropic106b10b1
5'-most EST
                   23631
Seq. No.
                   108290_1.R1040
Contig ID
                   uC-gmropic021h06b1
5'-most EST
                   BLASTX
Method
                   g2465923
NCBI GI
BLAST score
                   393
                   3.0e-43
E value
                   184
Match length
                   41
% identity
                  (AF024648) receptor-like serine/threonine kinase
NCBI Description
                   [Arabidopsis thaliana]
                   23632
Seq. No.
                   108298 1.R1040
Contig ID
                   trc700566092.h1
5'-most EST
                   BLASTX
Method
                   g3805956
NCBI GI
                   973
BLAST score
                   1.0e-106
E value
                   232
Match length
                   74
% identity
NCBI Description (Y13769) laccase [Populus balsamifera subsp. trichocarpa]
                   23633
Seq. No.
                   108308 1.R1040
 Contig ID
                   fua701041645.hl
 5'-most EST
                   BLASTX
Method
                   g130846
 NCBI GI
 BLAST score
                   438
                   2.0e-43
 E value
                   129
 Match length
```

BASIC FORM OF PATHOGENESIS-RELATED PROTEIN 1 PRECURSOR (PRP

1) >gi\_82185\_pir\_\_S04728 pathogenesis-related protein
homolog precursor - common tobacco >gi\_19972\_emb\_CAA32228\_

57

% identity

NCBI Description



(X14065) PRP 1 precursor (AA -23 to 154) [Nicotiana tabacum] >gi\_228620\_prf\_\_1807333A pathogenesis-related protein 1 [Nicotiana tabacum]

Seq. No. 23634 Contig ID 108309\_1.R1040 5'-most EST rca701001122.h1

Seq. No. 23635

Contig ID 108315\_1.R1040 5'-most EST jsh701064948.h1

Method BLASTX
NCBI GI g2262117
BLAST score 374
E value 1.0e-35
Match length 111
% identity 65

NCBI Description (AC002343) auxin inducible protein isolog [Arabidopsis

thaliana]

Seq. No. 23636

Contig ID 108317\_1.R1040 5'-most EST pxt700941703.h1

Method BLASTX
NCBI GI g2911040
BLAST score 141
E value 5.0e-09
Match length 47
% identity 64

NCBI Description (AL021961) receptor protein kinase - like protein

[Arabidopsis thaliana]

Seq. No. 23637

Contig ID 108325\_1.R1040 5'-most EST awf700842044.h1

Seq. No. 23638

Contig ID 108341\_1.R1040 5'-most EST jC-gmro02910002b03a1

Seq. No. 23639

Contig ID 108347\_1.R1040 5'-most EST sat701002864.h1

Seq. No. 23640

Contig ID 108361\_1.R1040

5'-most EST uC-gmflminsoy025c08b1

Method BLASTX
NCBI GI g3355465
BLAST score 758
E value 2.0e-80
Match length 203
% identity 69

NCBI Description (AC004218) putative Ser/Thr protein kinase [Arabidopsis

thaliana]

Seq. No. 23641

3753



Contig ID 108378\_1.R1040 5'-most EST trc700566257.h1

Method BLASTX
NCBI GI g3128192
BLAST score 391
E value 3.0e-38
Match length 96
% identity 77

NCBI Description (AC004521) axi 1-like protein [Arabidopsis thaliana]

Seq. No. 23642

Contig ID 108385\_1.R1040 5'-most EST kl1701203351.h1

Method BLASTX
NCBI GI g3894168
BLAST score 249
E value 6.0e-21
Match length 164
% identity 34

NCBI Description (AC005312) similar to phloem-specific lectin [Arabidopsis

thaliana]

Seq. No. 23643

Contig ID 108400\_1.R1040 5'-most EST trc700568314.h1

Seq. No. 23644

Contig ID 108421\_1.R1040 5'-most EST trc700566347.h1

Seq. No. 23645

Contig ID 108423\_1.R1040 5'-most EST jC-gmle01810042c04a1

Seq. No. 23646

Contig ID 108429\_1.R1040 5'-most EST pmv700890861.h1

Seq. No. 23647

Contig ID 108438 1.R1040 5'-most EST zsg701120812.h1

Seq. No. 23648

Contig ID 108453\_1.R1040 5'-most EST pxt700946257.h1

Seq. No. 23649

Contig ID 108460\_1.R1040 5'-most EST zsg701129572.h1

Method BLASTX
NCBI GI g4559352
BLAST score 142
E value 6.0e-09
Match length 105
% identity 39

NCBI Description (AC006585) putative DNA binding protein [Arabidopsis

thaliana]



```
23650
Seq. No.
                  108465 1.R1040
Contig ID
                  trc700566424.hl
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4115905
BLAST score
                  422
E value
                  1.0e-41
Match length
                  106
% identity
                  71
                  (AF072131) secondary xylem cellulose synthase [Populus
NCBI Description
                  tremuloides]
                  23651
Seq. No.
Contig ID
                  108481 1.R1040
                  pmv700894042.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3510250
BLAST score
                  262
                  7.0e-28
E value
                  106
Match length
% identity
                  63
                  (AC005310) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  23652
                  108489 1.R1040
Contig ID
5'-most EST
                  trc700566477.h1
Method
                  BLASTX
NCBI GI
                  g2702270
BLAST score
                  261
                  5.0e-23
E value
                  67
Match length
% identity
                  70
                  (AC003033) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  23653
                  108509 1.R1040
Contig ID
5'-most EST
                  trc700566495.h1
                  BLASTX
Method
NCBI GI
                  q1871192
BLAST score
                  178
E value
                  7.0e-13
Match length
                  85
% identity
                   44
NCBI Description
                   (U90439) Cys3His zinc finger protein isolog [Arabidopsis
                  thaliana]
                  23654
Seq. No.
Contig ID
                  108516 1.R1040
5'-most EST
                  sat701006122.h1
```

Contig ID 108528 1.R1040 5'-most EST jsh701064493.h1

Method BLASTX
NCBI GI g2980788
BLAST score 226



E value 3.0e-18 Match length 113 % identity 49

NCBI Description (AL022197) putative protein [Arabidopsis thaliana]

Seq. No. 23656

Contig ID 108552\_1.R1040 5'-most EST uC-gmropic075d12b1

Seq. No. 23657

Contig ID 108552 2.R1040 5'-most EST hrw701063092.h1

Seq. No. 23658

Contig ID 108587\_1.R1040

5'-most EST g4436981

Seq. No. 23659

Contig ID 108595\_1.R1040 5'-most EST leu701149306.h1

Seq. No. 23660

Contig ID 108614\_1.R1040 5'-most EST hyd700728310.h1

Method BLASTX
NCBI GI g1362091
BLAST score 317
E value 7.0e-47
Match length 133
% identity 63

NCBI Description cellulase (EC 3.2.1.4) precursor - tomato >gi 924622

(U20590) endo-1,4-beta-glucanase precursor [Solanum

lycopersicum]

Seq. No. 23661

Contig ID 108627\_1.R1040 5'-most EST trc700566711.h1

Seq. No. 23662

Contig ID 108636\_1.R1040 5'-most EST trc700566736.h1

Method BLASTX
NCBI GI g3142298
BLAST score 260
E value 6.0e-23
Match length 72
% identity 69

NCBI Description (AC002411) Strong similarity to protein SBT1 gb X98929 from

Lycopersicum esculentum. [Arabidopsis thaliana]

Seq. No. 23663

Contig ID 108641\_2.R1040 5'-most EST fua701043343.h1

Method BLASTX
NCBI GI g4138343
BLAST score 206
E value 7.0e-21



Match length 125 % identity 45

NCBI Description (AJ011979) RNA-directed RNA polymerase [Petunia x hybrida]

Seq. No. 23664

Contig ID 108648\_1.R1040 5'-most EST crh700855849.h1

Seq. No. 23665

Contig ID 108652\_1.R1040 5'-most EST trc700566857.h1

Seq. No. 23666

Contig ID 108655\_1.R1040 5'-most EST trc700566855.h1

Seq. No. 23667

Contig ID 108666\_1.R1040 5'-most EST trc700566786.h1

Seq. No. 23668

Contig ID 108674\_1.R1040 5'-most EST uC-gmropic056g10b1

Seq. No. 23669

Contig ID 108694\_1.R1040

5'-most EST jC-gmle01810055a07a1

Method BLASTX
NCBI GI g3033400
BLAST score 590
E value 4.0e-61
Match length 150
% identity 72

NCBI Description (AC004238) putative Ser/Thr protein kinase [Arabidopsis

thaliana]

Seq. No. 23670

Contig ID 108722\_1.R1040 5'-most EST zzp700831393.h1

Seq. No. 23671

Contig ID 108725\_1.R1040 5'-most EST trc700567013.h1

Method BLASTX
NCBI GI g2444176
BLAST score 311
E value 8.0e-29
Match length 95
% identity 66

NCBI Description (U94782) unconventional myosin [Helianthus annuus]

Seq. No. 23672

Contig ID 108743\_1.R1040 5'-most EST ary700764471.h1

Method BLASTX
NCBI GI g2935416
BLAST score 646

```
1.0e-67
E value
                    178
Match length
% identity
                    72
                    (AF047896) isoflavone reductase homolog [Betula pendula]
NCBI Description
                    23673
Seq. No.
                    108764 1.R1040
Contig ID
                    uC-gmrominsoy320b06b1
5'-most EST
                    23674
Seq. No.
                    108764 2.R1040
Contig ID
                    jex700\overline{9}03774.h1
 5'-most EST
                    23675
 Seq. No.
                    108778 1.R1040
 Contig ID
                    trc700567311.hl
 5'-most EST
                    23676
 Sea. No.
                    108782 1.R1040
 Contig ID
                    jC-gms\overline{t}02400005b09d1
 5'-most EST
```

BLASTX Method g2655008 NCBI GI 188 BLAST score 5.0e-14 E value

87 Match length 47 % identity

(AF017144) (1-4)-beta-mannan endohydrolase [Lycopersicon NCBI Description

esculentum]

23677 Seq. No.

108787 1.R1040 Contig ID vzy700750815.h1 5'-most EST

BLASTX Method g2895510 NCBI GI 1161 BLAST score 1.0e-128 E value 283 Match length 79 % identity

(AF033204) putative pectin methylesterase [Arabidopsis NCBI Description

thaliana]

23678 Seq. No.

108801 1.R1040 Contig ID ncj700976408.hl 5'-most EST

23679 Seq. No.

108806 1.R1040 Contig ID awf700843372.h1 5'-most EST

BLASTX Method q3367591 NCBI GI BLAST score 391 3.0e - 38E value Match length 100 77 % identity

(AL031135) putative protein [Arabidopsis thaliana] NCBI Description

23680 Seq. No.

3758



Contig ID 108807 1.R1040

5'-most EST jC-gmfl02220069f10a1

Method BLASTX
NCBI GI g4559334
BLAST score 262
E value 2.0e-22
Match length 160
% identity 36

NCBI Description (AC007087) unknown protein [Arabidopsis thaliana]

Seq. No. 23681

Contig ID 108818 1.R1040 5'-most EST trc700567162.h1

Method BLASTX
NCBI GI g4105190
BLAST score 234
E value 1.0e-19
Match length 94
% identity 51

NCBI Description (AF044127) peroxisomal short-chain alcohol dehydrogenase

[Homo sapiens]

Seq. No. 23682

Contig ID 108825\_1.R1040 5'-most EST zsg701122784.h1

Seq. No. 23683

Contig ID 108831\_1.R1040 5'-most EST ncj700975648.h1

Method BLASTX
NCBI GI g1871192
BLAST score 160
E value 2.0e-10
Match length 69
% identity 52

% identity 52

NCBI Description (U90439) Cys3His zinc finger protein isolog [Arabidopsis

thaliana]

Seq. No. 23684

Contig ID 108840\_1.R1040 5'-most EST 2lv700807673.h1

Method BLASTN
NCBI GI g287567
BLAST score 229
E value 1.0e-126
Match length 421
% identity 89

NCBI Description Vigna radiata auxin-regulated mRNA

Seq. No. 23685

Contig ID 108845\_1.R1040 5'-most EST g5666683

Seq. No. 23686

Contig ID 108846 1.R1040 5'-most EST trc700567392.h1



Contig ID 108854\_1.R1040

5'-most EST uC-gmflminsoy061c12b1

Method BLASTX
NCBI GI g4580523
BLAST score 280
E value 7.0e-25
Match length 134
% identity 53

NCBI Description (AF036305) scarecrow-like 8 [Arabidopsis thaliana]

Seq. No. 23688

Contig ID 108857\_1.R1040 5'-most EST zzp700830732.h1

Method BLASTX
NCBI GI g3881381
BLAST score 318
E value 2.0e-29
Match length 121
% identity 51

NCBI Description (Z68270) Similarity to Yeast Man(0)-alpha-mannosidase

(SW:MNS1\_YEAST); cDNA EST EMBL:D71247 comes from this gene; cDNA EST EMBL:D73896 comes from this gene [Caenorhabditis

elegans]

Seq. No. 23689

Contig ID 108876\_1.R1040

5'-most EST jC-gmle01810013h08d1

Seq. No. 23690

Contig ID 108904\_1.R1040 5'-most EST wrg700786852.h2

Method BLASTX
NCBI GI g3559805
BLAST score 300
E value 2.0e-27
Match length 84
% identity 73

NCBI Description (AJ006787) putative phytochelatin synthetase [Arabidopsis

thaliana]

Seq. No. 23691

Contig ID 108911\_1.R1040 5'-most EST sat701010923.h1

Method BLASTX
NCBI GI g3025329
BLAST score 322
E value 2.0e-29
Match length 140
% identity 49

NCBI Description HYPOTHETICAL 25.4 KD PROTEIN F53F4.3 IN CHROMOSOME V

>gi\_3877534\_emb\_CAB01212\_ (Z77663) Similarity to S.pombe hypothetical proteinSPAC4G9.01 (TR:E223656) [Caenorhabditis

elegans]

Seq. No. 23692

Contig ID 108912 1.R1040



zsg701129343.h1 5'-most EST BLASTN Method NCBI GI g4567193 BLAST score 48 E value 4.0e-18 Match length 234 84 % identity Arabidopsis thaliana chromosome II BAC T26C19 genomic NCBI Description sequence, complete sequence 23693 Seq. No. 108921 1.R1040 Contig ID leu701147438.hl 5'-most EST BLASTX Method g2444174 NCBI GI BLAST score 1087 1.0e-119 E value Match length 287 76 % identity NCBI Description (U94781) unconventional myosin [Helianthus annuus] 23694 Seq. No. 108933 1.R1040 Contig ID sat701011677.hl 5'-most EST BLASTX Method NCBI GI q1771160 964 BLAST score 1.0e-105 E value Match length 245 71 % identity (X98929) SBT1 [Lycopersicon esculentum] NCBI Description >gi\_3687305 emb\_CAA06999 (AJ006378) subtilisin-like protease [Lycopersicon esculentum] 23695 Seq. No. 108938 1.R1040 Contig ID asn701135903.hl 5'-most EST BLASTX Method g2887310 NCBI GI 236 BLAST score 5.0e-20 E value 80 Match length 55 % identity (Y15846) TSI-1 protein [Lycopersicon esculentum] NCBI Description 23696 Seq. No. 108964 1.R1040 Contig ID  $jC-gmf\overline{1}02220070d02a1$ 5'-most EST 23697 Seq. No. 108969 1.R1040

Contig ID trc700567581.hl 5'-most EST

23698 Seq. No.

108980 1.R1040 Contig ID jex700907649.hl 5'-most EST



Seq. No. 23699

Contig ID 108983\_1.R1040 5'-most EST pmv700893637.h1

Seq. No. 23700

Contig ID 108987\_1.R1040 5'-most EST fua701040935.h1

Method BLASTX
NCBI GI g2745849
BLAST score 278
E value 1.0e-24
Match length 88
% identity 59

NCBI Description (AF039201) germin-like protein; PcGER1 [Pinus caribaea]

Seq. No. 23701

Contig ID 108995\_1.R1040 5'-most EST rlr700897343.h1

Seq. No. 23702

Contig ID 109006\_1.R1040

5'-most EST jC-gmf102220125f04a1 .

Seq. No. 23703

Contig ID 109008\_1.R1040 5'-most EST sat701008093.h1

Seq. No. 23704

Contig ID 109048\_1.R1040 5'-most EST cks700764739.h1

Seq. No. 23705

Contig ID 109054 1.R1040 5'-most EST ncj700980265.h1

Method BLASTX
NCBI GI g3850568
BLAST score 317
E value 2.0e-29
Match length 86
% identity 69

NCBI Description (AC005278) Similar to hypothetical protein SPAC2F7.14c gi 1052797 from Schizosaccharomyces pombe cosmid gb\_Z50142.

[Arabidopsis thaliana]

Seq. No. 23706

Contig ID 109077 1.R1040

5'-most EST uC-gmflminsoy016d04b1

Method BLASTN
NCBI GI g2266946
BLAST score 243
E value 1.0e-134
Match length 503
% identity 87

NCBI Description Gossypium hirsutum phosphoenolpyruvate carboxylase 1

(PEPC1) mRNA, complete cds

Seq. No. 23707

BLAST score

E value Match length 7.0e-37



```
109081 1.R1040
Contig ID
                  fC-gmf1700906134r6
5'-most EST
                  BLASTX
Method
                  g3641868
NCBI GI
                   285
BLAST score
                   3.0e-25
E value
                  86
Match length
                   65
% identity
NCBI Description (AJ011012) hypothetical protein [Cicer arietinum]
                   23708
Seq. No.
                   109081 2.R1040
Contig ID
                   q4397595
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3641868
BLAST score
                   312
                   1.0e-28
E value
                   106
Match length
% identity
NCBI Description (AJ011012) hypothetical protein [Cicer arietinum]
                   23709
Seq. No.
                   109102 1.R1040
Contig ID
                   hyd700727215.h1
5'-most EST
                   23710
Seq. No.
                   109102 2.R1040
Contig ID
                   seb700\overline{6}52818.h1
5'-most EST
                   23711
Seq. No.
                   109110 1.R1040
Contig ID
                   zhf700952679.h1
5'-most EST
                   23712
Seq. No.
                   109110 2.R1040
Contig ID
5'-most EST
                   jex700902953.hl
                   23713
Seq. No.
                   109123 1.R1040
Contig ID
5'-most EST
                   q5057977
                   BLASTX
Method
                   g3924603
NCBI GI
                   766
BLAST score
                   2.0e-81
E value
Match length
                   188
                   74
% identity
                   (AF069442) putative WD-repeat protein [Arabidopsis
NCBI Description
                   thaliana]
                   23714
Seq. No.
                   109125 1.R1040
 Contig ID
 5'-most EST
                   zzp700830233.h1
                   BLASTX
Method
                   g3540181
NCBI GI
                   383
```



% identity 51
NCBI Description (AC004122) Unknown protein [Arabidopsis thaliana]

Seq. No. 23715

Contig ID 109128 1.R1040 5'-most EST kl1701205286.h1

Seq. No. 23716

Contig ID 109131\_1.R1040 5'-most EST trc700568033.h1

Seq. No. 23717

Contig ID 109137\_1.R1040 5'-most EST smc700745842.h1

Seq. No. 23718

Contig ID 109138\_1.R1040 5'-most EST trc700568074.h1

Seq. No. 23719

Contig ID 109146\_1.R1040 5'-most EST leu701152056.h1

Seq. No. 23720

Contig ID 109152\_1.R1040 5'-most EST jC-gmle01810078c07d1

Seq. No. 23721

Contig ID 109178\_1.R1040

5'-most EST uC-gmflminsoy027h03b1

Seq. No. 23722

Contig ID 109192\_1.R1040 5'-most EST trc700568365.h1

Seq. No. 23723

Contig ID 109200\_1.R1040 5'-most EST trc700568380.h1

Seq. No. 23724

Contig ID 109201\_1.R1040

5'-most EST g5606950

Seq. No. 23725

Contig ID 109211\_1.R1040 5'-most EST dpv701098227.h1

Seq. No. 23726

Contig ID 109225\_1.R1040

5'-most EST uC-gmflminsoy072c05b1

Seq. No. 23727

Contig ID 109234\_1.R1040 5'-most EST rlr700898979.h1

Seq. No. 23728

Contig ID 109241\_1.R1040



```
uC-gmrominsoy311a12b1
5'-most EST
                  BLASTX
Method
                   q4455342
NCBI GI
BLAST score
                   310
                   2.0e-28
E value
                   126
Match length
% identity
                  (AL035522) O-methyltransferase-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   23729
Seq. No.
                   109246 1.R1040
Contig ID
                   trc700568509.h1
5'-most EST
Seq. No.
                   23730
                   109258 1.R1040
Contig ID
                   trc700568532.h1
5'-most EST
                   23731
Seq. No.
                   109260 1.R1040
Contig ID
                   trc700\overline{5}68542.h1
5'-most EST
                   23732
Seq. No.
                   109282 1.R1040
Contig ID
                   jsh701066123.hl
5'-most EST
Method
                   BLASTX
                   g4093169
NCBI GI
BLAST score
                   601
                   4.0e-62
E value
                   161
Match length
                   70
% identity
                   (AF095933) p20-Arc [Dictyostelium discoideum]
NCBI Description
                   23733
Seq. No.
                   109282 2.R1040
Contig ID
                   smc700750138.h1
5'-most EST
                   BLASTX
Method
                   g4093169
NCBI GI
                   241
BLAST score
                   2.0e-20
E value
                   63
Match length
                   75
% identity
NCBI Description (AF095933) p20-Arc [Dictyostelium discoideum]
Seq. No.
                   23734
                   109293 1.R1040
Contig ID
                   rca700\overline{9}98403.h1
5'-most EST
                   23735
Seq. No.
                   109294 1.R1040
Contig ID
5'-most EST
                   trc700568631.hl
                   23736
Seq. No.
                   109298 1.R1040
Contig ID
5'-most EST
                   trc700\overline{5}68655.h1
```

BLASTX

g322787

Method NCBI GI



BLAST score 496 E value 6.0e-50 Match length 220 % identity 45

NCBI Description pyruvate kinase (EC 2.7.1.40), cytosolic - potato

Seq. No. 23737

Contig ID 109319\_1.R1040 5'-most EST seb700647913.h1

Seq. No. 23738

Contig ID 109321\_1.R1040 5'-most EST seb700647922.h1

Method BLASTX
NCBI GI g1352077
BLAST score 216
E value 4.0e-17
Match length 83
% identity 46

NCBI Description BETA-GALACTOSIDASE PRECURSOR (LACTASE)

(EXO-(1-->4)-BETA-D-GALACTANASE) >gi\_971485\_emb\_CAA58734\_

(X83854) putative beta-galactosidase/galactanase [Lycopersicon esculentum] >gi\_4138139\_emb\_CAA10174\_ (AJ012797) ss-galactosidase [Lycopersicon esculentum]

Seq. No. 23739

Contig ID 109321\_2.R1040 5'-most EST seb700649844.h1

Seq. No. 23740

Contig ID 109328\_1.R1040 5'-most EST jC-gmro02910032b10a1

Method BLASTX
NCBI GI g1706323
BLAST score 349
E value 1.0e-34
Match length 160
% identity 56

NCBI Description ORNITHINE DECARBOXYLASE (ODC) >gi\_2118242\_pir\_\_S64704

ornithine decarboxylase (EC 4.1.1.17) - jimsonweed

>gi 871008 emb CAA61121 (X87847) ornithine decarboxylase

[Datura stramonium]

Seq. No. 23741

Contig ID 109330\_1.R1040 5'-most EST jC-gmle01810021e05a1

Method BLASTX
NCBI GI g4220535
BLAST score 448
E value 2.0e-44
Match length 122
% identity 75

NCBI Description (AL035356) clathrin coat assembly like protein [Arabidopsis

thaliana]

Seq. No. 23742

Contig ID 109340 1.R1040



5'-most EST seb700648013.h1

Seq. No. 23743

Contig ID 109349 1.R1040 5'-most EST jsh701067554.h1

Method BLASTX
NCBI GI g2506788
BLAST score 245
E value 7.0e-21
Match length 87
% identity 15

NCBI Description GERANYLGERANYL TRANSFERASE TYPE II BETA SUBUNIT (RAB

GERANYLGERANYLTRANSFERASE BETA SUBUNIT) (RAB GERANYL-GERANYLTRANSFERASE BETA SUBUNIT) (RAB GG TRANSFERASE) (RAB GGTASE) >gi\_1332508\_emb\_CAA66638\_ (X98001) geranylgeranyl transferase II [Homo sapiens]

Seq. No. 23744

Contig ID 109350 1.R1040 5'-most EST sat701012374.h1

Seq. No. 23745

Contig ID 109360\_1.R1040 5'-most EST seb700648073.h1

Seq. No. 23746

Contig ID 109362\_1.R1040 5'-most EST seb700648088.h1

Seq. No. 23747

Contig ID 109376\_1.R1040

5'-most EST jC-gmle01810067f07d1

Seq. No. 23748

Contig ID 109382 1.R1040 5'-most EST gsv701047511.h1

Seq. No. 23749

Contig ID 109390 1.R1040 5'-most EST pxt700946219.h1

Seq. No. 23750

Contig ID 109395\_1.R1040 5'-most EST seb700653651.h1

Method BLASTX
NCBI GI g3056595
BLAST score 246
E value 4.0e-21
Match length 108
% identity 45

NCBI Description (AC004255) T1F9.16 [Arabidopsis thaliana]

Seq. No. 23751

Contig ID 109398 1.R1040 5'-most EST gsv701054636.h1

Method BLASTX NCBI GI g2688839

```
BLAST score
                   785
                   8.0e-84
E value
                   180
Match length
% identity
                   83
                   (AF003347) ATP phosphoribosyltransferase [Thlaspi
NCBI Description
                   goesingense]
                   23752
Seq. No.
                   109398 2.R1040
Contig ID
                   jC-gmf\overline{1}02220138e02a1
5'-most EST
                   BLASTX
Method
                   g2688839
NCBI GI
                   320
BLAST score
                   1.0e-29
E value
Match length
                   74
                   82
% identity
                   (AF003347) ATP phosphoribosyltransferase [Thlaspi
NCBI Description
                   goesingense]
                   23753
Seq. No.
                   109403 1.R1040
Contig ID
                   jC-gmro02910025g03a1
5'-most EST
                   BLASTX
Method
                   g2191135
NCBI GI
                   163
BLAST score
                   2.0e-11
E value
                   55
Match length
                   56
% identity
                   (AF007269) A IG002N01.14 gene product [Arabidopsis
NCBI Description
                   thaliana]
                   23754
Seq. No.
                   109446 1.R1040
Contig ID
                   seb700648412.hl
5'-most EST
                   23755
Seq. No.
                   109449 1.R1040
Contig ID
                   jC-gmro02910002g05a1
5'-most EST
                    23756
Seq. No.
                   109457 1.R1040
Contig ID
                    seb700\overline{6}48441.h1
5'-most EST
```

Method BLASTX
NCBI GI g3746060
BLAST score 215
E value 2.0e-17
Match length 51
% identity 76

NCBI Description (AC005311) unknown protein [Arabidopsis thaliana]

Seq. No. 23757

Contig ID 109458\_1.R1040 5'-most EST seb700648435.h1

Seq. No. 23758

Contig ID 109467 1.R1040 5'-most EST seb700648448.h1



Method BLASTX
NCBI GI g2245378
BLAST score 336
E value 8.0e-32
Match length 84
% identity 75

NCBI Description (U83245) auxin response factor 1 [Arabidopsis thaliana]

Seq. No. 23759

Contig ID 109489\_1.R1040 5'-most EST kl1701208829.h1

Seq. No. 23760

Contig ID 109498\_1.R1040

5'-most EST g5605936

Seq. No. 23761

Contig ID 109503\_1.R1040 5'-most EST seb700648511.h1

Method BLASTX
NCBI GI g3451066
BLAST score 369
E value 2.0e-35
Match length 107
% identity 61

NCBI Description (AL031326) hypothetical protein [Arabidopsis thaliana]

Seq. No. 23762

Contig ID 109532\_1.R1040 5'-most EST leu701152277.h1

Seq. No. 23763

Contig ID 109532\_2.R1040 5'-most EST seb700648584.h1

Seq. No. 23764

Contig ID 109533\_1.R1040 5'-most EST seb700648585.h1

Method BLASTN
NCBI GI g3204133
BLAST score 305
E value 1.0e-171
Match length 946
% identity 85

NCBI Description Cicer arietinum mRNA for beta-galactosidase, partial

Seq. No. 23765

Contig ID 109543\_1.R1040 5'-most EST seb700654283.h1

Seq. No. 23766

Contig ID 109554\_1.R1040 5'-most EST seb700648631.h1

Method BLASTX
NCBI GI g2829879
BLAST score 219
E value 9.0e-18



Match length 84 % identity 58

NCBI Description (AC002396) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 23767

Contig ID 109554 2.R1040 5'-most EST smc700747909.h1

Seq. No. 23768

Contig ID 109555\_1.R1040 5'-most EST seb700648635.h1

Method BLASTX
NCBI GI g4309697
BLAST score 288
E value 9.0e-26
Match length 87
% identity 62

NCBI Description (AC006266) putative DNA-directed RNA polymerase subunit

[Arabidopsis thaliana]

Seq. No. 23769

Contig ID 109556\_1.R1040 5'-most EST seb700651589.h1

Method BLASTX
NCBI GI g2181184
BLAST score 170
E value 3.0e-12
Match length 52
% identity 52

NCBI Description (Y13577) JR3 protein [Arabidopsis thaliana]

Seq. No. 23770

Contig ID 109557\_1.R1040 5'-most EST kl1701206374.h1

Seq. No. 23771

Contig ID 109569\_1.R1040 5'-most EST seb700649418.h1

Seq. No. 23772

Contig ID 109581\_1.R1040 5'-most EST seb700648692.h1

Seq. No. 23773

Contig ID 109588 1.R1040 5'-most EST seb700648801.h1

Seq. No. 23774

Contig ID 109598\_1.R1040 5'-most EST seb700648727.h1

Seq. No. 23775

Contig ID 109598 2.R1040

5'-most EST g4301687

Seq. No. 23776

Contig ID 109612\_1.R1040



```
jC-gmro02800028b05d1
5'-most EST
                  23777
Seq. No.
                  109618 1.R1040
Contig ID
                  jC-gmro02800031b05a1
5'-most EST
                  23778
Seq. No.
                  109618 2.R1040
Contig ID
                  uC-gmropic024a09b1
5'-most EST
                  23779
Seq. No.
                  109624 1.R1040
Contig ID
                  seb700648803.hl
5'-most EST
                  BLASTX
Method
                  g3249081
NCBI GI
                  208
BLAST score
                  6.0e-22
E value
                  114
Match length
                  9
% identity
                  (AC004473) Strong similarity to AROGP2 gene gb_1762634 from
NCBI Description
                  Lycopersicon esculentum. [Arabidopsis thaliana]
                  23780
Seq. No.
                  109656 1.R1040
Contig ID
5'-most EST
                  uC-gmflminsoy019c06b1
                  BLASTX
Method
                  g3080412
NCBI GI
                  149
BLAST score
                   4.0e-10
E value
                  159
Match length
% identity
                   34
                  (AL022604) putative protein [Arabidopsis thaliana]
NCBI Description
                   23781
Seq. No.
                   109658 1.R1040
Contig ID
5'-most EST
                   seb700648857.hl
                   BLASTX
Method
                   g2583131
NCBI GI
                   143
BLAST score
E value
                   4.0e-09
                   61
Match length
                   38
% identity
                  (AC002387) putative pectinesterase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   23782
                   109663 1.R1040
Contig ID
5'-most EST
                   seb700649244.hl
                   BLASTX
Method
NCBI GI
                   g2191136
BLAST score
                   362
                   9.0e-35
E value
Match length
                   98
% identity
                   65
                   (AF007269) Similar to UTP-Glucose Glucosyltransferase;
NCBI Description
```

[Arabidopsis thaliana]

coded for by A. thaliana cDNA T46230; coded for by A. thaliana cDNA H76538; coded for by A. thaliana cDNA H76290



Seq. No. 23783 Contig ID 109676\_1.R1040

5'-most EST seb700649406.h1
Method BLASTX
NCBI GI q3776564

NCBI GI g3776564
BLAST score 229
E value 4.0e-19
Match length 51
% identity 78

NCBI Description (AC005388) Similar to hypothetical protein T1D16.16

gi\_3075397 from A. thaliana BAC gb\_AC004484. [Arabidopsis

thaliana]

Seq. No. 23784

Contig ID 109678\_1.R1040 5'-most EST seb700648905.h1

Seq. No. 23785

Contig ID 109680\_1.R1040 5'-most EST pcp700993083.h1

Seq. No. 23786

Contig ID 109690\_1.R1040 5'-most EST seb700648927.h1

Seq. No. 23787

Contig ID 109709\_1.R1040 5'-most EST seb700648983.h1

Seq. No. 23788

Contig ID 109714\_1.R1040 5'-most EST zsg701121658.h1

Seq. No. 23789

Contig ID 109722\_1.R1040 5'-most EST zhf700958155.h1

Seq. No. 23790

Contig ID 109727\_1.R1040 5'-most EST kl1701211735.h1

Method BLASTX
NCBI GI g3831443
BLAST score 352
E value 3.0e-33
Match length 106
% identity 69

NCBI Description (AC005819) putative auxin-regulated protein [Arabidopsis

thaliana]

Seq. No. 23791

Contig ID 109733\_1.R1040 5'-most EST seb700649029.h1

Method BLASTX
NCBI GI g2511693
BLAST score 586
E value 1.0e-60



Match length 153 % identity 69

NCBI Description (Z99954) cysteine proteinase precursor [Phaseolus vulgaris]

Seq. No. 23792

Contig ID 109734\_1.R1040 5'-most EST seb700649434.h1

Seq. No. 23793

Contig ID 109740\_1.R1040 5'-most EST seb700649043.h1

Seq. No. 23794

Contig ID 109744\_1.R1040 5'-most EST jsh701066883.h1 Method BLASTN

NCBI GI g2502086
BLAST score 64
E value 1.0e-27
Match length 160
% identity 92

NCBI Description Vigna radiata adenosine triphosphatase mRNA, complete cds

Seq. No. 23795

Contig ID 109758\_1.R1040 5'-most EST seb700649119.h1

Seq. No. 23796

Contig ID 109762 1.R1040 5'-most EST ncj700980219.h1

Seq. No. 23797

Contig ID 109787\_1.R1040 5'-most EST zhf700962266.h1

Method BLASTX
NCBI GI g3928097
BLAST score 254
E value 6.0e-22
Match length 121
% identity 37

NCBI Description (AC005770) unknown protein, 5' partial [Arabidopsis

thaliana]

Seq. No. 23798

Contig ID 109832\_1.R1040 5'-most EST sat701011960.h1

Method BLASTX
NCBI GI g4580398
BLAST score 477
E value 2.0e-47
Match length 245
% identity 42

NCBI Description (AC007171) putative protein kinase APK1A [Arabidopsis

thaliana]

Seq. No. 23799

Contig ID 109839 1.R1040



```
jC-gmle01810012g05a1
5'-most EST
Method
                   BLASTX
                   a4038592
NCBI GI
BLAST score
                   207
                   6.0e-16
E value
Match length
                   213
% identity
                   31
                   (Y10403) RNA-directed RNA polymerase [Lycopersicon
NCBI Description
                   esculentum]
                   23800
Seq. No.
Contig ID
                   109854 1.R1040
5'-most EST
                   kl1701208265.h1
                   23801
Seq. No.
                   109887 1.R1040
Contig ID
                   sat701002956.hl
5'-most EST
                   BLASTX
Method
                   g1839188
NCBI GI
                   402
BLAST score
                   9.0e-39
E value
                   166
Match length
                   66
% identity
                  (U86081) root hair defective 3 [Arabidopsis thaliana]
NCBI Description
                   23802
Seq. No.
                   109888 1.R1040
Contig ID
                   seb700650839.hl
5'-most EST
Method
                   BLASTX
                   g1531758
NCBI GI
                   552
BLAST score
                   7.0e-57
E value
                   115
Match length
% identity
                   88
                   (X98772) AUX1 [Arabidopsis thaliana] >gi 3335360 (AC003028)
NCBI Description
                   unknown protein [Arabidopsis thaliana]
                   23803
Seq. No.
                   109888 2.R1040
Contig ID
                   seb700649355.hl
5'-most EST
                   BLASTX
Method
                   q1531758
NCBI GI
BLAST score
                   480
E value
                   2.0e-48
                   112
Match length
                   79
% identity
                   (X98772) AUX1 [Arabidopsis thaliana] >gi_3335360 (AC003028)
NCBI Description
                   unknown protein [Arabidopsis thaliana]
                   23804
Seq. No.
                   109905 1.R1040
Contig ID
                   zhf700\overline{9}54489.h1
5'-most EST
                   BLASTX
Method
```

NCBI GI g2853087
BLAST score 222
E value 5.0e-18
Match length 74



% identity 59
NCBI Description (AL021768) putative protein [Arabidopsis thaliana]

Seq. No. 23805

Contig ID 109910\_1.R1040

5'-most EST jC-gmf102220148f03a1

Method BLASTX
NCBI GI g2829912
BLAST score 233
E value 1.0e-26
Match length 101
% identity 59

NCBI Description (AC002291) Similar ATP-dependent RNA Helicase [Arabidopsis

thaliana]

Seq. No. 23806

Contig ID 109913\_2.R1040 5'-most EST epx701\overline{10}8646.h1

Seq. No. 23807

Contig ID 109918\_1.R1040 5'-most EST seb700649394.h1

Seq. No. 23808

Contig ID 109943\_1.R1040 5'-most EST jC-gmst02400064h01d1

Seq. No. 23809

Contig ID 109964\_1.R1040 5'-most EST hyd700729257.h1

Seq. No. 23810

Contig ID 109989\_1.R1040

NCBI Description (AC002328) F20N2.2 [Arabidopsis thaliana]

Seq. No. 23811

Contig ID 110016\_1.R1040 5'-most EST epx701108846.h1

Method BLASTX
NCBI GI g4239986
BLAST score 166
E value 2.0e-11
Match length 117
% identity 33

NCBI Description (AB017165) PIG-L [Homo sapiens]

Seq. No. 23812

Contig ID 110024\_1.R1040 5'-most EST seb700649626.h1

Method BLASTX



q1169586 NCBI GI 272 BLAST score 4.0e-24 E value 59 Match length % identity

FRUCTOSE-1, 6-BISPHOSPHATASE, CYTOSOLIC NCBI Description

(D-FRUCTOSE-1, 6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE) (CY-F1) >gi\_542079\_pir\_\_S41287 fructose-bisphosphatase (EC

3.1.3.11) - potato >gi 440591\_emb\_CAA54265\_ (X76946)

fructose-1,6-bisphosphatase [Solanum tuberosum]

23813 Seq. No.

110039 2.R1040 Contig ID 5'-most EST wvk700682147.h1

Seq. No. 23814

110047 1.R1040 Contig ID ncj700983762.hl 5'-most EST

23815 Seq. No.

Contiq ID 110051 1.R1040 jC-gmst02400023a07a1 5'-most EST

23816 Seq. No.

110052 1.R1040 Contig ID seb700649664.h1 5'-most EST

Seq. No. 23817

110064 1.R1040 Contig ID

uC-gmrominsoy142f04b1 5'-most EST

BLASTX Method g2944417 NCBI GI 475 BLAST score 8.0e-48 E value 132 Match length 68 % identity

NCBI Description (AF049881) peroxidase FLXPER4 [Linum usitatissimum]

23818 Seq. No.

110066 1.R1040 Contig ID seb700649682.hl 5'-most EST

23819 Seq. No.

110078 1.R1040 Contig ID jC-gmro02910024g07a15'-most EST

BLASTX Method q4128197 NCBI GI 157 BLAST score 2.0e-10 E value 95 Match length % identity

(U75273) acyl-CoA binding protein [Arabidopsis thaliana] NCBI Description

23820 Seq. No.

110078 2.R1040 Contig ID smc700747176.hl 5'-most EST



Seq. No. 23821

Contig ID 110078\_3.R1040 5'-most EST ncj700982102.h1

Seq. No. 23822

Contig ID 110078\_4.R1040 5'-most EST epx701109554.h1

Seq. No. 23823

Contig ID 110093\_1.R1040 5'-most EST uaw700661220.h1

Seq. No. 23824

Contig ID 110093\_2.R1040 5'-most EST jsh701063913.h1

Method BLASTX
NCBI GI g4490302
BLAST score 143
E value 5.0e-09
Match length 72
% identity 39

NCBI Description (AL035678) Tic22-like protein [Arabidopsis thaliana]

Seq. No. 23825

Contig ID 110103\_1.R1040

NCBI Description P.vulgaris hydroxyproline-rich glycoprotein (HRGP) mRNA, 3'

end

Seq. No. 23826

Contig ID 110103\_2.R1040 5'-most EST jsh701066721.h1

Method BLASTN
NCBI GI g169348
BLAST score 130
E value 6.0e-67
Match length 299
% identity 76

NCBI Description P.vulgaris hydroxyproline-rich glycoprotein (HRGP) mRNA, 3'

end

Seq. No. 23827

Contig ID 110152\_1.R1040 5'-most EST seb700649862.h1

Seq. No. 23828

Contig ID 110176\_1.R1040 5'-most EST seb700650030.h1

Method BLASTX
NCBI GI g2262105
BLAST score 261



E value 8.0e-23 Match length 119 % identity 45

NCBI Description (AC002343) unknown protein [Arabidopsis thaliana]

Seq. No. 23829

Contig ID 110181\_1.R1040 5'-most EST seb700649884.h1

Seq. No. 23830

Contig ID 110182\_1.R1040 5'-most EST fC-gmse700671753h2

Method BLASTX
NCBI GI g2314805
BLAST score 849
E value 4.0e-91
Match length 195
% identity 81

NCBI Description (U85045) 2-oxoglutarate-dependent dioxygenase [Pisum

sativum] >gi 2316036 (AF001219) gibberellin 3

 $\texttt{beta-hydroxy}\overline{\texttt{l}} \texttt{ase} \texttt{ [Pisum sativum]}$ 

Seq. No. 23831

Contig ID 110202\_1.R1040 5'-most EST seb700649958.h1

Seq. No. 23832

Contig ID 110204\_1.R1040 5'-most EST jex700908585.h1

Method BLASTX
NCBI GI g3367523
BLAST score 537
E value 9.0e-55
Match length 152
% identity 66

NCBI Description (AC004392) ESTs gb\_AA728658 and gb\_N95943 come from this

gene. [Arabidopsis thaliana]

Seq. No. 23833

Contig ID 110210\_1.R1040 5'-most EST uC-gmropic044a07b1

23834

Seq. No.

Contig ID 110231 1.R1040 5'-most EST smc700748267.h1

Method BLASTX
NCBI GI g2388970
BLAST score 140
E value 1.0e-08
Match length 76
% identity 36

NCBI Description (Z98979) tat binding homolog [Schizosaccharomyces pombe]

Seq. No. 23835

Contig ID 110233\_1.R1040 5'-most EST seb700650050.h1

Method BLASTX



NCBI GI g1653513 BLAST score 177 E value 4.0e-20 Match length 90 % identity 56

NCBI Description (D90914) hypothetical protein [Synechocystis sp.]

Seq. No. 23836

Contig ID 110249 1.R1040 5'-most EST hrw701059574.h1

Seq. No. 23837

Contig ID 110254\_1.R1040 5'-most EST seb700650117.h1

Seq. No. 23838

Contig ID 110259\_1.R1040 5'-most EST uaw700661064.h1

Seq. No. 23839

Contig ID 110267\_1.R1040

5'-most EST jC-gmro02910046e12d1

Seq. No. 23840

Contig ID 110287\_1.R1040 5'-most EST seb700650150.h1

Method BLASTX
NCBI GI g2443329
BLAST score 155
E value 4.0e-10
Match length 47
% identity 66

NCBI Description (D86122) Mei2-like protein [Arabidopsis thaliana]

Seq. No. 23841

Contig ID 110296\_1.R1040 5'-most EST gsv701048944.h1

Seq. No. 23842

Contig ID 110303 1.R1040 5'-most EST pxt700941593.h1

Seq. No. 23843

Contig ID 110305\_1.R1040 5'-most EST fua701037360.h1

Seq. No. 23844

Contig ID 110305\_2.R1040 5'-most EST zzp700831375.h1

Seq. No. 23845

Contig ID 110307\_1.R1040 5'-most EST ncj700978635.h1

Method BLASTX
NCBI GI g3080426
BLAST score 192
E value 5.0e-15



Match length 81 % identity 51

NCBI Description (AL022604) putative protein [Arabidopsis thaliana]

Seq. No. 23846

Contig ID 110334\_1.R1040 5'-most EST fC-gmst700650236r1

Method BLASTX
NCBI GI g3201554
BLAST score 174
E value 1.0e-12
Match length 47
% identity 66

NCBI Description (AJ006501) beta-D-glucosidase [Tropaeolum majus]

Seq. No. 23847

Contig ID 110347\_1.R1040 5'-most EST seb700650254.h1

Method BLASTX
NCBI GI g542804
BLAST score 265
E value 5.0e-23
Match length 170
% identity 34

NCBI Description DNA-directed DNA polymerase alpha/primase complex chain B -

human >gi\_439601 (L24559) DNA polymerase alpha [Homo

sapiens] >gi\_4505929\_ref\_NP\_002680.1\_pPOLA\_polymerase (DNA

directed), alpha

Seq. No. 23848

Contig ID 110348\_2.R1040 5'-most EST fua701037806.h1

Seq. No. 23849

Contig ID 110348\_3.R1040 5'-most EST sat701005215.h1

Seq. No. 23850

Contig ID 110352\_1.R1040 5'-most EST seb700650260.h1

Method BLASTX
NCBI GI g3386604
BLAST score 180
E value 8.0e-13
Match length 146
% identity 32

NCBI Description (AC004665) putative protein kinase [Arabidopsis thaliana]

Seq. No. 23851

Contig ID 110355\_1.R1040 5'-most EST asn701132361.h1

Method BLASTX
NCBI GI g4220524
BLAST score 262
E value 3.0e-29
Match length 149
% identity 50



NCBI Description (AL035356) putative protein [Arabidopsis thaliana]

Seq. No. 23852

Contig ID 110357\_1.R1040

5'-most EST g4397265

Seq. No. 23853

Contig ID 110361\_1.R1040 5'-most EST zsg701124642.h1

Seq. No. 23854

Contig ID 110378\_1.R1040

5'-most EST g4286021

Seq. No. 23855

Contig ID 110397\_1.R1040

5'-most EST uC-gmflminsoy077e10b1

Seq. No. 23856

Contig ID 110401\_1.R1040 5'-most EST seb700651956.h1

Seq. No. 23857

Contig ID 110406\_1.R1040 5'-most EST art700605475.h2

Method BLASTX
NCBI GI g4038594
BLAST score 643
E value 2.0e-67
Match length 150
% identity 79

NCBI Description (AJ222798) tDET1 protein [Lycopersicon esculentum]

>gi\_4454332\_emb\_CAA11914\_ (AJ224356) tDET1 protein

[Lycopersicon esculentum]

Seq. No. 23858

Contig ID 110411\_1.R1040

5'-most EST uC-gmflminsoy024d03b1

Seq. No. 23859

Contig ID 110416\_1.R1040 5'-most EST smc700745869.h1

Seq. No. 23860

Contig ID 110423\_1.R1040 5'-most EST kl1701210049.h1

Method BLASTX
NCBI GI g3805851
BLAST score 314
E value 3.0e-29
Match length 96
% identity 59

NCBI Description (AL031986) putative protein [Arabidopsis thaliana]

Seq. No. 23861

Contig ID 110424\_1.R1040

5'-most EST uC-gmrominsoy052b12b1



Method BLASTX
NCBI GI g2829868
BLAST score 266
E value 3.0e-23
Match length 55
% identity 93

NCBI Description (AC002396) Unknown protein [Arabidopsis thaliana]

Seq. No. 23862

Contig ID 110424 2.R1040 5'-most EST hyd700729291.h1

Method BLASTN
NCBI GI g2749918
BLAST score 49
E value 1.0e-18
Match length 113
% identity 86

NCBI Description Arabidopsis thaliana chromosome I BAC F316 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 23863

Contig ID 110434 1.R1040 5'-most EST hyd700728989.h1

Method BLASTX
NCBI GI g2443751
BLAST score 393
E value 3.0e-53
Match length 131
% identity 85

NCBI Description (AF020303) fumarase [Arabidopsis thaliana] >gi\_2529676

(AC002535) putative fumarase [Arabidopsis thaliana]

Seq. No. 23864

Contig ID 110438\_1.R1040 5'-most EST hyd700729104.h1

Method BLASTX
NCBI GI g1351791
BLAST score 443
E value 7.0e-44
Match length 172
% identity 15

NCBI Description HYPOTHETICAL 57.0 KD TRP-ASP REPEATS CONTAINING PROTEIN IN

CPR4-SSK22 INTERGENIC REGION >gi\_83249\_pir\_\_S19487 hypothetical protein YCR072c - yeast (Saccharomyces cerevisiae) >gi\_1907211\_emb\_CAA42270\_ (X59720) YCR072c,

len:515 [Saccharomyces cerevisiae]

Seq. No. 23865

Contig ID 110446\_1.R1040 5'-most EST zsg701118463.h1

Method BLASTX
NCBI GI g2842490
BLAST score 437
E value 4.0e-43
Match length 113
% identity 69

NCBI Description (AL021749) heat-shock protein [Arabidopsis thaliana]



Seq. No. 23866

Contig ID 110451\_1.R1040

5'-most EST jC-gmf1022220131b10a1

Method BLASTX
NCBI GI g4544404
BLAST score 269
E value 1.0e-23
Match length 127
% identity 43

NCBI Description (AC007047) unknown protein [Arabidopsis thaliana]

Seq. No. 23867

Contig ID 110458\_1.R1040 5'-most EST asn701138541.h1

Seq. No. 23868

Contig ID 110473\_1.R1040 5'-most EST seb700650538.h1

Seq. No. 23869

Contig ID 110485\_1.R1040 5'-most EST zhf700963181.h1

Seq. No. 23870

Contig ID 110487\_1.R1040

5'-most EST g5126646

Seq. No. 23871

Contig ID 110490\_1.R1040 5'-most EST pmv700889860.h1

Method BLASTX
NCBI GI g4249419
BLAST score 194
E value 5.0e-15
Match length 47
% identity 79

NCBI Description (AC006072) hypothetical protein, 3' partial [Arabidopsis

.thaliana]

Seq. No. 23872

Contig ID 110494 1.R1040 5'-most EST sat701003472.h1

Method BLASTX
NCBI GI g1170660
BLAST score 254
E value 5.0e-22
Match length 77
% identity 69

NCBI Description MEVALONATE KINASE (MK) >gi\_541880\_pir\_\_S42088 mevalonate

kinase (EC 2.7.1.36) - Arabidopsis thaliana

>gi\_456614\_emb\_CAA54820\_ (X77793) mevalonate kinase

[Arabidopsis thaliana]

Seq. No. 23873

Contig ID 110500 1.R1040 5'-most EST seb700650587.h1

Match length

NCBI Description

% identity

128

60



```
23874
Seq. No.
                  110511 1.R1040
Contig ID
5'-most EST
                   seb700650602.hl
Method
                  BLASTX
                  q4406384
NCBI GI
                   345
BLAST score
                   2.0e-67
E value
                   165
Match length
                   78
% identity
NCBI Description (AF112303) serine acetyltransferase [Arabidopsis thaliana]
                   23875
Seq. No.
                   110559 1.R1040
Contig ID
5'-most EST
                   seb700650723.hl
Method
                   BLASTX
                   g1076603
NCBI GI
                   305
BLAST score
                   5.0e-28
E value
                   106
Match length
% identity
                   63
NCBI Description vsf-1 protein - tomato
                   23876
Seq. No.
                   110563 1.R1040
Contig ID
                   jC-gmr002910046d06a1
5'-most EST
                   23877
Seq. No.
                   110575 1.R1040
Contig ID
                   jC-gmf102220054e11a1
5'-most EST
                   BLASTX
Method
                   g4567283
NCBI GI
                   579
BLAST score
                   1.0e-59
E value
Match length
                   237
                   54
% identity
NCBI Description (AC006841) unknown protein [Arabidopsis thaliana]
                   23878
Seq. No.
                   110577 1.R1040
Contig ID
                   leu701\overline{1}50019.h1
5'-most EST
                   23879
Seq. No.
                   110578 1.R1040
Contig ID
5'-most EST
                   zhf700954539.h1
Seq. No.
                   23880
                   110585 1.R1040
Contig ID
                   jC-gmro02910071g06a1
5'-most EST
Method
                   BLASTX
                   g2194121
NCBI GI
BLAST score
                   330
                   2.0e-30
E value
```

3784

(qb ATCD1). EST gb ATTS4338 comes from this gene.

(AC002062) Strong similarity to Arabidopsis cyclin delta-1



## [Arabidopsis thaliana]

```
Seq. No.
                   23881
                  110585 2.R1040
Contig ID
                   jC-qmf102220081g12a1
5'-most EST
                   BLASTX
Method
                   g3915635
NCBI GI
BLAST score
                   773
                   3.0e-82
E value
                   259
Match length
                   63
% identity
                  CYCLIN DELTA-1 >gi 2995130 emb CAA58285 (X83369) cyclin
NCBI Description
                   delta-1 [Arabidopsis thaliana]
                   23882
Seq. No.
                   110591 1.R1040
Contig ID
                   seb700\overline{6}52385.h1
5'-most EST
Seq. No.
                   23883
                   110605 1.R1040
Contig ID
                   epx701110057.hl
5'-most EST
                   BLASTX
Method
                   g2462834
NCBI GI
BLAST score
                   179
                   4.0e-13
E value
Match length
                   75
                   44
% identity
                   (AF000657) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   23884
Seq. No.
                   110618 1.R1040
Contig ID
5'-most EST
                   seb700\overline{6}50836.h1
                   23885
Seq. No.
                   110622 1.R1040
Contig ID
5'-most EST
                   fC-qmst700650840f1
Method
                   BLASTX
                   q3860163
NCBI GI
BLAST score
                   229
                   1.0e-32
E value
                   287
Match length
                   34
% identity
                   (AF098962) disease resistance protein RPP1-WsA [Arabidopsis
NCBI Description
                   thaliana]
                   23886
Seq. No.
                   110629 1.R1040
Contig ID
                   zhf700954025.hl
5'-most EST
                   23887
Seq. No.
                   110632 1.R1040
Contig ID
                   vwf700675110.h1
5'-most EST
                   BLASTX
Method
                   g2208899
NCBI GI
                   405
BLAST score
```

4.0e-39

233

E value

Match length



```
% identity
                  (AB004795) dipeptidyl aminopeptidase [Pseudomonas sp.]
NCBI Description
                   23888
Seq. No.
                   110636 1.R1040
Contig ID
                   seb700\overline{6}50859.h1
5'-most EST
                   BLASTX
Method
                   g3413700
NCBI GI
BLAST score
                   214
                   3.0e-17
E value
                   65
Match length
                   65
% identity
                   (AC004747) putative YME1 protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   23889
                   110645 1.R1040
Contig ID
                   seb700\overline{6}50870.h1
5'-most EST
                   23890
Seq. No.
                   110664 1.R1040
Contig ID
                   seb700\overline{6}50891.h1
5'-most EST
                   BLASTX
Method
                   g2959781
NCBI GI
                   282
BLAST score
                   1.0e-31
E value
                   109
Match length
% identity
                   67
                   (AJ223508) Zwille protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   23891
                   110666 1.R1040
Contig ID
                   seb700650893.h1
5'-most EST
                   23892
Seq. No.
                   110675 1.R1040
Contig ID
5'-most EST
                   seb700650909.h1
                   23893
Seq. No.
                   110692 1.R1040
Contig ID
5'-most EST
                   seb700\overline{6}50928.h1
                   BLASTX
Method
                   q2459435
NCBI GI
BLAST score
                    162
                    3.0e-11
E value
Match length
                    47
                    66
% identity
                    (AC002332) putative serine carboxypeptidase [Arabidopsis
NCBI Description
                    thaliana]
Seq. No.
                    23894
                    110693 1.R1040
Contig ID
                    seb700650929.h1
5'-most EST
```

Method BLASTX g3559805 NCBI GI BLAST score 934 1.0e-101 E value 205 Match length



% identity 80
NCBI Description (AJ006787) putative phytochelatin synthetase [Arabidopsis thaliana]

Seq. No. 23895

Contig ID 110702\_1.R1040 5'-most EST kl1701206348.h1

Method BLASTX
NCBI GI 94432846
BLAST score 389
E value 2.0e-37
Match length 120
% identity 62

NCBI Description (AC006283) unknown protein [Arabidopsis thaliana]

Seq. No. 23896

Contig ID 110704 1.R1040 5'-most EST txt700732294.h1

Seq. No. 23897

Contig ID 110705\_1.R1040 5'-most EST fC-gmst700650943f1

Method BLASTX
NCBI GI g2062174
BLAST score 380
E value 2.0e-36
Match length 108
% identity 69

NCBI Description (AC001645) transcription factor (TINY) isolog [Arabidopsis

thaliana]

Seq. No. 23898

Contig ID 110707\_1.R1040 5'-most EST fC-gmst700650945f1

Method BLASTX
NCBI GI g2997755
BLAST score 362
E value 4.0e-38
Match length 291
% identity 36

NCBI Description (AF054823) TFIIH transcription/DNA repair factor p52

subunit [Mus musculus]

Seq. No. 23899

Contig ID 110730\_1.R1040 5'-most EST wvk700682821.h1

Method BLASTX
NCBI GI g2213611
BLAST score 228
E value 7.0e-19
Match length 76
% identity 58

NCBI Description (ACO00103) F21J9.5 [Arabidopsis thaliana]

Seq. No. 23900

Contig ID 110732\_1.R1040 5'-most EST seb700650986.h1



Seq. No. 23901

Contig ID 110737\_1.R1040 5'-most EST jC-gmf102220142e08a1

Seq. No. 23902

Contig ID 110737 2.R1040 5'-most EST seb700650995.h1

Seq. No. 23903

Contig ID 110750\_1.R1040

5'-most EST uC-gmflminsoy045f06b1

Method BLASTX
NCBI GI g3128192
BLAST score 451
E value 2.0e-68
Match length 168
% identity 76

NCBI Description (AC004521) axi 1-like protein [Arabidopsis thaliana]

Seq. No. 23904

Contig ID 110767\_1.R1040 5'-most EST seb700651036.h1

Seq. No. 23905

Contig ID 110771\_1.R1040 5'-most EST zhf700961474.h1

Seq. No. 23906

Contig ID 110778\_1.R1040 5'-most EST seb700651048.h1

Seq. No. 23907

Contig ID 110798\_1.R1040 5'-most EST seb700651071.h1

Seq. No. 23908

Contig ID 110802\_1.R1040 5'-most EST pmv700893183.h1

Method BLASTX
NCBI GI g557472
BLAST score 779
E value 1.0e-82
Match length 572
% identity 34

NCBI Description (U15178) arabinosidase [Bacteroides ovatus]

Seq. No. 23909

Contig ID 110814\_1.R1040 5'-most EST seb700651087.h1

Seq. No. 23910

Contig ID 110829\_1.R1040 5'-most EST seb700651113.h1

Method BLASTX NCBI GI g2833460 BLAST score 150



1.0e-09 E value Match length 50 56 % identity

RIBOFLAVIN-SPECIFIC DEAMINASE >gi\_1001153\_dbj\_BAA10295\_ NCBI Description

(D64001) riboflavin biosynthesis protein [Synechocystis

23911 Seq. No.

110840\_1.R1040 Contig ID

uC-gmrominsoy158e11b1 5'-most EST

BLASTX Method g3482918 NCBI GI 402 BLAST score 1.0e-55 E value Match length 127 85 % identity

(AC003970) Similar to ATP-citrate-lyase [Arabidopsis NCBI Description

thaliana]

23912 Seq. No.

110840 2.R1040 Contig ID vwf700678665.h1 5'-most EST

BLASTX Method g3482918 NCBI GI BLAST score 536 5.0e-55 E value 118 Match length 83 % identity

(AC003970) Similar to ATP-citrate-lyase [Arabidopsis NCBI Description

thaliana]

23913 Seq. No.

110851 1.R1040 Contig ID 5'-most EST awf700839240.h1

23914 Seq. No.

110853 1.R1040 Contig ID

q4302988 5'-most EST BLASTX Method NCBI GI g1943751 501 BLAST score E value 1.0e-50 157 Match length % identity

(U93845) Arabidopsis thaliana ER-type calcium pump NCBI Description protein, complete sequence >gi\_2078292 (U96455) ER-type

Ca2+-pumping ATPase; ECA1p [Arabidopsis thaliana]

23915 Seq. No.

110872 1.R1040 Contig ID seb700651214.h1 5'-most EST

Seq. No. 23916

110882 1.R1040 Contig ID seb700651225.h1 5'-most EST

Seq. No. 23917

```
tig ID 110883_1
```

Contig ID 110883\_1.R1040 5'-most EST seb700651277.h1 Method BLASTX

NCBI GI g3377517 BLAST score 284 E value 2.0e-25 Match length 93

% identity 54 NCBI Description (AF073361) nitrate transporter NTL1 [Arabidopsis thaliana]

Seq. No. 23918

Contig ID 110899\_1.R1040 5'-most EST fua701041340.h1

Method BLASTX
NCBI GI g116923
BLAST score 217
E value 2.0e-17
Match length 185
% identity 31

NCBI Description COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-COP)

>gi\_111414\_pir\_\_S13520 beta-COP protein - rat
>gi\_55819\_emb\_CAA40505\_ (X57228) beta COP [Rattus

norvegicus]

Seq. No. 23919

Contig ID 110902\_1.R1040 5'-most EST seb700651250.h1

Seq. No. 23920

Contig ID 110903\_1.R1040 5'-most EST fC-gmst700651292f6

Seq. No. 23921

Contig ID 110913\_1.R1040 5'-most EST seb700651279.h1

Method BLASTN
NCBI GI g2345147
BLAST score 111
E value 2.0e-55
Match length 302
% identity 87

NCBI Description Pisum sativum developmentally regulated GTP binding protein

(PsDRG1) mRNA, complete cds

Seq. No. 23922

Contig ID 110915\_1.R1040 5'-most EST seb700651270.h1

Method BLASTX
NCBI GI g1421730
BLAST score 394
E value 3.0e-38
Match length 127
% identity 59

NCBI Description (U43082) RF2 [Zea mays]

Seq. No. 23923

Contig ID 110916\_1.R1040



```
hvd700727907.hl
5'-most EST
Method
                  BLASTX
                  q4538929
NCBI GI
                  514
BLAST score
                  4.0e-52
E value
Match length
                  167
                  63
% identity
                  (AL049483) putative nucleic acid binding protein
NCBI Description
                  [Arabidopsis thaliana]
                  23924
Seq. No.
                  110926_1.R1040
Contig ID
5'-most EST
                  jC-gmro02910056b06a1
Method
                  BLASTX
                  q2827143
NCBI GI
BLAST score
                  1169
                  1.0e-129
E value
                  240
Match length
                  92
% identity
                  (AF027174) cellulose synthase catalytic subunit
NCBI Description
                   [Arabidopsis thaliana]
                  23925
Seq. No.
Contig ID
                  110932 1.R1040
                  sat701014324.hl
5'-most EST
                  BLASTX
Method
                  a4006829
NCBI GI
                  549
BLAST score
E value
                  2.0e-56
                  141
Match length
                  76
% identity
                  (AC005970) putative protein kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   23926
                   110934 1.R1040
Contig ID
5'-most EST
                  seb700651295.h1
                   23927
Seq. No.
                   110938 1.R1040
Contig ID
5'-most EST
                  rlr700896910.h1
Method
                  BLASTX
                   g3834307
NCBI GI
BLAST score
                   542
E value
                   2.0e-55
Match length
                   161
% identity
                   61
                  (AC005679) Strong similarity to gene T10I14.120 gi_2832679
NCBI Description
                   ESTs gb N65887 and gb N65627 come from this gene.
                   [Arabidopsis thaliana]
```

putative protein from Arabidopsis thaliana BAC gb\_AL021712.

23928 Seq. No.

110942 1.R1040 Contig ID 5'-most EST  $seb700\overline{6}51317.h1$ 

BLASTX Method g4314356 NCBI GI BLAST score 206



E value 2.0e-16 Match length 112 % identity 37

NCBI Description (AC006340) putative anthocyanidin-3-glucoside rhamnosyltransferase [Arabidopsis thaliana]

Seq. No. 23929

Contig ID 110947\_1.R1040 5'-most EST seb700651322.h1

Method BLASTX
NCBI GI g4115383
BLAST score 379
E value 1.0e-36
Match length 108
% identity 79

NCBI Description (AC005967) receptor-like protein kinase [Arabidopsis

thaliana]

Seq. No. 23930

Contig ID 110971\_1.R1040 5'-most EST pxt700943933.h1

Method BLASTX
NCBI GI 94249418
BLAST score 334
E value 9.0e-31
Match length 211
% identity 32

NCBI Description (AC006072) putative zinc-finger protein (C-x8-C-x5-C-x3-H

type domains), 5' partial [Arabidopsis thaliana]

Seq. No. 23931

Contig ID 110971\_2.R1040 5'-most EST zzp700832879.h1

Method BLASTX
NCBI GI g3738297
BLAST score 204
E value 4.0e-16
Match length 93
% identity 11

NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]

Seq. No. 23932

Contig ID 110974\_1.R1040

5'-most EST uC-gmflminsoy082e05b1

Method BLASTX
NCBI GI g2914707
BLAST score 171
E value 5.0e-12
Match length 110
% identity 7

NCBI Description (AC003974) putative disease resistance protein (Cf-2.2)

[Arabidopsis thaliana] >gi\_3298554 (AC004681) putative

disease resistance protein [Arabidopsis thaliana]

Seq. No. 23933

Contig ID 110976\_1.R1040 5'-most EST sat701011636.h1



Method BLASTX
NCBI GI g3924594
BLAST score 305
E value 1.0e-27
Match length 89
% identity 24

NCBI Description (AF069442) putative ribonucleoprotein [Arabidopsis thaliana] >gi\_4262139\_gb\_AAD14439\_ (AC005275) putative

ribonucleoprotein [Arabidopsis thaliana]

Seq. No. 23934

Contig ID 110981\_1.R1040 5'-most EST seb700651363.h1

Seq. No. 23935

Contig ID 110984\_1.R1040 5'-most EST jC-gmle01810048g02d1

Method BLASTX
NCBI GI g3757521
BLAST score 178
E value 8.0e-13
Match length 83
% identity 45

NCBI Description (AC005167) unknown protein [Arabidopsis thaliana]

Seq. No. 23936

Contig ID 110984 2.R1040 5'-most EST sat701009016.h1

Seq. No. 23937

Contig ID 111004\_1.R1040 5'-most EST jC-gmf102220065g12a1

Method BLASTX
NCBI GI g4049514
BLAST score 299
E value 5.0e-27
Match length 128
% identity 26

NCBI Description (AL034563) putative yeast CF Ib (RNA3' Cleavage factor Ib) homolog; ribonucleoprotein [Schizosaccharomyces pombe]

Seq. No. 23938

Contig ID 111006\_1.R1040 5'-most EST gsv701044346.h1

Seq. No. 23939

Contig ID 111023\_1.R1040 5'-most EST seb700651420.h1

Method BLASTX
NCBI GI g3668086
BLAST score 255
E value 1.0e-21
Match length 70
% identity 84

NCBI Description (AC004667) unknown protein [Arabidopsis thaliana]

Seq. No. 23940



Contig ID 111030\_1.R1040 5'-most EST smc700746246.h1

Method BLASTX
NCBI GI g3482980
BLAST score 275
E value 5.0e-24
Match length 153
% identity 42

NCBI Description (AL031369) hypothetical protein [Arabidopsis thaliana]

Seq. No. 23941

Contig ID 111030\_2.R1040 5'-most EST smc700744911.h1

Method BLASTX
NCBI GI g4567257
BLAST score 159
E value 7.0e-11
Match length 111
% identity 33

NCBI Description (AC007070) hypothetical protein [Arabidopsis thaliana]

Seg. No. 23942

Contig ID 111039\_1.R1040 5'-most EST zhf700954607.h1

Method BLASTX
NCBI GI g2191144
BLAST score 185
E value 1.0e-13
Match length 62
% identity 53

NCBI Description (AF007269) A\_IG002N01.24 gene product [Arabidopsis

thaliana]

Seq. No. 23943

Contig ID 111059\_1.R1040 5'-most EST kl1701206223.h1

Seq. No. 23944

Contig ID 111065\_1.R1040 5'-most EST seb700651488.h1

Method BLASTX
NCBI GI g4467095
BLAST score 290
E value 2.0e-26
Match length 133
% identity 59

NCBI Description (AL035538) putative protein [Arabidopsis thaliana]

Seq. No. 23945

Contig ID 111065\_2.R1040 5'-most EST jC-gmf102220054b09d1

Method BLASTX
NCBI GI g4467095
BLAST score 276
E value 2.0e-24
Match length 107
% identity 62

NCBI Description (AL035538) putative protein [Arabidopsis thaliana] 23946 Seq. No. 111066 1.R1040 Contig ID 5'-most EST jex700907270.h1 23947 Seq. No. 111066 2.R1040 Contig ID wvk700683188.hl 5'-most EST Seq. No. 23948 111083 1.R1040 Contig ID pxt700942992.h1 5'-most EST Method BLASTX g2190543 NCBI GI BLAST score 389 E value 2.0e-37 114 % identity 69 NCBI Description

Match length (AC001229) EST gb\_N37484 comes from this gene. [Arabidopsis thaliana]

23949 Seq. No. 111083 2.R1040 Contig ID uC-gmropic008d02b1 5'-most EST

Seq. No. 23950 111083 3.R1040 Contig ID 5'-most EST k11701205711.hl

23951 Seq. No. 111083 4.R1040 Contig ID fua701040912.hl 5'-most EST

23952 Seq. No. 111108 1.R1040 Contig ID q4395963 5'-most EST

BLASTX Method g4262186 NCBI GI 878 BLAST score 1.0e-94 E value 232 Match length 75 % identity

(ACO05508) Highly similar to cullin 3 [Arabidopsis NCBI Description

thaliana]

23953 Seq. No.

111110 1.R1040 Contig ID 5'-most EST g4287386 Method BLASTX

NCBI GI g2702271 235 BLAST score 1.0e-19 E value 109 Match length % identity 50

(AC003033) unknown protein [Arabidopsis thaliana] NCBI Description



```
23954
Seq. No.
                   111116 1.R1040
Contig ID
                   seb700651543.hl
5'-most EST
Seq. No.
                   23955
                   111118 1.R1040
Contig ID
                   seb700651544.hl
5'-most EST
                   23956
Seq. No.
                   111137 1.R1040
Contig ID
                   ckk700\overline{6}05704.h2
5'-most EST
                   BLASTX
Method
                   g100673
NCBI GI
BLAST score
                   446
E value
                   2.0e-44
Match length
                   95
% identity
NCBI Description DNA-binding protein GT-2 - rice (fragment)
                   23957
Seq. No.
                   111148 1.R1040
Contig ID
                   seb700\overline{6}51590.h1
5'-most EST
                   BLASTX
Method
                   g3334441
NCBI GI
                   171
BLAST score
                   3.0e-12
E value
Match length
                   48
% identity
                   60
                   HYPOTHETICAL 47.9 KD PROTEIN T517.9 IN CHROMOSOME II
NCBI Description
                   >gi 2642161 (AC003000) hypothetical protein [Arabidopsis
                   thaliana]
                   23958
Seq. No.
                   111150 1.R1040
Contig ID
                   seb700\overline{6}51593.h1
5'-most EST
                   23959
Seq. No.
                    111157 1.R1040
Contig ID
                   uC-gmflminsoy118e04b1
5'-most EST
                    23960
Seq. No.
                    111158 1.R1040
Contig ID
                    seb700651607.hl
5'-most EST
                    BLASTX
Method
NCBI GI
                    q2894568
                    227
BLAST score
                    4.0e-19
E value
                    82
Match length
% identity
NCBI Description (AL021890) putative protein [Arabidopsis thaliana]
```

23961 Seq. No.

111166 1.R1040 Contig ID uC-gmropic030b02b1 5'-most EST

Method BLASTX q4454467 NCBI GI 196 BLAST score



E value 9.0e-15 Match length 128 % identity 34

NCBI Description (AC006234) unknown protein [Arabidopsis thaliana]

Seq. No. 23962

Contig ID 111174\_1.R1040 5'-most EST seb700651633.h1

Method BLASTN
NCBI GI g169157
BLAST score 216
E value 1.0e-118
Match length 388
% identity 89

NCBI Description Pisum sativum serine hydroxymethyltransferase mRNA,

complete cds

Seq. No. 23963

Contig ID 111176 1.R1040 5'-most EST dpv701098532.h1

Seq. No. 23964

Contig ID 111180\_1.R1040 5'-most EST seb700651649.h1

Method BLASTX
NCBI GI g4006827
BLAST score 202
E value 4.0e-16
Match length 63
% identity 60

NCBI Description (AC005970) subtilisin-like protease [Arabidopsis thaliana]

Seq. No. 23965

Contig ID 111200\_1.R1040 5'-most EST jex700909114.h1

Method BLASTN
NCBI GI g4567259
BLAST score 86
E value 3.0e-40

Match length 378 % identity 62

NCBI Description Arabidopsis thaliana chromosome II BAC F3K23 genomic

sequence, complete sequence

Seq. No. 23966

Contig ID 111205\_1.R1040 5'-most EST seb700651682.h1

Method BLASTX
NCBI GI g2213629
BLAST score 332
E value 2.0e-30
Match length 277
% identity 31

NCBI Description (AC000103) F21J9.21 [Arabidopsis thaliana]

Seq. No. 23967

Contig ID 111205 2.R1040

3797



```
q5510185
5'-most EST
Seq. No.
                  23968
Contig ID
                  111229 1.R1040
                   seb700651727.hl
5'-most EST
                   23969
Seq. No.
                   111237 1.R1040
Contig ID
                   jsh701064233.hl
5'-most EST
Seq. No.
                   23970
                   111246 1.R1040
Contig ID
                   ncj700985555.h1
5'-most EST
                   23971
Seq. No.
Contig ID
                   111268 1.R1040
                   wvk700680707.h1
5'-most EST
                   23972
Seq. No.
                   111272 1.R1040
Contig ID
5'-most EST
                   sat701013451.h1
Seq. No.
                   23973
                   111290 1.R1040
Contig ID
                   uC-gmrominsoy129e08b1
5'-most EST
                   BLASTX
Method
                   g2245139
NCBI GI
BLAST score
                   158
E value
                   3.0e-10
                   127
Match length
% identity
                   41
                   (Z97344) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   23974
Seq. No.
                   111291 1.R1040
Contig ID
                   seb700\overline{6}51832.h1
5'-most EST
                   BLASTX
Method
                   g1705508
NCBI GI
                   179
BLAST score
                   3.0e-13
E value
                   95
Match length
                   45
% identity
                   BONE MARROW STROMAL ANTIGEN 2 (BST-2)
NCBI Description
                   >gi_1082259_pir__A56836 bone marrow stromal cell surface
                   protein BST-2 - human >gi_506861_dbj_BAA05679_ (D28137)
                   BST-2 [Homo sapiens]
                   23975
Seq. No.
                   111295 1.R1040
Contig ID
```

ary700764468.hl 5'-most EST

23976 Seq. No.

111295 2.R1040 Contig ID

5'-most EST jC-qmro02910063h04a1

Seq. No. 23977

111303 1.R1040 Contig ID



```
5'-most EST
                  fua701037172.hl
                  23978
Seq. No.
                  111308 1.R1040
Contig ID
                  seb700651860.hl
5'-most EST
                  BLASTN
Method
                  q2345147
NCBI GI
                  236
BLAST score
                  1.0e-130
E value
                  312
Match length
                  94
% identity
NCBI Description Pisum sativum developmentally regulated GTP binding protein
                   (PsDRG1) mRNA, complete cds
                   23979
Seq. No.
                   111324 1.R1040
Contig ID
                   jC-qmle01810083e04a1
5'-most EST
                   23980
Seq. No.
                   111325 1.R1040
Contig ID
                   seb700651894.hl
5'-most EST
                   BLASTX
Method
                   q1762584
NCBI GI
                   300
BLAST score
                   2.0e-27
E value
                   99
Match length
                   18
% identity
                   (U63373) polygalacturonase isoenzyme 1 beta subunit homolog
NCBI Description
                   [Arabidopsis thaliana]
                   23981
Seq. No.
                   111341 1.R1040
Contig ID
                   bth700847362.h1
5'-most EST
                   BLASTN
Method
                   g2342673
NCBI GI
BLAST score
                   36
                   6.0e-11
E value
                   60
Match length
                   90
 % identity
                   Sequence of BAC F7G19 from Arabidopsis thaliana chromosome
NCBI Description
                   1, complete sequence [Arabidopsis thaliana]
                   23982
 Seq. No.
                   111345 1.R1040
 Contig ID
                   seb700651941.hl
 5'-most EST
                   23983
 Seq. No.
                   111357 1.R1040
 Contig ID
                   leu701150517.h1
 5'-most EST
                   BLASTX
 Method
                   g1256771
 NCBI GI
 BLAST score
                   396
                   2.0e-38
 E value
                   95
 Match length
```

75

NCBI Description (U51270) COP9 [Spinacia oleracea]

% identity



Contig ID 111374 1.R1040

5'-most EST uC-gmflminsoy119g03b1

Method BLASTX
NCBI GI g2459408
BLAST score 393
E value 5.0e-38
Match length 120
% identity 64

NCBI Description (AC002332) unknown protein [Arabidopsis thaliana]

>gi\_2924769 (AC002334) unknown protein [Arabidopsis

thaliana]

Seq. No. 23985

Contig ID 111379\_1.R1040 5'-most EST seb700652008.h1

Seq. No. 23986

Contig ID 111387\_1.R1040 5'-most EST fde700872189.h1

Method BLASTX
NCBI GI g3169010
BLAST score 161
E value 4.0e-11
Match length 66
% identity 53

NCBI Description (AJ006412) putative GTP-binding protein [Homo sapiens]

Seq. No. 23987

Contig ID 111401\_1.R1040 5'-most EST seb700652053.h1

Method BLASTX
NCBI GI g3928099
BLAST score 340
E value 5.0e-32
Match length 123
% identity 27

NCBI Description (AC005770) unknown protein [Arabidopsis thaliana]

Seq. No. 23988

Contig ID 111406\_1.R1040 5'-most EST kmv700740293.h1

Method BLASTX
NCBI GI g4455192
BLAST score 254
E value 7.0e-22
Match length 82
% identity 30

NCBI Description (AL035440) putative protein [Arabidopsis thaliana]

Seq. No. 23989

Contig ID 111409\_1.R1040 5'-most EST seb700652074.h1

Seq. No. 23990

Contig ID 111418\_1.R1040

5'-most EST g5678016



Method BLASTN NCBI GI g2656027 BLAST score 38

E value 8.0e-12 Match length 227 % identity 82

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MJH22

Seq. No. 23991

Contig ID 111429\_1.R1040 5'-most EST gsv701055201.h1

Method BLASTX
NCBI GI g2244981
BLAST score 173
E value 2.0e-12
Match length 37
% identity 86

NCBI Description (Z97340) similarity to proline-rich protein APG -

Arabidopsis [Arabidopsis thaliana]

Seq. No. 23992

Contig ID 111431\_1.R1040 5'-most EST fua701042912.h1

Method BLASTX
NCBI GI g3023637
BLAST score 603
E value 2.0e-62
Match length 255
% identity 47

NCBI Description PROBABLE ATP-DEPENDENT RNA HELICASE HRH1 (DEAH BOX PROTEIN

8) >gi\_1362899\_pir\_\_A56236 probable RNA helicase 1 - human >gi\_807817 dbj\_BAA09078\_ (D50487) RNA helicase (HRH1) [Homo

sapiens]

Seq. No. 23993

Contig ID 111474\_1.R1040 5'-most EST uC-gmronoir029c10b1

Method BLASTX
NCBI GI g1665771
BLAST score 255
E value 1.0e-21
Match length 225
% identity 26

NCBI Description (D87440) Similar to Plasmodium falciparum glutamic acid-rich protein precursor (A54514) [Homo sapiens]

Seq. No. 23994

Contig ID 111486\_1.R1040 5'-most EST kl1701215160.h1

Method BLASTX
NCBI GI g3004565
BLAST score 237
E value 5.0e-35
Match length 146
% identity 23

NCBI Description (AC003673) putative protein kinase [Arabidopsis thaliana]



Contig ID 111506\_1.R1040 5'-most EST bth700848002.h1

Method BLASTX
NCBI GI g2190553
BLAST score 255
E value 6.0e-42
Match length 134
% identity 67

NCBI Description (AC001229) Strong similarity to Arabidopsis

zeta-crystallin-like protein (gb Z49268). [Arabidopsis

thaliana]

Seq. No. 23996

Contig ID 111528\_1.R1040 5'-most EST seb700652444.h1

Seq. No. 23997

Contig ID 111532\_1.R1040 5'-most EST fde700876126.h1

Method BLASTN
NCBI GI g1370199
BLAST score 54
E value 2.0e-21
Match length 188
% identity 83

NCBI Description L.japonicus mRNA for small GTP-binding protein, RAC1

Seq. No. 23998

Contig ID 111537\_1.R1040 5'-most EST seb700652332.h1

Seq. No. 23999

Contig ID 111549 1.R1040 5'-most EST seb700652349.h1

Method BLASTN
NCBI GI g2760172
BLAST score 57
E value 6.0e-23
Match length 230
% identity 86

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MUB3, complete sequence [Arabidopsis thaliana]

Seq. No. 24000

Contig ID 111563 1.R1040 5'-most EST zhf700955923.h1

Seq. No. 24001

Contig ID 111565\_1.R1040 5'-most EST epx701105753.h1

Seq. No. 24002

Contig ID 111604\_1.R1040 5'-most EST leu701144462.h1

Method BLASTX



```
NCBI GI g3128194
BLAST score 577
E value 2.0e-59
Match length 171
% identity 65
NCBI Description (AC00452
```

NCBI Description (AC004521) putative heme A:farnesyltransferase [Arabidopsis

thaliana]

Seq. No. 24003

Contig ID 111607 1.R1040

5'-most EST uC-gmflminsoy099b02b1

Seq. No. 24004

Contig ID 111612\_1.R1040 5'-most EST jC-gmle01810083f05a1

Method BLASTX
NCBI GI g4510348
BLAST score 518
E value 2.0e-52
Match length 147
% identity 67

NCBI Description (AC006921) unknown protein [Arabidopsis thaliana]

Seq. No. 24005

Contig ID 111631\_1.R1040 5'-most EST seb700652482.h1

Method BLASTX
NCBI GI g4512659
BLAST score 595
E value 1.0e-61
Match length 176
% identity 66

NCBI Description (AC006931) putative protein kinase [Arabidopsis thaliana]

>gi\_4544465\_gb\_AAD22372.1\_AC006580\_4 (AC006580) putative

protein kinase [Arabidopsis thaliana]

Seq. No. 24006

Contig ID 111634 1.R1040 5'-most EST seb700652487.h1

Method BLASTX
NCBI GI g2244865
BLAST score 166
E value 1.0e-11
Match length 36
% identity 72

NCBI Description (Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No. 24007

Contig ID 111638 1.R1040 5'-most EST seb700652492.h1

Method BLASTX
NCBI GI 94539460
BLAST score 146
E value 3.0e-09
Match length 101
% identity 7

NCBI Description (AL049500) putative protein [Arabidopsis thaliana]



```
24008
Seq. No.
Contig ID
                   111651 1.R1040
5'-most EST
                   vwf700673542.hl
Method
                   BLASTX
NCBI GI
                   q4249385
BLAST score
                   443
E value
                   5.0e-44
Match length
                  88
% identity
                   91
NCBI Description (AC005966) T2K10.11 [Arabidopsis thaliana]
Seq. No.
                   24009
                   111659 1.R1040
Contig ID
5'-most EST
                   gsv701049542.h1
Seq. No.
                   24010
Contig ID
                   111665 1.R1040
                   seb700\overline{6}52544.h1
5'-most EST
Method
                  BLASTX
                   q3152593
NCBI GI
BLAST score
                   274
E value
                   7.0e-24
Match length
                   225
% identity
NCBI Description
                  (AC002986) Contains similarity to thyroid receptor
                   interactor gb L40410 from Homo sapiens. [Arabidopsis
                   thaliana]
Seq. No.
                   24011
                   111682 1.R1040
Contig ID
5'-most EST
                   seb700\overline{652584.h1}
Method
                   BLASTX
NCBI GI
                   q3983665
BLAST score
                   423
E value
                   8.0e-42
Match length
                   119
                   71
% identity
NCBI Description (AB011271) importin-beta2 [Oryza sativa]
                   24012
Seq. No.
                   111737 1.R1040
Contig ID
5'-most EST
                   zzp700834286.h1
                   BLASTX
Method
NCBI GI
                   g2262157
BLAST score
                   476
E value
                   7.0e-48
Match length
                   146
% identity
                  (AC002329) putative ligand-gated ion channel protein
NCBI Description
```

Contig ID 111751\_1.R1040 5'-most EST seb700652710.h1

Seq. No. 24014

[Arabidopsis thaliana]



Contig ID 111758\_1.R1040 5'-most EST seb700652718.h1

Method BLASTX
NCBI GI g2829889
BLAST score 288
E value 1.0e-25
Match length 71
% identity 75

NCBI Description (AC002396) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 24015

Contig ID 111793\_1.R1040 5'-most EST seb700652765.h1

Seq. No. 24016

Contig ID 111808\_1.R1040 5'-most EST seb700652783.h1

Seq. No. 24017

Contig ID 111827\_1.R1040 5'-most EST seb700652815.h1

Method BLASTX
NCBI GI g3560144
BLAST score 272
E value 4.0e-26
Match length 191
% identity 40

NCBI Description (AL031534) putative asparagine synthase

[Schizosaccharomyces pombe]

Seq. No. 24018

Contig ID 111864\_1.R1040 5'-most EST seb700652861.h1

Method BLASTX
NCBI GI g3183454
BLAST score 241
E value 2.0e-20
Match length 98
% identity 49

NCBI Description HYPOTHETICAL 30.7 KD PROTEIN IN MCPC-KINA INTERGENIC REGION >gi 2632217\_emb\_CAA10859\_ (AJ222587) YkwC protein [Bacillus

subtilis] >gi\_2633767\_emb\_CAB13269\_ (Z99111) similar to 3-hydroxyisobutyrate dehydrogenase [Bacillus subtilis]

Seq. No. 24019

Contig ID 111892\_1.R1040 5'-most EST uC-gmronoir004e09b1

Seq. No. 24020

Contig ID 111924\_1.R1040

5'-most EST uC-gmflminsoy064e03b1

Seq. No. 24021

Contig ID 111924 2.R1040 5'-most EST gsv701043859.h1

Seq. No. 24022



```
111930 1.R1040
Contig ID
                   q4397601
5'-most EST
                   24023
Seq. No.
                   111940 1.R1040
Contig ID
                   ncj700983214.hl
5'-most EST
                   24024
Seq. No.
                   111944 1.R1040
Contig ID
                   zhf700\overline{9}63949.h1
5'-most EST
                   24025
Seq. No.
                   111968 1.R1040
Contig ID
                   seb700\overline{6}52991.h1
5'-most EST
                   24026
Seq. No.
                   111979 1.R1040
Contig ID
                   fC-qmst700653015f1
5'-most EST
                   BLASTX
Method
                   g1020315
NCBI GI
                    422
BLAST score
                    5.0e-41
E value
                    230
Match length
                    43
% identity
                   (U36310) glycerol-3-phosphate dehydrogenase [Homo sapiens]
NCBI Description
                    >gi_1389721 (U40367) glycerol-3-phosphate dehydrogenase
                    [Homo sapiens]
                    24027
Seq. No.
                    111991 1.R1040
Contig ID
                    seb700\overline{6}53032.h1
5'-most EST
                    BLASTX
Method
                    g434765
NCBI GI
                    150
BLAST score
                    6.0e-10
 E value
                    52
 Match length
                    56
 % identity
                    (D21262) ORF [Homo sapiens]
 NCBI Description
                    24028
 Seq. No.
                    112001 1.R1040
 Contig ID
                    seb700653044.hl
 5'-most EST
                    24029
 Seq. No.
                    112016 1.R1040
 Contig ID
                    seb700\overline{6}53076.h1
 5'-most EST
                    BLASTX
 Method
                    g3327868
 NCBI GI
 BLAST score
                     144
                     5.0e-09
 E value
 Match length
                     101
                     38
 % identity
                     (AB012912) COP1-Interacting Protein 7 (CIP7) [Arabidopsis
 NCBI Description
                     thaliana]
```

Contig ID 112025\_1.R1040

3806



uC-gmronoir015e11b1 5'-most EST BLASTX Method g417036 NCBI GI 150 BLAST score 1.0e-09 E value 89 Match length % identity TRANSLATION INITIATION FACTOR EIF-2B DELTA SUBUNIT (EIF-2B NCBI Description GDP-GTP EXCHANGE FACTOR) (GUANINE NUCLEOTIDE EXCHANGE FACTOR SUBUNIT GCD7) (GCD COMPLEX SUBUNIT GCD7) >gi\_477773\_pir\_\_B48156 translation regulator GCD7 - yeast (Saccharomyces cerevisiae) >gi\_171576 (L07116) guanine nucleotide exchange factor, eIF-2B, delta subunit [Saccharomyces cerevisiae] >gi\_596047 (U17243) Subunit of the guanine nucleotide exchange factor for EIF-2 [Saccharomyces cerevisiae] 24031 Seq. No. 112050 1.R1040 Contig ID  $seb700\overline{6}53125.h1$ 5'-most EST Seq. No. 24032 112052 1.R1040 Contig ID seb700653127.hl 5'-most EST BLASTX Method g123613 NCBI GI 438 BLAST score 3.0e-43E value Match length 99 80 % identity HEAT SHOCK COGNATE 70 KD PROTEIN 1 >gi\_100222\_pir\_\_S14949 NCBI Description heat shock cognate protein 70 - tomato >gi 19256 emb CAA37970 (X54029) heat shock protein cognate 70 [Lycopersicon esculentum] 24033 Seq. No. 112065 1.R1040 Contig ID seb700653146.hl 5'-most EST 24034 Seq. No. 112096 1.R1040 Contig ID seb700653184.h1 5'-most EST BLASTX Method g2494144 NCBI GI 151 BLAST score 9.0e-10 E value 52 Match length 65 % identity (AC002329) predicted leucine-rich protein [Arabidopsis NCBI Description thaliana] 24035 Seq. No.

112116 1.R1040 Contig ID zzp700834570.h1 5'-most EST

BLASTX Method q2947063 NCBI GI 182 BLAST score



2.0e-13 E value Match length 68 % identity 51

(AC002521) putative Ser/Thr protein kinase [Arabidopsis NCBI Description

thaliana]

Seq. No. Contig ID

24036 112119 1.R1040

5'-most EST

uC-gmrominsoy104a03b1

Method BLASTX NCBI GI g2505876 BLAST score 279 7.0e-25 E value 57 Match length

% identity 89

NCBI Description (Y12776) MYB-related protein [Arabidopsis thaliana]

Seq. No.

24037

Contig ID 5'-most EST 112120 1.R1040 kl1701210710.h1

Seq. No.

24038

Contig ID 5'-most EST 112124 1.R1040 dpv701103013.h1

Method BLASTX NCBI GI g3935157 BLAST score 234 E value 3.0e-19 Match length 78 55

% identity NCBI Description

(AC005106) T25N20.21 [Arabidopsis thaliana]

Seq. No.

24039

Contig ID 5'-most EST 112127 1.R1040 leu701149661.h1

Seq. No.

24040

Contig ID 5'-most EST 112127 2.R1040 asj700967378.hl

Seq. No.

24041

Contig ID

112133 1.R1040

5'-most EST

jC-gmro02910022c02a1

Seq. No.

24042

Contig ID 5'-most EST 112134 2.R1040 leu701148549.h1

Seq. No.

24043

Contig ID

112138 1.R1040

5'-most EST

uC-gmflminsoy064e04b1

Seq. No.

24044

Contig ID 5'-most EST 112147 1.R1040 fua701042588.hl

Method NCBI GI BLASTN g16220



BLAST score 87 E value 4.0e-41 Match length 257 % identity 86

NCBI Description A.thaliana mRNA for mitochondrial chaperonin hsp60

Seq. No. 24045

Contig ID 112162\_1.R1040 5'-most EST seb700653434.h1

Seq. No. 24046

Contig ID 112163\_1.R1040 5'-most EST gsv701052749.h1

Seq. No. 24047

Contig ID 112173\_1.R1040 5'-most EST kl1701213309.h1

Method BLASTX
NCBI GI g1208886
BLAST score 226
E value 3.0e-18
Match length 158
% identity 31

NCBI Description (U50135) coded for by C. elegans cDNA yk46f1.3; coded for

by C. elegans cDNA yk46f1.5; weakly similar to S. cerevisiae vanadate resistance protein GOG5/VRG4

(GB:L33915) [Caenorhabditis elegans]

· Seq. No. 24048

Contig ID 112198\_1.R1040 5'-most EST fjg700968370.h1

Method BLASTX
NCBI GI g3044214
BLAST score 578
E value 1.0e-59
Match length 141
% identity 76

NCBI Description (AF057044) acyl-CoA oxidase [Arabidopsis thaliana]

Seq. No. 24049

Contig ID 112209\_1.R1040 5'-most EST jC-gmle01810041b02a1

Method BLASTX
NCBI GI g2244973
BLAST score 422
E value 2.0e-41
Match length 207
% identity 45

NCBI Description (Z97340) similarity to extensin class 1 protein

[Arabidopsis thaliana]

Seq. No. 24050

Contig ID 112241\_1.R1040 5'-most EST zhf700957041.h1

Seq. No. 24051

Contig ID 112264\_1.R1040

```
5'-most EST
                  kl1701214302.h1
Method
                  BLASTX
NCBI GI
                  g4249413
BLAST score
                  618
E value
                  6.0e-64
Match length
                  141
% identity
NCBI Description (AC006072) unknown protein [Arabidopsis thaliana]
                  24052
Seq. No.
Contig ID
                  112264 2.R1040
5'-most EST
                  jC-gmle01810077d10d1
Seq. No.
                  24053
Contig ID
                  112271 1.R1040
5'-most EST
                  zhf700955122.h1
Method
                  BLASTX
NCBI GI
                  g687844
BLAST score
                  201
                  5.0e-16
E value
Match length
                  86
% identity
                  7
                 (U21320) contains TPR domain-like repeats [Caenorhabditis
NCBI Description
                  elegans]
Seq. No.
                  24054
                  112275 1.R1040
Contig ID
5'-most EST
                  seb700653435.hl
Seq. No.
                  24055
                  112303_1.R1040
Contig ID
5'-most EST
                  zhf700963447.h1
Method
                  BLASTN
NCBI GI
                  g4151065
BLAST score
                  209
E value
                  1.0e-114
Match length
                  603
                  84
% identity
NCBI Description N.tabacum mRNA for ribonucleotide reductase, clone R1-1
Seq. No.
                  24056
Contig ID
                  112319 1.R1040
                  crh700852313.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3152576
BLAST score
                  360
E value
                  3.0e-34
Match length
                  121
% identity
                  54
NCBI Description (AC002986) Similar to liver-specific transport protein
                  gb L27651 from Rattus norviegicus. [Arabidopsis thaliana]
```

Contig ID 112331\_1.R1040 5'-most EST sat701010490.h1

Method BLASTX NCBI GI g4006909



```
BLAST score
                   221
E value
                   4.0e-18
Match length
                   67
% identity
                   66
NCBI Description (Z99708) putative protein [Arabidopsis thaliana]
                   24058
Seq. No.
Contig ID
                   112336 1.R1040
5'-most EST
                  rca701000871.hl
Method
                  BLASTX
NCBI GI
                  q1935912
BLAST score
                  286
E value
                  1.0e-25
                  123
Match length
                   44
% identity
NCBI Description (U77346) LLS1 [Zea mays]
Seq. No.
                  24059
Contig ID
                   112359 1.R1040
5'-most EST
                   fC-gmst700653543a5
Method
                  BLASTX
NCBI GI
                  q861157
BLAST score
                   694
E value
                   3.0e-73
Match length
                  174
% identity
                  74
NCBI Description
                   [Vicia faba]
```

(Z35163) cell wall invertase II; beta-furanofructosídase

24060 Seq. No. Contig ID 112364 1.R1040 jC-gmf102220053d04a1 5'-most EST Method BLASTX

NCBI GI g1706256 BLAST score 330 E value 9.0e-31 105 Match length % identity 58

NCBI Description PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 10 (PPIASE) (ROTAMASE)

(CYCLOPHILIN-10) >gi\_733577 (U23453) similar to

peptidyl-prolyl cis-trans isomerase (PPIASE) (CYCLOPHILIN) [Caenorhabditis elegans] >gi 1155225 (U34954) cyclophilin

isoform 10 [Caenorhabditis elegans]

Seq. No. 24061

112371 2.R1040 Contig ID 5'-most EST eep700870304.h1

Method BLASTN NCBI GI g2264318 BLAST score 50 E value 5.0e-19 Match length 163 % identity

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MUP24, complete sequence [Arabidopsis thaliana]

Seq. No. 24062

Match length

111



```
112376 1.R1040
Contig ID
5'-most EST
                  leu701150803.hl
Method
                  BLASTX
NCBI GI
                  q4314355
BLAST score
                  282
                  4.0e-25
E value
Match length
                  125
% identity
                  46
NCBI Description (AC006340) unknown protein [Arabidopsis thaliana]
                  24063
Seq. No.
                  112379 1.R1040
Contig ID
5'-most EST
                  seb700653565.hl
                  BLASTX
Method
NCBI GI
                  g3695019
BLAST score
                  338
E value
                  3.0e-41
Match length
                  157
% identity
NCBI Description (AF055848) subtilisin-like protease [Arabidopsis thaliana]
Seq. No.
                  24064
                  112407 1.R1040
Contig ID
                  seb700653663.hl
5'-most EST
                  24065
Seq. No.
Contig ID
                  112414 1.R1040
5'-most EST
                  dpv701102410.hl
Method
                  BLASTX
NCBI GI
                   q4510400
BLAST score
                   196
                   8.0e-15
E value
Match length
                   49
                  76
% identity
                  (AC006587) putative vacuolar-type H(+)-ATPase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                   24066
Contig ID
                   112421 1.R1040
5'-most EST
                   uC-gmfIminsoy032f08b1
Method
                  BLASTX
                   g4038491
NCBI GI
BLAST score
                   810
E value
                  7.0e-87
Match length
                  194
                   80
% identity
NCBI Description
                  (AJ131705) poly(ADP-ribose) polymerase [Arabidopsis
                  thaliana]
                   24067
Seq. No.
                  112424 1.R1040
Contig ID
5'-most EST
                  seb700653629.hl
Method
                  BLASTX
NCBI GI
                  g4544431
BLAST score
                  472
E value
                  1.0e-47
```



% identity 79

NCBI Description (AC006955) hypothetical protein [Arabidopsis thaliana]

Seq. No. 24068

Contig ID 112427\_1.R1040 5'-most EST seb700653634.h1

Method BLASTX
NCBI GI g1491712
BLAST score 182
E value 2.0e-13
Match length 75
% identity 51

NCBI Description (X99961) unknown [Homo sapiens]

Seq. No. 24069

Contig ID 112431\_1.R1040

5'-most EST jC-gmro02910038a10a1

Method BLASTN
NCBI GI g3695060
BLAST score 60
E value 5.0e-25
Match length 144
% identity 85

NCBI Description Lotus japonicus rac GTPase activating protein 2 mRNA,

partial cds

Seq. No. 24070

Contig ID 112431\_2.R1040

5'-most EST jC-gmf\(\bar{1}\)02220101b06a1

Seq. No. 24071

Contig ID 112451\_1.R1040 5'-most EST uC-gmropic111b03b1

Seq. No. 24072

Contig ID 112463 1.R1040 5'-most EST seb700653674.h1

Seq. No. 24073

Contig ID 112477 1.R1040 5'-most EST seb700653690.h1

Seq. No. 24074

Contig ID 112533\_1.R1040 5'-most EST seb700653765.h1

Method BLASTX
NCBI GI g4433618
BLAST score 202
E value 1.0e-15
Match length 90
% identity 52

NCBI Description (AF107585) putative myosin heavy chain [Dendrobium grex

Madame Thong-IN]

Seq. No. 24075

Contig ID 112533\_2.R1040 5'-most EST fua701041060.h1



Contig ID 112535\_1.R1040 5'-most EST smc700750054.h1

Method BLASTX
NCBI GI g1946355
BLAST score 259
E value 2.0e-22
Match length 90
% identity 53

NCBI Description (U93215) maize transposon MuDR mudrA protein isolog [Arabidopsis thaliana] >gi\_2880040 (AC002340) maize

transposon MuDR mudrA-like protein [Arabidopsis thaliana]

Seq. No. 24077

Contig ID 112535\_2.R1040 5'-most EST seb700653767.h1

Seq. No. 24078

Contig ID 112541\_1.R1040 5'-most EST seb700653779.h1

Method BLASTX
NCBI GI g1946367
BLAST score 158
E value 1.0e-10
Match length 107
% identity 36

NCBI Description (U93215) unknown protein [Arabidopsis thaliana]

Seq. No. 24079

Contig ID 112567\_1.R1040 5'-most EST fua701038969.h1

Method BLASTX
NCBI GI g2739366
BLAST score 330
E value 3.0e-31
Match length 209
% identity 38

NCBI Description (AC002505) SF16 like protein [Arabidopsis thaliana]

Seq. No. 24080

Contig ID 112569\_1.R1040 5'-most EST seb700653822.h1

Method BLASTX
NCBI GI g2642157
BLAST score 185
E value 1.0e-13
Match length 128
% identity 38

NCBI Description (AC003000) ankyrin-like protein [Arabidopsis thaliana]

Seq. No. 24081

Contig ID 112577\_1.R1040 5'-most EST jC-gmfI02220055e07a1

Seq. No. 24082

Contig ID 112625\_1.R1040



```
5'-most EST
                  seb700653892.h1
Method
                  BLASTX
NCBI GI
                  q3024689
BLAST score
                  146
E value
                  1.0e-09
Match length
                  87
                  36
% identity
                  TRANSCRIPTION INITIATION FACTOR TFIID 100 KD SUBUNIT
NCBI Description
                  (TAFII-100) (TAFII100) >gi 1491718 emb CAA64777 (X95525)
                  hTAFII100 [Homo sapiens]
Seq. No.
                  24083
                  112636 1.R1040
Contig ID
                  uC-gmrominsoy248g04b1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g3451074
BLAST score
                  220
E value
                  1.0e-17
Match length
                  87
% identity
                  55
NCBI Description (AL031326) putative protein [Arabidopsis thaliana]
                  24084
Seq. No.
Contig ID
                  112651 1.R1040
5'-most EST
                  fua701042788.h1
Seq. No.
                  24085
                  112654 1.R1040
Contig ID
5'-most EST
                  gsv701045294.h1
Seq. No.
                  24086
                  112673 1.R1040
Contig ID
5'-most EST
                  leu701153577.h1
Method
                  BLASTX
                  g1621268
NCBI GI
BLAST score
                  1055
E value
                  1.0e-115
                  276
Match length
                  52
% identity
NCBI Description (Z81012) unknown [Ricinus communis]
Seq. No.
                  24087
Contig ID
                  112674 1.R1040
5'-most EST
                  uC-gmrominsoy063g09b1
Method
                  BLASTX
                  g4454011
NCBI GI
BLAST score
                  895
E value
                  1.0e-146
Match length
                  377
% identity
                  66
NCBI Description (AL035396) putative protein [Arabidopsis thaliana]
```

Seq. No. 24088 Contig ID

112676 1.R1040 seb700654245.h1 5'-most EST

Method BLASTX NCBI GI g99992



BLAST score 325 E value 1.0e-30 Match length 87 % identity 38

NCBI Description protein disulfide-isomerase (EC 5.3.4.1) precursor - alfalfa (clone B2) >gi\_166418 (M82973) putative endomembrane protein; putative [Medicago sativa]

Seq. No. 24089

Contig ID 112681\_1.R1040 5'-most EST seb700654011.h1

Method BLASTX
NCBI GI g2980777
BLAST score 580
E value 1.0e-59
Match length 162
% identity 74

NCBI Description (AL022198) putative protein [Arabidopsis thaliana]

Seq. No. 24090

Contig ID 112683 1.R1040 5'-most EST zvp700764220.h1

Seq. No. 24091

Contig ID 112687\_1.R1040 5'-most EST leu701145562.h1

Method BLASTX
NCBI GI g3688284
BLAST score 204
E value 3.0e-16
Match length 61
% identity 67

NCBI Description (AJ011567) lanatoside 15'-O-acetylesterase [Digitalis

lanata]

Seq. No. 24092

Contig ID 112703\_1.R1040 5'-most EST jC-gmro02910074g05a1

Method BLASTX
NCBI GI g3292824
BLAST score 318
E value 3.0e-29
Match length 86
% identity 71

NCBI Description (AL031018) putative protein [Arabidopsis thaliana]

Seq. No. 24093

Contig ID 112703\_2.R1040 5'-most EST zzp700834585.h1

Method BLASTX
NCBI GI g3292824
BLAST score 416
E value 9.0e-41
Match length 110
% identity 73

NCBI Description (AL031018) putative protein [Arabidopsis thaliana]

Match length

% identity

120

44



```
Seq. No.
                   24094
                   112735 1.R1040
Contig ID
5'-most EST
                  nci700987754.h1
Method
                  BLASTX
NCBI GI
                   g1001263
BLAST score
                  189
                   3.0e-14
E value
                  90
Match length
% identity
                   48
NCBI Description (D64003) hypothetical protein [Synechocystis sp.]
                  24095
Seq. No.
                  112737 1.R1040
Contig ID
5'-most EST
                  seb700\overline{6}54115.h1
                  BLASTX
Method
NCBI GI
                  g3776557
BLAST score
                  218
E value
                   6.0e-18
Match length
                   65
                   52
% identity
                  (AC005388) Contains similarity to gi 2924495 hypothetical
NCBI Description
                  protein Rv1920 from Mycobacterium tuberculosis genome
                  gb AL022020. [Arabidopsis thaliana]
                   24096
Seq. No.
Contig ID
                   112744 1.R1040
5'-most EST
                   jC-qmro02910037h12a1
Method
                   BLASTX
NCBI GI
                   q1208784
BLAST score
                   404
E value
                   3.0e-39
                   124
Match length
                   57
% identity
NCBI Description (U48371) alcohol dehydrogenase [Pinus banksiana]
                   24097
Seq. No.
                   112744 2.R1040
Contig ID
5'-most EST
                   zhf700963088.h1
                  BLASTX
Method
                   g1076647
NCBI GI
BLAST score
                   253
E value
                   1.0e-21
Match length
                   78
% identity
                   62
                  alcohol dehydrogenase 2 - garden petunia >gi 829592
NCBI Description
                   (U25536) alcohol dehydrogenase-2 [Petunia hybrida]
                   24098
Seq. No.
                   112745 1.R1040
Contig ID
5'-most EST
                   seb700654124.h1
Method
                  BLASTX
                   g3242728
NCBI GI
BLAST score
                   130
E value
                   7.0e-14
```

NCBI Description (AC003040) unknown protein [Arabidopsis thaliana]



Contig ID 112765\_1.R1040 5'-most EST hyd700728025.h1

Method BLASTX
NCBI GI 94467126
BLAST score 303
E value 1.0e-36
Match length 307
% identity 34

NCBI Description (AL035538) guanine nucleotide-exchange protein-like

[Arabidopsis thaliana]

Seq. No. 24100

Contig ID 112769 1.R1040 5'-most EST ncj700988378.h1

Seq. No. 24101

Contig ID 112775\_1.R1040 5'-most EST pcp700994491.h1

Method BLASTX
NCBI GI g2244866
BLAST score 307
E value 5.0e-28
Match length 143
% identity 51

NCBI Description (Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No. 24102

Contig ID 112806 1.R1040 5'-most EST kl1701206321.h1

Seq. No. 24103

Contig ID 112815 1.R1040 5'-most EST seb700654217.h1

Seq. No. 24104

Contig ID 112818\_1.R1040 5'-most EST wrg700787833.h2

Method BLASTX
NCBI GI g559713
BLAST score 406
E value 6.0e-40
Match length 95
% identity 80

NCBI Description (D38552) The half39 protein is related to cyclophilin.

[Homo sapiens]

Seq. No. 24105

Contig ID 112826\_1.R1040 5'-most EST 2hf700960152.h1

Seq. No. 24106

Contig ID 112827 1.R1040 5'-most EST 2hf700958215.h1

Method BLASTX NCBI GI g3142289



BLAST score 323 E value 7.0e-30 Match length 123 % identity 49

NCBI Description (AC002411) Strong similarity to beta-keto-Coa synthase gb U37088 from Simmondsia chinensis. [Arabidopsis thaliana]

Seq. No. 24107

Contig ID 112827\_2.R1040 5'-most EST seb700654231.h1

Seq. No. 24108

Contig ID 112830\_1.R1040 5'-most EST kmv700741920.h1

Method BLASTN
NCBI GI g633606
BLAST score 170
E value 1.0e-90
Match length 393
% identity 86

NCBI Description P.sativum mRNA for chloroplastic outer envelope membrane

protein (OEP75)

Seq. No. 24109

Contig ID 112844\_1.R1040 5'-most EST seb700654254.h1

Seq. No. 24110

Contig ID 112856\_1.R1040 5'-most EST ncj700981950.h1

Seq. No. 24111

Contig ID 112863\_1.R1040 5'-most EST gsv701051226.h1

Method BLASTX
NCBI GI g3236238
BLAST score 249
E value 2.0e-21
Match length 94
% identity 53

NCBI Description (AC004684) putative ARF1 GTPase activating protein

[Arabidopsis thaliana] >gi\_4519792\_dbj\_BAA75744.1\_

(AB017876) Aspl [Arabidopsis thaliana]

Seq. No. 24112

Contig ID 112901\_1.R1040 5'-most EST fde700872625.h1

Method BLASTX
NCBI GI g3176709
BLAST score 628
E value 3.0e-65
Match length 307
% identity 44

NCBI Description (AC002392) putative anthranilate

N-hydroxycinnamoyl/benzoyltransferase [Arabidopsis

thaliana]



```
Seq. No.
                   24113
Contig ID
                   112918 1.R1040
5'-most EST
                   uaw700665247.h1
Seq. No.
                   24114
                   112922 1.R1040
Contig ID
5'-most EST
                   zvj700605156.h2
Seq. No.
                   24115
Contig ID
                   112929 1.R1040
5'-most EST
                   zvj700605168.h2
Method
                  BLASTX
NCBI GI
                  g1806142
BLAST score
                   341
E value
                   3.0e-32
                  99
Match length
                   69
% identity
NCBI Description (X97315) cdc2MsD [Medicago sativa]
                  24116
Seq. No.
                  112945 1.R1040
Contig ID
5'-most EST
                  pxt700946095.h1
                  BLASTX
Method
NCBI GI
                  g2245131
BLAST score
                  204
E value
                   8.0e-16
                  151
Match length
% identity
                  35
NCBI Description (297344) hypothetical protein [Arabidopsis thaliana]
                  24117
Seq. No.
                  112953 1.R1040
Contig ID
5'-most EST
                  hyd700728573.h1
Method
                  BLASTX
NCBI GI
                   q4454453
BLAST score
                   337
                   1.0e-51
E value
                  290
Match length
                   47
% identity
NCBI Description (AC006234) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   24118
Contig ID
                  112956 1.R1040
5'-most EST
                  zvj700\overline{6}05211.h2
                  BLASTX
Method
NCBI GI
                   q2104535
BLAST score
                   548
E value
                   3.0e-56
Match length
                  147
% identity
                  76
NCBI Description (AF001308) T10M13.13 [Arabidopsis thaliana]
```

Contig ID 112959 1.R1040 5'-most EST uxk700672792.h1

Method BLASTX NCBI GI 94063751

3820



BLAST score 292 E value 4.0e-26 Match length 199 % identity 32

NCBI Description (AC005851) putative white protein [Arabidopsis thaliana] >gi\_4510409\_gb\_AAD21495.1\_ (AC006929) putative white

protein [Arabidopsis thaliana]

Seq. No. 24120

Contig ID 112979\_1.R1040 5'-most EST jC-gmfl02220085b12a1

Method BLASTX
NCBI GI g2654868
BLAST score 366
E value 7.0e-35
Match length 163
% identity 50

NCBI Description (AF015301) RbohAp108 [Arabidopsis thaliana]

Seq. No. 24121

Contig ID 112983\_1.R1040 5'-most EST zvj700605251.h2

Method BLASTX
NCBI GI g3355490
BLAST score 226
E value 7.0e-19
Match length 69
% identity 58

NCBI Description (AC004218) putative dolichyl-phosphate

beta-glucosyltransferase [Arabidopsis thaliana]

Seq. No. 24122

Contig ID 112985\_1.R1040 5'-most EST zvj700605255.h2

Method BLASTX
NCBI GI g2462749
BLAST score 563
E value 8.0e-58
Match length 145
% identity 79

NCBI Description (AC002292) Putative Serine/Threonine protein kinase

[Arabidopsis thaliana]

Seq. No. 24123

Contig ID 112986\_1.R1040 5'-most EST zvj700605256.h2

Method BLASTX
NCBI GI g2191178
BLAST score 203
E value 4.0e-16
Match length 69
% identity 57

NCBI Description (AF007270) contains similarity to MIPP proteins

[Arabidopsis thaliana]

Seq. No. 24124

Contig ID 112991 1.R1040



5'-most EST zvj700605263.h2

Method BLASTX
NCBI GI g4580398
BLAST score 245
E value 4.0e-21
Match length 82
% identity 63

NCBI Description (AC007171) putative protein kinase APK1A [Arabidopsis

thaliana]

Seq. No. 24125

Contig ID 112998\_1.R1040 5'-most EST zvj700605273.h2

Seq. No. 24126

Contig ID 113002\_1.R1040 5'-most EST zvj700605277.h2

Method BLASTX
NCBI GI g1708971
BLAST score 518
E value 2.0e-52
Match length 235
% identity 46

NCBI Description (R)-MANDELONITRILE LYASE ISOFORM 1 PRECURSOR

(HYDROXYNITRILE LYASE 1) ((R)-OXYNITRILASE 1)

>gi\_421871\_pir\_\_S32156 mandelonitrile lyase (EC 4.1.2.10) -

black cherry >gi\_288116\_emb\_CAA51194\_ (X72617)

mandelonitrile lyase [Prunus serotina] >gi\_1730332 (U78814) (R)-(+)-mandelonitrile lyase isoform MDL1 precursor [Prunus serotina] >gi\_1090776 prf\_2019441A mandelonitrile lyase

[Prunus serotina]

Seq. No. 24127

Contig ID 113017\_1.R1040 5'-most EST art700605306.h2

Seq. No. 24128

Contig ID 113070\_1.R1040 5'-most EST xzy700966852.h1

Method BLASTN
NCBI GI g4220643
BLAST score 42
E value 4.0e-14
Match length 90
% identity 87

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MWD22, complete sequence [Arabidopsis thaliana]

Seq. No. 24129

Contig ID 113070\_2.R1040 5'-most EST uC-gmronoir020d04b1

Seq. No. 24130

Contig ID 113106\_1.R1040 5'-most EST jex700905323.h1

Seq. No. 24131



Contig ID

5'-most EST

113149 1.R1040

uC-gmrominsoy264h09b1

```
BLASTX
Method
                  g1174199
NCBI GI
BLAST score
                  235
E value
                  7.0e-20
                  112
Match length
                   52
% identity
NCBI Description (U44760) S25-PR6 [Nicotiana tabacum]
Seq. No.
                   24132
                   113151 1.R1040
Contig ID
                   art700605493.h2
5'-most EST
                   BLASTX
Method
                   q2827705
NCBI GI
BLAST score
                   214
                   4.0e-17
E value
Match length
                   141
% identity
NCBI Description (AL021684) predicted protein [Arabidopsis thaliana]
Seq. No.
                   113176 1.R1040
Contig ID
                   taw700658146.h1
5'-most EST
                   24134
Seq. No.
                   113180 1.R1040
Contig ID
                   jC-gmle01810052f01a1
5'-most EST
                   BLASTN
Method
NCBI GI
                   g829118
BLAST score
                   196
                   1.0e-106
E value
                   484
Match length
                   85
% identity
NCBI Description P.vulgaris gene for cyclophilin
Seq. No.
                   24135
                   113183 1.R1040
Contig ID
                   taw700654363.hl
5'-most EST
                   BLASTX
Method
                   g1871180
NCBI GI
BLAST score
                   254
                   1.0e-21
E value
                   133
Match length
                   47
% identity
                   (U90439) unknown protein [Arabidopsis thaliana]
NCBI Description
                   24136
Seq. No.
                   113192 1.R1040
Contig ID
                   k11701\overline{2}15241.h1
5'-most EST
                   BLASTX
Method
                   q4049401
NCBI GI
BLAST score
                   349
E value
                   4.0e-33
                   82
Match length
 % identity
NCBI Description (AJ131580) glutathione transferase AtGST 10 [Arabidopsis
```



## thaliana]

 Seq. No.
 24137

 Contig ID
 113194\_1.R1040

 5'-most EST
 fC-gmse700654386y1

 Method
 BLASTX

NCBI GI g2130082
BLAST score 680
E value 3.0e-71
Match length 310
% identity 46

NCBI Description protein kinase Xa21 (EC 2.7.1.-) - rice >gi\_1122443

(U37133) receptor kinase-like protein [Oryza sativa] >gi\_2586085 (U72723) receptor kinase-like protein [Oryza

longistaminata] >gi\_1586408\_prf\_\_2203451A receptor

kinase-like protein [Oryza sativa]

Seq. No. 24138

Contig ID 113220 1.R1040 5'-most EST taw700654435.h1

Seq. No. 24139

Contig ID 113227\_1.R1040 5'-most EST taw700654446.h1

Method BLASTX
NCBI GI g2462745
BLAST score 216
E value 6.0e-26
Match length 108
% identity 55

NCBI Description (AC002292) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 24140

Contig ID 113232\_1.R1040 5'-most EST taw700658808.h1

Seq. No. 24141

Contig ID 113233\_1.R1040

5'-most EST jC-gmro02800031d06a1

Method BLASTN
NCBI GI g3021343
BLAST score 277
E value 1.0e-154
Match length 534
% identity 88

NCBI Description Cicer arietinum mRNA for hypothetical protein homologous to

EST B23019

Seq. No. 24142

Contig ID 113233\_2.R1040

5'-most EST uC-gmrominsoy155b05b1

Seq. No. 24143

Contig ID 113233\_3.R1040 5'-most EST rlr700895471.h1

Method BLASTN NCBI GI g3021343



BLAST score 6.0e-64 E value 185 Match length 92 % identity

NCBI Description Cicer arietinum mRNA for hypothetical protein homologous to

EST B23019

24144 Seq. No.

113240 1.R1040 Contig ID taw700654472.h1 5'-most EST

BLASTN Method q938299 NCBI GI 64 BLAST score 1.0e-27 E value 236 Match length 83 % identity

NCBI Description V.ungiculata mRNA for unknown protein (A3 gene)

24145 Seq. No.

113268 1.R1040 Contig ID smc700744721.hl 5'-most EST

24146 Seq. No.

113293 1.R1040 Contig ID jC-gmro02910047h12a1 5'-most EST

BLASTX Method g2191136 NCBI GI 212 BLAST score 6.0e-17 E value 122 Match length % identity

(AF007269) Similar to UTP-Glucose Glucosyltransferase; NCBI Description

coded for by A. thaliana cDNA T46230; coded for by A.

thaliana cDNA H76538; coded for by A. thaliana cDNA H76290

[Arabidopsis thaliana]

24147 Seq. No.

113297 1.R1040 Contig ID gsv701051363.hl 5'-most EST

Seq. No. 24148

113298 1.R1040 Contig ID taw700654567.hl 5'-most EST

24149 Seq. No.

113299\_1.R1040 Contig ID

g5752943 5'-most EST BLASTX Method g3298441 NCBI GI 361 BLAST score 3.0e - 34E value 89 Match length % identity 78

(AB010879) chloroplast ribosomal protein L10 [Nicotiana NCBI Description

tabacum]

24150 Seq. No.



```
113299 2.R1040
Contig ID
5'-most EST
                   wvk700686195.h1
Method
                   BLASTX
NCBI GI
                   q3298441
BLAST score
                   373
E value
                   3.0e - 36
Match length
                   85
% identity
                   80
NCBI Description
                   (AB010879) chloroplast ribosomal protein L10 [Nicotiana
                   tabacum]
Seq. No.
                   24151
                   113319 1.R1040
Contig ID
5'-most EST
                  ncj700988593.h1
                  BLASTX
Method
NCBI GI
                   q2388582
BLAST score
                   538
E value
                   7.0e-55
                  140
Match length
% identity
                   68
                  (AC000098) Contains similarity to Rattus O-GlcNAc
NCBI Description
                   transferase (gb U76557). [Arabidopsis thaliana]
Seq. No.
                   24152
Contig ID
                   113345 1.R1040
5'-most EST
                   uC-gmrominsoy034c09b1
Seq. No.
                   24153
                   113353 1.R1040
Contig ID
5'-most EST
                   pmv700889074.h1
                   BLASTX
Method
NCBI GI
                   q4335773
BLAST score
                   269
E value
                   2.0e-23
Match length
                   151
% identity
                   51
NCBI Description
                  (AC006284) unknown protein [Arabidopsis thaliana]
Seq. No.
                   24154
                   113372 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy045g01b1
Seq. No.
                   24155
Contig ID
                   113394 1.R1040
5'-most EST
                   sat701012155.h1
Method
                   BLASTN
NCBI GI
                   q4567259
BLAST score
                   54
                   2.0e-21
E value
```

Match length 158 % identity 84

NCBI Description Arabidopsis thaliana chromosome II BAC F3K23 genomic

sequence, complete sequence

Seq. No. 24156

113400 1.R1040 Contig ID 5'-most EST xpa700797932.h1



Contig ID 113406\_1.R1040 5'-most EST fua701041972.h1

Seq. No. 24158

Contig ID 113419\_1.R1040 5'-most EST 2hf700959048.h1

Seq. No. 24159

Contig ID 113419\_2.R1040 5'-most EST jC-qmro02910069b06a1

Method BLASTX
NCBI GI g1653380
BLAST score 214
E value 6.0e-17

Match length 115 % identity 38

NCBI Description (D90913) hypothetical protein [Synechocystis sp.]

Seq. No. 24160

Contig ID 113424\_1.R1040 5'-most EST taw700654811.h1

Method BLASTX
NCBI GI g2224663
BLAST score 174
E value 1.0e-12
Match length 73
% identity 52

NCBI Description (AB002359) KIAA0361 [Homo sapiens]

Seq. No. 24161

Contig ID 113427\_1.R1040 5'-most EST taw700654815.h1

Seq. No. 24162

Contig ID 113436\_1.R1040 5'-most EST taw700654828.h1

Method BLASTX
NCBI GI g3451075
BLAST score 652
E value 6.0e-87
Match length 214
% identity 74

NCBI Description (AL031326) putative protein [Arabidopsis thaliana]

Seq. No. 24163

Contig ID 113489\_1.R1040 5'-most EST sat701013345.h1

Seq. No. 24164

Contig ID 113489\_2.R1040 5'-most EST taw700654903.h1

Seq. No. 24165

Contig ID 113507\_1.R1040 5'-most EST taw700654927.h1

3827



Method BLASTX
NCBI GI g3980406
BLAST score 275
E value 1.0e-24
Match length 90
% identity 58

NCBI Description (AC004561) putative tropinone reductase [Arabidopsis

thaliana]

Seq. No. 24166

Contig ID 113527\_1.R1040 5'-most EST awf700836851.h1

Method BLASTX
NCBI GI g3461815
BLAST score 166
E value 8.0e-12
Match length 45
% identity 69

NCBI Description (AC004138) hypothetical protein [Arabidopsis thaliana]

Seq. No. 24167

Contig ID 113529\_1.R1040 5'-most EST gsv701055015.h1

Seq. No. 24168

Contig ID 113533\_1.R1040 5'-most EST taw700655825.h1

Method BLASTX
NCBI GI g3080375
BLAST score 184
E value 5.0e-14
Match length 53
% identity 58

NCBI Description (AL022580) putative protein [Arabidopsis thaliana]

Seq. No. 24169

Contig ID 113558\_1.R1040 5'-most EST rlr700900137.h1

Method BLASTX
NCBI GI g1651907
BLAST score 325
E value 3.0e-30
Match length 113
% identity 55

NCBI Description (D90901) spore germination protein c2 [Synechocystis sp.]

Seq. No. 24170

Contig ID 113565\_1.R1040 5'-most EST jsh701064181.h1

Seq. No. 24171

Contig ID 113572 1.R1040 5'-most EST taw700655021.h1

Seq. No. 24172

Contig ID 113595\_1.R1040 5'-most EST leu701149275.h1



BLASTN Method NCBI GI g18651 BLAST score 486 0.0e+00E value 511 Match length 98 % identity

NCBI Description Soybean gene for heat shock protein Gmhsp17.9-D (class VI)

Seq. No.

24173 113595 2.R1040 Contig ID 5'-most EST hrw701060520.hl

Method BLASTN NCBI GI q18651 BLAST score 188 E value 1.0e-101 Match length 288 % identity 91

NCBI Description Soybean gene for heat shock protein Gmhspl7.9-D (class VI)

24174 Seq. No.

Contig ID 113595 3.R1040 5'-most EST awf700839582.h1

Method BLASTN NCBI GI g18651 BLAST score 149 E value 2.0e-78 217 Match length % identity 92

NCBI Description Soybean gene for heat shock protein Gmhspl7.9-D (class VI)

Seq. No.

24175 Contig ID 113597 1.R1040 5'-most EST kl1701214832.h1

Seq. No. 24176

Contig ID 113607 1.R1040

5'-most EST q4305882 Method BLASTX NCBI GI q3341687 BLAST score 161 2.0e-10 E value 82 Match length % identity 40

(AC003672) putative ras protein [Arabidopsis thaliana] NCBI Description

Seq. No. 24177

Contig ID 113611 1.R1040 rca700999535.hl 5'-most EST

Seq. No. 24178

Contig ID 113647 1.R1040 5'-most EST jsh701065654.hl

Method BLASTX g2289004 NCBI GI BLAST score 174 E value 7.0e-13 Match length 63



% identity 54

NCBI Description (AC002335) hypothetical protein [Arabidopsis thaliana] >gi 3763939 (AC004450) hypothetical protein [Arabidopsis

thaliana]

Seq. No. 24179

Contig ID 113663\_1.R1040

NCBI Description L.polyphyllus pPLB07 mRNA

Seq. No. 24180

Contig ID 113691 1.R1040 5'-most EST jC-gmle01810078a01d1

Seq. No. 24181

Contig ID 113721\_1.R1040 5'-most EST vzy700754933.h1

Method BLASTX
NCBI GI g1130682
BLAST score 361
E value 1.0e-49
Match length 125
% identity 75

NCBI Description (Z46959) acetohydroxyacid synthase [Gossypium hirsutum]

- Seq. No. 24182

Contig ID 113739\_1.R1040

5'-most EST uC-gmflminsoy057d07b1

Method BLASTX
NCBI GI g4566530
BLAST score 268
E value 2.0e-23
Match length 113
% identity 43

NCBI Description (AF109733) SWI/SNF-related, matrix-associated,

actin-dependent regulator of chromatin D1 [Homo sapiens]

Seq. No. 24183

Contig ID 113774\_1.R1040 5'-most EST zhf700959401.h1

Method BLASTX
NCBI GI g2462911
BLAST score 818
E value 1.0e-87
Match length 239
% identity 57

NCBI Description (283832) UDP-glucose: sterol glucosyltransferase [Avena

sativa]

Seq. No. 24184

Contig ID 113784 1.R1040



5'-most EST kl1701207679.h1

Method BLASTX
NCBI GI g4512616
BLAST score 352
E value 3.0e-33
Match length 127
% identity 60

NCBI Description (AC004793) Contains similarity to gi\_1653332 extragenic

suppressor (SuhB) from Synechocystis sp. gb\_D90912 and is a member of the Inositol monophophatase family PF\_00459. EST

gb\_AA597395 comes from this gene. [Arabidopsis tha

Seq. No. 24185

Contig ID 113785 1.R1040 5'-most EST taw700655525.h1

Method BLASTX
NCBI GI g4204286
BLAST score 174
E value 2.0e-21
Match length 146
% identity 47

NCBI Description (AC003027) Unknown protein [Arabidopsis thaliana]

Seq. No. 24186

Contig ID 113814\_1.R1040 5'-most EST rlr700901521.h1

Seq. No. 24187

Contig ID 113846\_1.R1040 5'-most EST taw700655657.h1

Seq. No. 24188

Contig ID 113848 1.R1040 5'-most EST pmv700892835.h1

Method BLASTX
NCBI GI g2655008
BLAST score 131
E value 5.0e-09
Match length 93
% identity 40

NCBI Description (AF017144) (1-4)-beta-mannan endohydrolase [Lycopersicon

esculentum]

Seq. No. 24189

Contig ID 113862\_1.R1040 5'-most EST taw700655701.h1

Seq. No. 24190

Contig ID 113883 1.R1040

5'-most EST g5677426

Seq. No. 24191

Contig ID 113909\_1.R1040

5'-most EST jC-gmfl02220115c05a1

Method BLASTX NCBI GI g4538928 BLAST score 268



E value 2.0e-23
Match length 102
% identity 61

NCBI Description (AL049483) putative protein [Arabidopsis thaliana]

Seq. No. 24192

Contig ID 113909 2.R1040 5'-most EST jC-gmle01810089f10d1

Method BLASTX
NCBI GI g4538928
BLAST score 196
E value 1.0e-14
Match length 55
% identity 75

NCBI Description (AL049483) putative protein [Arabidopsis thaliana]

Seq. No. 24193

Contig ID 113914\_1.R1040 5'-most EST smc700748821.h1

Method BLASTX
NCBI GI g2317908
BLAST score 424
E value 3.0e-45
Match length 139
% identity 37

NCBI Description (U89959) Unknown protein [Arabidopsis thaliana]

Seq. No. 24194

Contig ID 113923\_1.R1040 5'-most EST taw700655793.h1

Seq. No. 24195

Contig ID 113927\_1.R1040 5'-most EST asn701138430.h1

Method BLASTX
NCBI GI g4558659
BLAST score 678
E value 2.0e-71
Match length 183
% identity 68

NCBI Description (AC007063) unknown protein [Arabidopsis thaliana]

Seq. No. 24196

Contig ID 113945\_1.R1040 5'-most EST taw700655821.h1

Seq. No. 24197

Contig ID 113950\_1.R1040 5'-most EST rca701001106.h1

Method BLASTX
NCBI GI g4406804
BLAST score 318
E value 4.0e-29
Match length 90
% identity 54

NCBI Description (AC006304) proline iminopeptidase [Arabidopsis thaliana]



Seq. No. 24198

Contig ID 113990\_1.R1040

5'-most EST g5678039

Seq. No. 24199

Contig ID 114012 1.R1040 5'-most EST fjg700968490.h1

Seq. No. 24200

Contig ID 114037\_1.R1040 5'-most EST eep700869002.h1

Seq. No. 24201

Contig ID 114037 2.R1040 5'-most EST taw700660009.h1

Seq. No. 24202

Contig ID 114047\_1.R1040 5'-most EST wvk700682549.h2

Method BLASTX
NCBI GI g1354849
BLAST score 145
E value 6.0e-14
Match length 58
% identity 69

NCBI Description (U57350) epoxide hydrolase [Nicotiana tabacum]

Seq. No. 24203

Contig ID 114088 1.R1040 5'-most EST hyd700726394.h1

Method BLASTX
NCBI GI g2832618
BLAST score 630
E value 4.0e-68
Match length 231
% identity 29

NCBI Description (AL021711) putative protein [Arabidopsis thaliana]

Seq. No. 24204

Contig ID 114134\_1.R1040 5'-most EST pmv700891253.h1

Seq. No. 24205

Contig ID 114135\_1.R1040 5'-most EST taw700656248.h1

Method BLASTN
NCBI GI g2921509
BLAST score 98
E value 8.0e-48
Match length 186
% identity 88

NCBI Description Fritillaria agrestis clp-like energy-dependent protease

(clpP) mRNA, complete cds

Seq. No. 24206

Contig ID 114137\_1.R1040 5'-most EST zzp700829782.h1



```
BLASTX
Method
NCBI GI
                  q3023197
BLAST score
                  1081
E value
                  1.0e-118
Match length
                  257
% identity
                  80
                  14-3-3-LIKE PROTEIN D (SGF14D) >gi 1575731 (U70536) SGF14D
NCBI Description
                  [Glycine max]
Seq. No.
                  24207
                  114154 1.R1040
Contig ID
5'-most EST
                  g4299681
Method
                  BLASTX
NCBI GI
                  q4006919
BLAST score
                  262
E value
                  2.0e-22
Match length
                  70
% identity
                  76
NCBI Description (Z99708) ribosomal protein [Arabidopsis thaliana]
                  24208
Seq. No.
Contig ID
                  114156 1.R1040
5'-most EST
                  cle700967788.h1
Method
                  BLASTX
                  q4056487
NCBI GI
BLAST score
                  233
E value
                  1.0e-19
                  75
Match length
% identity
NCBI Description (AC005896) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  24209
                  114170 1.R1040
Contig ID
                  taw700656354.h1
5'-most EST
Seq. No.
                  24210
                  114179 1.R1040
Contig ID
5'-most EST
                  taw700656377.hl
Method
                  BLASTX
NCBI GI
                  g3953456
BLAST score
                  164
                  2.0e-11
E value
Match length
                  61
                  54
% identity
NCBI Description (AC002328) F20N2.1 [Arabidopsis thaliana]
Seq. No.
                  24211
                  114185 1.R1040
Contig ID
5'-most EST
                  leu701148703.h1
Method
                  BLASTX
                  g2494275
NCBI GI
BLAST score
                  148
E value
                  1.0e-09
```

Match length 36 % identity 69

NCBI Description ELONGATION FACTOR P (EF-P) >gi\_1399829 (U59235) elongation

factor P [Synechococcus PCC7942]



24212 Seq. No. 114186 1.R1040 Contig ID taw700656387.hl 5'-most EST BLASTN Method g18850 NCBI GI 33 BLAST score 4.0e-09 E value Match length 81 85 % identity NCBI Description H.lupulus (cv.Spalter) RNA (S10o) for 7S (SRP) RNA 24213 Seq. No. 114197 1.R1040 Contig ID smc700749687.hl 5'-most EST 24214 Seq. No. 114216 1.R1040 Contig ID taw700656449.h1 5'-most EST 24215 Seq. No. 114222 1.R1040 · Contig ID taw700656463.h1 5'-most EST BLASTN Method q1000861 NCBI GI BLAST score 208 1.0e-113 E value 212 Match length 100 % identity NCBI Description Homo sapiens creatine kinase B mRNA, complete cds 24216 Seq. No. 114223 1.R1040 Contig ID q5057720 5'-most EST Method BLASTX q2997591 NCBI GI 295 BLAST score 1.0e-26 E value 73 Match length 78 % identity (AF020814) glucose-6-phosphate/phosphate-translocator NCBI Description precursor [Pisum sativum] 24217 Seq. No. 114233 1.R1040 Contig ID wvk700682489.h2 5'-most EST 24218 Seq. No. 114236 1.R1040 Contig ID taw700656492.h1 5'-most EST 24219 Seq. No.

Contig ID 114240\_1.R1040 5'-most EST wvk700682505.h2

Method BLASTX
NCBI GI g2181184
BLAST score 216



E value 9.0e-18 Match length 86 % identity 50

NCBI Description (Y13577) JR3 protein [Arabidopsis thaliana]

Seq. No. 24220

Contig ID 114257\_1.R1040 5'-most EST wvk700682541.h2

Seq. No. 24221

Contig ID 114260 1.R1040

5'-most EST uC-gmrominsoy107a10b1

Method BLASTX
NCBI GI g3776567
BLAST score 279
E value 2.0e-24
Match length 215
% identity 39

NCBI Description (AC005388) Strong similarity to F21B7.33 gi\_2809264 from A.

thaliana BAC gb AC002560. EST gb N65119 comes from this

gene. [Arabidopsis thaliana]

Seq. No. 24222

Contig ID 114264\_1.R1040 5'-most EST smc700749333.h1

Method BLASTN
NCBI GI g642961
BLAST score 197
E value 1.0e-107
Match length 245
% identity 96

NCBI Description Human synaptotagmin I mRNA, 3' UTR

Seq. No. 24223

Contig ID 114283 1.R1040 5'-most EST asn701135868.h1

Seq. No. 24224

Contig ID 114298 1.R1040 5'-most EST gsv701050168.h1

Seq. No. 24225

Contig ID 114301\_1.R1040 5'-most EST taw700656635.h1

Seq. No. 24226

Contig ID 114304 1.R1040 5'-most EST taw700656769.h1

Seq. No. 24227

Contig ID 114307\_1.R1040 5'-most EST epx701106348.h1

Method BLASTX
NCBI GI g3249066
BLAST score 427
E value 5.0e-42
Match length 174

3836



% identity 65

NCBI Description (AC004473) Similar to S. cerevisiae SIK1P protein

gb 984964. ESTs gb\_F15433 and gb AA395158 come from this

gene. [Arabidopsis thaliana]

Seq. No. 24228

Contig ID 114315\_1.R1040 5'-most EST taw700656672.h1

Seq. No. 24229

Contig ID 114319\_1.R1040 5'-most EST taw700658889.h1

Seq. No. 24230

Contig ID 114321 2.R1040 5'-most EST taw700656686.h1

Seq. No. 24231

Contig ID 114324\_1.R1040 5'-most EST taw700656695.h1

Seq. No. 24232

Contig ID 114329 1.R1040 5'-most EST fua701040964.h1

Seq. No. 24233

Contig ID 114348\_1.R1040 5'-most EST kl1701213230.h1

Method BLASTX
NCBI GI g3080447
BLAST score 480
E value 1.0e-47
Match length 314
% identity 42

NCBI Description (AL022605) putative protein [Arabidopsis thaliana]

Seq. No. 24234

Contig ID 114350\_1.R1040 5'-most EST taw700656771.h1

Method BLASTX
NCBI GI g4263509
BLAST score 365
E value 4.0e-35
Match length 99
% identity 71

NCBI Description (AC004044) hypothetical protein [Arabidopsis thaliana]

Seq. No. 24235

Contig ID 114358\_1.R1040 5'-most EST taw700656788.h1

Seq. No. 24236

Contig ID 114359\_1.R1040 5'-most EST kmv700738368.h1

Method BLASTX NCBI GI g4455209 BLAST score 229



E value 4.0e-19 Match length 74 64 % identity

NCBI Description (AL035440) putative Proline synthetase associated protein

[Arabidopsis thaliana]

24237 Seq. No.

114359 2.R1040 Contig ID 5'-most EST wrg700787109.h2

Seq. No. 24238

114362 1.R1040 Contig ID taw700656794.h1 5'-most EST

Seq. No. 24239

114376 1.R1040 Contig ID 5'-most EST taw700656819.h1

24240 Seq. No.

114391 1.R1040 Contig ID 5'-most EST pcp700994484.h1

Seq. No. 24241

Contig ID 114411 1.R1040 5'-most EST zsg701122666.h1

Method BLASTX NCBI GI g4454051 BLAST score 1379 E value 1.0e-153 Match length 327 % identity 76

(AL035394) putative polygalacturonase [Arabidopsis NCBI Description

thaliana]

Seq. No. 24242

Contig ID 114420 1.R1040 5'-most EST taw700657705.h1

24243 Seq. No.

114430 1.R1040 Contig ID 5'-most EST jC-gmle01810062c05a1

Seq. No. 24244

114432 1.R1040 Contig ID taw700656920.h1 5'-most EST

BLASTX Method NCBI GI q4455171 BLAST score 243 2.0e-26 E value Match length 88

% identity

NCBI Description (AL035521) hypothetical protein [Arabidopsis thaliana]

Seq. No. 24245

114444 1.R1040 Contig ID 5'-most EST jC-gmle01810072b06d1

Method BLASTX



```
g1653513
NCBI GI
BLAST score
                   144
                   6.0e-09
E value
Match length
                   58
                   47
% identity
NCBI Description (D90914) hypothetical protein [Synechocystis sp.]
                  24246
Seq. No.
Contig ID
                   114445 1.R1040
5'-most EST
                  taw700656950.hl
                  24247
Seq. No.
                  114493 1.R1040
Contig ID
                   jC-qmle01810033f04d1
```

5'-most EST jC-gmle0181
Method BLASTX
NCBI GI g728777
BLAST score 243
E value 2.0e-20
Match length 99

% identity 49
NCBI Description ACTIVATOR 1 36 KD SUBUNIT (REPLICATION FACTOR C 36 KD SUBUNIT) (A1 36 KD SUBUNIT) (RF-C 36 KD SUBUNIT) (RFC36)

>gi\_1498257 (L07540) replication factor C, 36-kDa subunit

[Homo sapiens]

Seq. No. 24248

Contig ID 114505\_1.R1040 5'-most EST taw700657086.h1

Seq. No. 24249

Contig ID 114530\_1.R1040 5'-most EST hyd700728314.h1

Seq. No. 24250

Contig ID 114547 1.R1040

5'-most EST jC-gmf102220065d08d1

Method BLASTX
NCBI GI g133872
BLAST score 222
E value 4.0e-18
Match length 52
% identity 87

NCBI Description 30S RIBOSOMAL PROTEIN S1, CHLOROPLAST PRECURSOR (CS1)

>gi\_282838\_pir\_\_S26494 ribosomal protein S1, chloroplast spinach >gi\_322404\_pir\_\_A44121 small subunit ribosomal
protein CS1, CS-S2 - spinach >gi\_18060\_emb\_CAA46927\_
(X66135) ribosomal protein S1 [Spinacia oleracea]
>gi\_170143 (M82923) chloroplast ribosomal protein S1

[Spinacia oleracea]

Seq. No. 24251

Contig ID 114555\_1.R1040 5'-most EST rca701002166.h1

Method BLASTX
NCBI GI g3335378
BLAST score 160
E value 9.0e-11



85 Match length % identity

(AC003028) Myb-related transcription activator [Arabidopsis NCBI Description

thaliana]

24252 Seq. No.

114562 1.R1040 Contig ID taw700657164.hl 5'-most EST

BLASTX Method g4406769 NCBI GI 500 BLAST score 1.0e-50 E value 161 Match length 63 % identity

NCBI Description (AC006836) putative translin [Arabidopsis thaliana]

Seq. No.

24253 114592 1.R1040 Contig ID uaw700660832.hl 5'-most EST

24254 Seq. No.

114592 2.R1040 Contig ID uC-gmronoir065g12b1 5'-most EST

24255 Seq. No.

114609 1.R1040 Contig ID  $sat701\overline{0}06531.h1$ 5'-most EST

24256 Seq. No.

114619 1.R1040 Contig ID taw700657237.h1 5'-most EST

BLASTN Method g2224548 NCBI GI 246 BLAST score 1.0e-136 E value 265 Match length 99 % identity

NCBI Description Human mRNA for KIAA0304 gene, complete cds

24257 Seq. No.

114628 1.R1040 Contig ID 5'-most EST sat701003878.h1

24258 Seq. No.

114656 1.R1040 Contig ID zsq701122177.h1 5'-most EST

BLASTN Method g534971 NCBI GI BLAST score 170 8.0e-91 E value 322 Match length % identity 88

V.faba (var. minor) mRNA for alpha 1,4-glucan phosphorylase NCBI Description

L isoform

24259 Seq. No.

114663 1.R1040 Contig ID



```
5'-most EST
                  taw700659976.h1
Method
                  BLASTX
NCBI GI
                  a4006902
BLAST score
                  194
E value
                  2.0e-15
Match length
                  43
% identity
                  77
NCBI Description
                  (Z99708) putative protein [Arabidopsis thaliana]
Seq. No.
                  24260
                  114679 1.R1040
Contig ID
                  txt700736068.h1
5'-most EST
Seq. No.
                  24261
                  114683 1.R1040
Contig ID
5'-most EST
                  jC-gmf102220142d03a1
```

Seq. No. 24262 Contig ID 114683 2.R1040

5'-most EST g5677171

24263 Seq. No. 114699 1.R1040 Contig ID 5'-most EST taw700657360.h1

24264 Seq. No.

Contig ID 114701 1.R1040 5'-most EST uC-gmflminsoy046b10b1 Method BLASTX NCBI GI g1877183 BLAST score 184

2.0e-13 E value Match length 95 40 % identity

NCBI Description (Y11586) putative mitochondrial matrix protein

[Chlamydomonas reinhardtii]

Seq. No. 24265 Contig ID 114705 1.R1040 5'-most EST jC-gmle01810051a08d1

Seq. No. 24266

114705 2.R1040 Contig ID 5'-most EST taw700660326.hl

24267 Seq. No.

114721 1.R1040 Contig ID 5'-most EST jex700907350.h1

BLASTX Method g2335096 NCBI GI BLAST score 163 E value 2.0e-11 Match length 52 % identity

NCBI Description (AC002339) hypothetical protein [Arabidopsis thaliana]

Seq. No. 24268



```
114744 1.R1040
Contig ID
                  taw700657441.hl
5'-most EST
                  24269
Seq. No.
                  114760 1.R1040
Contig ID
                  taw700657467.hl
5'-most EST
                  BLASTX
Method
NCBI GI
                  g2632105
                  505
BLAST score
                  2.0e-51
E value
                  118
Match length
                  81
% identity
                   (Z98760) arginyl-tRNA synthetase [Arabidopsis thaliana]
NCBI Description
                   >qi 4539426 emb CAB38959.1_ (AL049171) arginyl-tRNA
                   synthetase [Arabidopsis thaliana]
                   24270
Seq. No.
                   114765 1.R1040
Contig ID
                   taw700657475.h1
5'-most EST
                   BLASTX
Method
                   g3242701
NCBI GI
BLAST score
                   185
                   5.0e-14
E value
                   43
Match length
% identity
NCBI Description (AC003040) hypothetical protein [Arabidopsis thaliana]
                   24271
Seq. No.
                   114767 1.R1040
Contig ID
                   xzy700966802.hl
5'-most EST
                   BLASTX
Method
                   g4455246
NCBI GI
                   355
BLAST score
                   6.0e-40
E value
                   146
Match length
                   59
% identity
NCBI Description (AL035523) putative protein [Arabidopsis thaliana]
                   24272
Seq. No.
                   114785 1.R1040
Contig ID
                   smc700744591.hl
 5'-most EST
                   BLASTX
Method
                   q2443329
NCBI GI
BLAST score
                   161
                   4.0e-11
E value
                   86
Match length
                   41
 % identity
                   (D86122) Mei2-like protein [Arabidopsis thaliana]
 NCBI Description
                   24273
 Seq. No.
                   114789 1.R1040
 Contig ID
                   taw700657695.hl
 5'-most EST
                   BLASTX
 Method
 NCBI GI
                   q4455335
 BLAST score
                   390
 E value
                   5.0e-38
```

3842

89

Match length



% identity

NCBI Description (AL035525) putative protein [Arabidopsis thaliana]

Seq. No.

24274

Contig ID 5'-most EST

114793 1.R1040 taw700657521.h1

Seq. No.

24275

Contig ID 5'-most EST 114804 1.R1040 fde700874313.h1

Seq. No.

24276

Contig ID 5'-most EST 114808 1.R1040 taw700<del>6</del>59114.h1

Seq. No.

24277

Contig ID 5'-most EST 114830 1.R1040 taw700659141.h1

Seq. No.

24278

Contig ID

114833 1.R1040

5'-most EST

jC-qmro02910023e05d1

Method NCBI GI BLASTX

q4454019

BLAST score

190

E value

4.0e-14

Match length

177

% identity

32

NCBI Description

(AL035396) SRG1-like protein [Arabidopsis thaliana]

Seq. No.

24279

Contig ID

114836 1.R1040

5'-most EST

taw700659148.h1

Seq. No.

24280

Contig ID 5'-most EST 114844 1.R1040 taw700659163.h1

Method

BLASTX

NCBI GI

g1463123

BLAST score

235

E value

1.0e-19

Match length

58

% identity

83

NCBI Description

(U34817) violaxanthin de-epoxidase precursor [Nicotiana

tabacum]

Seq. No.

24281

Contig ID

114854 1.R1040

5'-most EST

 $a55090\overline{4}2$ BLASTX

Method

NCBI GI

g2190551

BLAST score E value

157 4.0e-10

Match length

48

% identity

62

NCBI Description

(AC001229) Similar to C. elegans hypothetical protein K07C5.6 (gb Z71181). ESTs gb H36844, gb AA394956 come from



## this gene. [Arabidopsis thaliana]

24282 Seq. No. 114854 2.R1040 Contig ID pcp700989558.hl 5'-most EST

BLASTX Method NCBI GI q4006865 BLAST score 1238 E value 1.0e-136 Match length 326 70 % identity

(Z99707) putative protein [Arabidopsis thaliana] NCBI Description

Seq. No. 24283

114881 1.R1040 Contig ID 5'-most EST uC-gmropic105d03b1

Method BLASTX NCBI GI g1617268 BLAST score 627 E value 1.0e-65 Match length 149 75 % identity

NCBI Description (Z72153) acyl CoA synthetase [Brassica napus]

24284 Seq. No.

Contig ID 114892 1.R1040 5'-most EST taw700657652.hl

Method BLASTX NCBI GI g3608495 BLAST score 917 E value 2.0e-99 213 Match length % identity 88

(AF089738) plastid division protein FtsZ [Arabidopsis NCBI Description thaliana] >gi\_4510351\_gb\_AAD21440.1\_ (AC006921) plastid

division protein FtsZ [Arabidopsis thaliana]

24285 Seq. No.

114894 1.R1040 Contig ID 5'-most EST uaw700662114.h1

Method BLASTX NCBI GI g3386600 BLAST score 497 E value 2.0e-50 Match length 112 87 % identity

(AC004665) putative glycoprotein [Arabidopsis thaliana] NCBI Description

Seq. No.

24286 114903 1.R1040 Contig ID 5'-most EST smc700744669.hl

Seq. No. 24287

Contig ID 114916 1.R1040 5'-most EST leu701149828.h1

Method BLASTX NCBI GI q2353173



BLAST score 252 E value 5.0e-23 Match length 77 % identity 75

NCBI Description (AF015543) sigma factor 2 [Arabidopsis thaliana]

Seq. No. 24288

Contig ID 114950 1.R1040

5'-most EST uC-gmflminsoy057g07b1

Seq. No. 24289

Contig ID 114953\_1.R1040 5'-most EST taw700657749.h1

Seq. No. 24290

Contig ID 114965\_1.R1040 5'-most EST ncj700980857.h1

Method BLASTX
NCBI GI g2832661
BLAST score 249
E value 5.0e-29
Match length 92
% identity 75

NCBI Description (AL021710) pherophorin - like protein [Arabidopsis

thaliana]

Seq. No. 24291

Contig ID 114986\_1.R1040 5'-most EST taw700658430.h1

Method BLASTX
NCBI GI g4567316
BLAST score 258
E value 1.0e-22
Match length 77

% identity 62

NCBI Description (AC005956) hypothetical protein [Arabidopsis thaliana]

Seq. No. 24292

Contig ID 115000\_1.R1040 5'-most EST taw700657820.h1

Seq. No. 24293

Contig ID 115013\_1.R1040 5'-most EST smc700749638.h1

Seq. No. 24294

Contig ID 115015\_1.R1040 5'-most EST taw700659441.h1

Seq. No. 24295

Contig ID 115016\_1.R1040 5'-most EST taw700659442.h1

Seq. No. 24296

Contig ID 115025\_1.R1040 5'-most EST g5753439

Method BLASTX



NCBI GI g465898 BLAST score 220 E value 8.0e-18 Match length 151 % identity 36

NCBI Description HYPOTHETICAL HELICASE K12H4.8 IN CHROMOSOME III

>gi\_630692\_pir\_\_S44849 K12H4.8 protein - Caenorhabditis
elegans >gi\_289703 (L14331) homology with eukaryotic

initiation factor-4A (eIF-4A) and E. coli Ribonuclease III;

coded for by C. elegans cDNA GenBank: T02268; putative

[Caenorhabditis elegans]

Seq. No. 24297

Contig ID 115034 1.R1040 5'-most EST taw700657866.h1

Seq. No. 24298

Contig ID 115039\_1.R1040 5'-most EST asn701136693.h1

Method BLASTX
NCBI GI g2443329
BLAST score 833
E value 2.0e-89
Match length 208
% identity 75

NCBI Description (D86122) Mei2-like protein [Arabidopsis thaliana]

Seq. No. 24299

Contig ID 115042\_1.R1040 5'-most EST smc700749676.h1

Seq. No. 24300

Contig ID 115043\_1.R1040 5'-most EST taw700657878.h1

Seq. No. 24301

Contig ID 115070\_1.R1040 5'-most EST hyd700728695.h1

Seq. No. 24302

Contig ID 115071 1.R1040

5'-most EST jC-gmro02910010d03a1

Seq. No. 24303

Contig ID 115073\_1.R1040 5'-most EST wrg700788649.h1

Seq. No. 24304

Contig ID 115084\_1.R1040 5'-most EST awf700842952.h1

Method BLASTX
NCBI GI g505267
BLAST score 149
E value 8.0e-10
Match length 101
% identity 41

NCBI Description (X77111) chitinase, class V [Nicotiana tabacum]



Seq. No. 24305

Contig ID 115100\_1.R1040 5'-most EST fC-gmse700659340f5

Method BLASTX
NCBI GI g2495184
BLAST score 1077
E value 1.0e-118
Match length 271
% identity 75

NCBI Description PROTOPORPHYRINOGEN OXIDASE, CHLOROPLAST PRECURSOR (PPO)

>gi\_1877018\_dbj\_BAA11820\_ (D83139) protoporphyrinogen

oxidase [Arabidopsis thaliana]

Seq. No. 24306

Contig ID 115105\_1.R1040 5'-most EST uaw700660753.h1

Method BLASTX
NCBI GI g2583112
BLAST score 224
E value 1.0e-18
Match length 96
% identity 46

NCBI Description (AC002387) putative PD1-like DNA-binding protein

[Arabidopsis thaliana]

Seq. No. 24307

Contig ID 115118\_1.R1040 5'-most EST taw700657981.h1

Method BLASTN
NCBI GI g1524177
BLAST score 116
E value 2.0e-58
Match length 228
% identity 88

NCBI Description M.sativa mRNA for proteasome subunit

Seq. No. 24308

Contig ID 115170\_1.R1040 5'-most EST uaw700666512.h1

Seq. No. 24309

Contig ID 115183 1.R1040 5'-most EST leu701157244.h1

Method BLASTX
NCBI GI g1699023
BLAST score 988
E value 1.0e-107
Match length 233
% identity 81

NCBI Description (U78866) putative arginine-aspartate-rich RNA binding

protein [Arabidopsis thaliana] >gi\_1699051 (U78867)
putative aspartate-arginine-rich mRNA binding protein

[Arabidopsis thaliana]

Seq. No. 24310

Contig ID 115192\_1.R1040



```
5'-most EST
                   jsh701066286.h1
Method
                   BLASTX
NCBI GI
                   g4538974
BLAST score
                   261
                   1.0e-22
E value
Match length
                   94
                   57
% identity
```

(AL049487) hypothetical protein [Arabidopsis thaliana] NCBI Description

24311 Seq. No. Contig ID 115204 1.R1040

5'-most EST taw700658109.hl

24312 Seq. No.

115217 1.R1040 Contig ID 5'-most EST taw700658127.h1

24313 Seq. No.

115221 1.R1040 Contig ID 5'-most EST uaw700660923.h1

Seq. No. 24314

115225 1.R1040 Contig ID

5'-most EST jC-gmro02910009f10a1

Method BLASTX g3193300 NCBI GI BLAST score 319 E value 2.0e-29 Match length 138 % identity 49

NCBI Description (AF069298) No definition line found [Arabidopsis thaliana]

Seq. No. 24315

115231 1.R1040 Contig ID 5'-most EST zsg701123179.h1

Seq. No. 24316

115234 1.R1040 Contig ID

5'-most EST jC-gmro02800038d07d1

Seq. No. 24317

115259 1.R1040 Contig ID 5'-most EST jC-gmle01810008f05d1

Seq. No. 24318

115273 1.R1040 Contig ID 5'-most EST fC-gmse700658206r6

Method BLASTX NCBI GI q1280611 BLAST score 482 2.0e-48 E value Match length 126 % identity

NCBI Description (U53860) steroid reductase DET2 [Arabidopsis thaliana]

Seq. No. 24319

Contig ID 115284 1.R1040

3848



5'-most EST fde700872745.h1 BLASTX Method g3212867 NCBI GI 440 BLAST score 1.0e-43 E value 136 Match length 59 % identity (AC004005) unknown protein [Arabidopsis thaliana] NCBI Description 24320 Seq. No. 115293 1.R1040 Contig ID uC-gmropic044a11b1 5'-most EST Method BLASTX NCBI GI q4490333 147 BLAST score 2.0e-09 E value 70 Match length 60 % identity (AL035656) EF-Hand containing protein-like [Arabidopsis NCBI Description thaliana] 24321 Seq. No. 115295 1.R1040 Contig ID vwf700677174.hl 5'-most EST 24322 Seq. No. 115300 1.R1040 Contig ID wrg700788077.hl 5'-most EST BLASTX Method g3096910 NCBI GI 1300 BLAST score 1.0e-144 E value 294 Match length 82 % identity (AJ005813) neoxanthin cleavage enzyme [Arabidopsis NCBI Description thaliana] 24323 Seq. No. 115315 1.R1040 Contig ID uC-gmropic043e03b1 5'-most EST BLASTX Method NCBI GI q2252843 BLAST score 324 E value 9.0e-30 168 Match length 48 % identity (AF013293) No definition line found [Arabidopsis thaliana] NCBI Description Seq. No. 24324 115333 1.R1040 Contig ID 5'-most EST gsv701045358.hl

Seq. No. 24325

Contig ID 115340\_1.R1040 5'-most EST taw700658304.h1

Method BLASTN NCBI GI g198573

3849



BLAST score 131 E value 1.0e-67 Match length 208 % identity 93

NCBI Description Mouse hydrophilic protein (KE2 wt) mRNA, complete cds

Seq. No. 24326

Contig ID 115341\_1.R1040 5'-most EST taw700658311.h1

Method BLASTN
NCBI GI g204681
BLAST score 140
E value 6.0e-73
Match length 159
% identity 97

NCBI Description Rattus rattus mitochondrial IF1 protein mRNA, complete cds

Seq. No. 24327

Contig ID 115342\_1.R1040 5'-most EST taw700658368.h1

Method BLASTN
NCBI GI g55627
BLAST score 302
E value 1.0e-169
Match length 323
% identity 98

NCBI Description Messenger RNA for rat preproalbumin

Seq. No. 24328

Contig ID 115351\_1.R1040 5'-most EST taw700658317.h1

Method BLASTN
NCBI GI g1747520
BLAST score 82
E value 2.0e-38
Match length 246
% identity 83

NCBI Description Homo sapiens microsomal glutathione S-transferase 2 (MGST2) mRNA, complete cds >gi\_4505180\_ref\_NM\_002413.1\_MGST2\_ Homo

sapiens microsomal glutathione S-transferase 2 (MGST2)

mRNA, and translated products

Seq. No. 24329

Contig ID 115355\_1.R1040 5'-most EST smc700745575.h1

Seq. No. 24330

Contig ID 115356\_1.R1040 5'-most EST taw700658325.h1

Method BLASTN
NCBI GI g472851
BLAST score 191
E value 1.0e-103
Match length 279
% identity 92

NCBI Description Mus musculus RNA1 homolog (Fug1) mRNA, complete cds



Seq. No. 24331

Contig ID 115357\_1.R1040 5'-most EST taw700658443.h1

Method BLASTN
NCBI GI g204075
BLAST score 275
E value 1.0e-153
Match length 275

% identity 100 NCBI Description Rat fatty liver acid binding protein (FABP) mRNA, complete

cds. >gi\_204083\_gb\_J00732\_RATFABPL Rat liver fatty acid

binding protein (FABP) mRNA

Seq. No. 24332

Contig ID 115362\_1.R1040 5'-most EST taw700658339.h1

Method BLASTN
NCBI GI g4006931
BLAST score 143
E value 9.0e-75
Match length 275
% identity 88

NCBI Description Bos taurus mRNA for b17.2 subunit of NADH:ubiquinone

oxidoreductase complex (complex I)

Seq. No. 24333

Contig ID 115366\_1.R1040

5'-most EST jC-gmro02910008g11d1

Seq. No. 24334

Contig ID 115368\_1.R1040 5'-most EST smc700745548.h1 Method BLASTN

Method BLASTN
NCBI GI g3341993
BLAST score 59
E value 1.0e-24
Match length 151
% identity 85

NCBI Description Homo sapiens mitochondrial proteolipid 68MP homolog mRNA, nuclear gene encoding mitochondrial protein, complete cds

Seq. No. 24335

Contig ID 115369\_1.R1040 5'-most EST taw700658350.h1

Method BLASTN
NCBI GI g603497
BLAST score 117
E value 3.0e-59
Match length 231
% identity 88

NCBI Description Mouse thymic stromal cell mRNA for TLSF-beta, complete cds

Seq. No. 24336

Contig ID 115372 1.R1040 5'-most EST smc700745541.h1

Method BLASTN NCBI GI g467779



BLAST score 81 E value 8.0e-38 Match length 120 % identity 93

NCBI Description M.musculus peroxisome proliferator-activated receptor alpha

gene. Exon

Seq. No. 24337

Contig ID 115376 1.R1040 5'-most EST taw700658361.h1

Method BLASTN
NCBI GI g2959435
BLAST score 186
E value 1.0e-100
Match length 194
% identity 99

NCBI Description Rattus sp. mRNA for NADH-cytochrome b5 reductase, complete

cds

Seq. No. 24338

Contig ID 115379\_1.R1040 5'-most EST taw700658366.h1

Seq. No. 24339

Contig ID 115380\_1.R1040 5'-most EST taw700658367.h1 Method BLASTN

Method BLASTN
NCBI GI g2072091
BLAST score 61
E value 6.0e-26
Match length 137

Match length 137 % identity 87

NCBI Description Rattus norvegicus Na+-Ca+ exchanger (NCX1) gene, exon 1-Ht

Seq. No. 24340

Contig ID 115390\_1.R1040 5'-most EST smc700745516.h1

Method BLASTN
NCBI GI g1020410
BLAST score 242
E value 1.0e-134
Match length 270
% identity 99

NCBI Description Rattus norvegicus mRNA for selenoprotein P, complete cds

Seq. No. 24341

Contig ID 115395\_1.R1040 5'-most EST taw700658391.h1

Method BLASTN
NCBI GI g204516
BLAST score 103
E value 6.0e-51
Match length 115
% identity 97

NCBI Description Rat liver glutathione S-transferase Yc subunit mRNA,

complete cds



Seq. No. 24342

Contig ID 115408\_1.R1040 5'-most EST taw700658427.h1

Method BLASTN
NCBI GI g2317645
BLAST score 55
E value 3.0e-22
Match length 147
% identity 85

NCBI Description Homo sapiens mRNA for smallest subunit of ubiquinol-cytochrome c reductase, complete cds

Seq. No. 24343

Contig ID 115414\_1.R1040 5'-most EST smc700745658.h1

Seq. No. 24344

Contig ID 115415\_1.R1040 5'-most EST smc700745655.h1

Seq. No. 24345

Contig ID 115423\_1.R1040 5'-most EST smc700745643.h1

Seq. No. 24346

Contig ID 115424\_1.R1040 5'-most EST taw700658455.h1

Seq. No. 24347

Contig ID 115428\_1.R1040 5'-most EST smc700745636.h1

Seq. No. 24348

Contig ID 115429\_1.R1040 5'-most EST taw700658463.h1

Method BLASTN
NCBI GI g862386
BLAST score 93
E value 6.0e-45
Match length 226
% identity 87

NCBI Description Rattus norvegicus purine specific Na+ nucleoside

cotransporter (SPNT) mRNA, complete cds

Seq. No. 24349

Contig ID 115437\_1.R1040 5'-most EST taw700658478.h1

Method BLASTN
NCBI GI g202270
BLAST score 145
E value 5.0e-76
Match length 219
% identity 92

NCBI Description Mus musculus UCR-motif DNA-binding protein (UCRBP) mRNA,

complete cds

Seq. No. 24350



Contig ID 115450\_1.R1040 5'-most EST taw700658514.h1

Seq. No. 24351

Contig ID 115452\_1.R1040 5'-most EST taw700658518.h1

Method BLASTN
NCBI GI g3217024
BLAST score 55
E value 3.0e-22
Match length 207
% identity 82

NCBI Description Homo sapiens DNA sequence from PAC 97D16 on chromosome

6p21.3-22.2. Contains an unknown pseudogene, a 60S Ribosomal protein L24 (L30) LIKE pseudogene and histone genes H2BFC (H2B/c), H4FFP (H4/f pseudogene), H2AFC (H2A/c

Seq. No. 24352

Contig ID 115453\_1.R1040 5'-most EST fC-gmse700658166f5

Method BLASTN
NCBI GI g307145
BLAST score 239
E value 1.0e-132
Match length 419
% identity 89

NCBI Description Human lysyl oxidase-like protein mRNA, complete cds

Seq. No. 24353

Contig ID 115459\_1.R1040 5'-most EST smc700745364.h1

Seq. No. 24354

Contig ID 115467\_1.R1040 5'-most EST fC-gmse700658543f1

Method BLASTN
NCBI GI g2267160
BLAST score 574
E value 0.0e+00
Match length 663
% identity 96

NCBI Description Rattus norvegicus CD94 (Cd94) mRNA, complete cds

Seq. No. 24355

Contig ID 115471\_1.R1040 5'-most EST fC-gmse700658550g1

Method BLASTN
NCBI GI g485402
BLAST score 835
E value 0.0e+00
Match length 839
% identity 100

NCBI Description Rat mRNA for RAC protein kinase alpha, complete cds

Seq. No. 24356

Contig ID 115475 1.R1040 5'-most EST smc700745339.h1



Method BLASTN
NCBI GI g3242170
BLAST score 131
E value 1.0e-67
Match length 210
% identity 91

NCBI Description Homo sapiens DNA sequence from PAC 232K4 on chromosome 6p22.3. Contains the JUMONJI gene for a hypothetical 141.7 kD protein. Contains ESTs, STSs, a CA repeat polymorphism

and genomic marker D6S260", complete sequence [H

Seq. No. 24357

Contig ID 115480\_1.R1040 5'-most EST smc700745333.h1

Method BLASTN
NCBI GI g205795
BLAST score 223
E value 1.0e-122
Match length 258
% identity 96

NCBI Description Rat nuclear pore complex protein mRNA sequence

Seq. No. 24358

Contig ID 115487\_1.R1040 5'-most EST smc700745325.h1

Seq. No. 24359

Contig ID 115508\_1.R1040 5'-most EST taw700658605.h1

Seq. No. 24360

Contig ID 115512\_1.R1040 5'-most EST taw700658609.h1

Method BLASTN
NCBI GI g57040
BLAST score 193
E value 1.0e-105
Match length 193
% identity 100

NCBI Description R.norvegicus mRNA for calmodulin (pRCM1)

Seq. No. 24361

Contig ID 115514 1.R1040 5'-most EST smc700748686.h1

Method BLASTN
NCBI GI g191139
BLAST score 161
E value 1.0e-85
Match length 197
% identity 95

NCBI Description Chinese hamster metallothionein II (MT-II) mRNA

Seq. No. 24362

Contig ID 115519 1.R1040 5'-most EST smc700745479.h1

Method BLASTN NCBI GI g1710211



```
BLAST score 91
E value 8.0e-44
Match length 219
% identity 85
NCBL Description Human C
```

NCBI Description Human clone 23732 mRNA, partial cds

Seq. No. 24363

Contig ID 115529\_1.R1040 5'-most EST smc700748654.h1

Method BLASTN
NCBI GI g1842210
BLAST score 215
E value 1.0e-118
Match length 233
% identity 99

NCBI Description R.norvegicus mRNA for carnitine/acylcarnitine carrier

protein

Seq. No. 24364

Contig ID 115531\_1.R1040 5'-most EST smc700745451.h1

Seq. No. 24365

Contig ID 115540\_1.R1040 5'-most EST smc700745436.h1

Method BLASTN
NCBI GI g2078459
BLAST score 39
E value 9.0e-13
Match length 125
% identity 83

NCBI Description Human cosmid clone LUCA17 from 3p21.3, complete sequence

[Homo sapiens]

Seq. No. 24366

Contig ID 115542\_1.R1040 5'-most EST smc700745433.h1

Seq. No. 24367

Contig ID 115543\_1.R1040 5'-most EST taw700658667.h1

Method BLASTN
NCBI GI g3719432
BLAST score 241
E value 1.0e-133
Match length 245
% identity 100

NCBI Description Rattus norvegicus tip associating protein (TAP) mRNA,

complete cds

Seq. No. 24368

Contig ID 115545\_1.R1040 5'-most EST taw700658669.h1

Method BLASTN
NCBI GI g1906793
BLAST score 239
E value 1.0e-132



Match length 239 % identity 100

NCBI Description Rattus norvegicus mRNA for phosphatidylinositol 4-kinase,

complete cds

Seq. No. 24369

Contig ID 115550\_1.R1040 5'-most EST smc700745416.h1

Method BLASTN
NCBI GI g2113880
BLAST score 74
E value 1.0e-33
Match length 202
% identity 90

NCBI Description Mus musculus Hifla gene, exon 2 to 15 and 2 joined CDS's

Seq. No. 24370

Contig ID 115551\_1.R1040 5'-most EST taw700658682.h1

Seq. No. 24371

Contig ID 115554\_1.R1040 5'-most EST smc700745411.h1

Seq. No. 24372

Contig ID 115555\_1.R1040 5'-most EST taw700658687.h1

Seq. No. 24373

Contig ID 115557 1.R1040 5'-most EST smc700745407.h1

Method BLASTN
NCBI GI g671559
BLAST score 177
E value 4.0e-95
Match length 205
% identity 97

NCBI Description M.musculus mRNA for centrosomin B

Seq. No. 24374

Contig ID 115559 1.R1040 5'-most EST taw700658694.h1

Seq. No. 24375

Contig ID 115580\_1.R1040 5'-most EST taw700658783.h1

Seq. No. 24376

Contig ID 115588 1.R1040

5'-most EST jC-gmst02400061c03a1

Seq. No. 24377

Contig ID 115618 1.R1040

5'-most EST jC-gmst02400076f10al

Seq. No. 24378

Contig ID 115620\_1.R1040

3857



5'-most	EST	smc700747281.h	1
omosc	LOT	SMC/UU/4/201.	[]

 Seq. No.
 24379

 Contig ID
 115624\_1.R1040

Contig ID 115624 1.RI040 5'-most EST smc700747272.h1

Seq. No. 24380

Contig ID 115629\_1.R1040 5'-most EST xpa700793958.h1

Seq. No. 24381

Contig ID 115650\_1.R1040

5'-most EST uC-gmflminsoy056f10b1

Seq. No. 24382

Contig ID 115660\_1.R1040 5'-most EST taw700658871.h1

Seq. No.

Contig ID 115688\_1.R1040

5'-most EST uC-gmrominsoy108d10b1

24383

Method BLASTX
NCBI GI g1916290
BLAST score 305
E value 2.0e-27
Match length 187
% identity 43

NCBI Description (U89876) ALY [Mus musculus]

Seq. No. 24384

Contig ID 115688\_2.R1040 5'-most EST taw700658922.h1

Method BLASTX
NCBI GI g1916290
BLAST score 105
E value 2.0e-10
Match length 71

% identity 56

NCBI Description (U89876) ALY [Mus musculus]

Seq. No. 24385

Contig ID 115703\_1.R1040 5'-most EST gsv701050921.h1

Seq. No. 24386

Contig ID 115736 1.R1040 5'-most EST taw700659023.h1

Seq. No. 24387

Contig ID 115750 1.R1040 5'-most EST taw700659042.h1

Method BLASTX
NCBI GI g2459440
BLAST score 775
E value 2.0e-82
Match length 247
% identity 61

3858

NCBI Description



```
NCBI Description (AC002332) putative receptor kinase [Arabidopsis thaliana]
                  24388
Seq. No.
                  115772 1.R1040
Contig ID
                  taw700659073.hl
5'-most EST
                  BLASTN
Method
NCBI GI
                  q563624
                  68
BLAST score
                  7.0e-30
E value
                  96
Match length
                   94
% identity
NCBI Description S.tuberosum (PU141) mRNA for U14 small nucleolar RNA
                   24389
Seq. No.
                   115775 1.R1040
Contig ID
                   jC-gmf102220052c06a1
5'-most EST
                   24390
Seq. No.
                   115787 1.R1040
Contig ID
                   uC-gmrominsoy222h12b1
5'-most EST
                   24391
Seq. No.
                   115798 1.R1040
Contig ID
                   taw700659120.hl
5'-most EST
                   24392
Seq. No.
                   115813 1.R1040
Contig ID
                   taw700659159.hl
5'-most EST
                   BLASTX
Method
                   q4512670
NCBI GI
BLAST score
                   389
                   2.0e-37
E value
                   201
Match length
% identity
                   40
                   (AC006931) putative cytochrome P450 [Arabidopsis thaliana]
NCBI Description
                   24393
Seq. No.
                   115825 1.R1040
Contig ID
                   pxt700946090.hl
5'-most EST
                   BLASTX
Method
                   q2739376
NCBI GI
BLAST score
                   484
                   1.0e-48
E value
Match length
                   129
 % identity
                   (AC002505) putative permease [Arabidopsis thaliana]
NCBI Description
 Seq. No.
                   24394
                   115833 1.R1040
Contig ID
                   taw700659189.h1
 5'-most EST
                   BLASTX
Method
                   g3252794
NCBI GI
 BLAST score
                   345
                   8.0e-33
 E value
                   92
 Match length
                   68
 % identity
                   (AB015615) isoamylase [Oryza sativa]
```



24395 Seq. No.

115869 1.R1040 Contig ID smc700744746.hl 5'-most EST

BLASTX Method NCBI GI q4454015 BLAST score 173 E value 1.0e-12 Match length 46 70 % identity

(AL035396) putative protein [Arabidopsis thaliana] NCBI Description

Seq. No.

24396 Contig ID 115903 1.R1040 5'-most EST taw700660601.h1

Seq. No.

24397

Contig ID 5'-most EST 115930 1.R1040 smc700744857.hl

Seq. No.

24398

Contig ID 5'-most EST 115936 1.R1040 pxt700943420.h1

Method BLASTX NCBI GI q1723239 BLAST score 391 E value 4.0e-38 Match length 111 % identity 63

HYPOTHETICAL 35.7 KD PROTEIN C26A3.11 IN CHROMOSOME I NCBI Description

>gi 1177358 emb CAA93234 (Z69240) putative amidohydrolase

[Schizosaccharomyces pombe]

Seq. No. 24399

115980 1.R1040 Contig ID 5'-most EST taw700660375.h1

Seq. No. 24400

115991 1.R1040 Contig ID 5'-most EST taw700659555.h1

Seq. No. 24401

116000 1.R1040 Contig ID 5'-most EST asn701139071.hl

Method BLASTX NCBI GI g1717755 BLAST score 473 E value 2.0e-47 Match length 174 52 % identity

TROPINONE REDUCTASE HOMOLOG (P29X) >gi 539028 pir\_ C48674 NCBI Description

tropinone reductase homolog - jimsonweed >gi\_424158 (L20475) 29kDa protein; high homology to aa sequence of

tropinone reductases [Datura stramonium]

Seq. No. 24402

Contig ID 116010 1.R1040



```
epx701108925.h1
5'-most EST
                  24403
Seq. No.
                  116013 1.R1040
Contig ID
5'-most EST
                  pcp700989813.hl
Method
                  BLASTX
                  a2864616
NCBI GI
                  300
BLAST score
                  2.0e-27
E value
                  71
Match length
% identity
NCBI Description (AL021811) hypothetical protein [Arabidopsis thaliana]
                  24404
Seq. No.
                  116022 1.R1040
Contig ID
                   zzp700834706.hl
5'-most EST
                  BLASTX
Method
                   g4206195
NCBI GI
                   201
BLAST score
                   2.0e-15
E value
                   45
Match length
% identity
                   (AF071527) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   >gi 4262169_gb_AAD14469_ (AC005275) hypothetical protein
                   [Arabidopsis thaliana]
                   24405
Seq. No.
                   116034 1.R1040
Contig ID
5'-most EST
                   smc700748227.h1
                   24406
Seq. No.
                   116040 1.R1040
Contig ID
                   fua701037973.h1
5'-most EST
                   24407
Seq. No.
                   116048 1.R1040
Contig ID
5'-most EST
                   taw700659648.hl
Seq. No.
                   24408
                   116072 1.R1040
Contig ID
                   taw700659687.h1
5'-most EST
                   BLASTX
Method
                   q4218154
NCBI GI
                   173
BLAST score
                   1.0e-12
E value
                   74
Match length
                   41
% identity
                   (AJ132706) hypothetical protein [Anabaena variabilis]
NCBI Description
                   24409
Seq. No.
                   116078 1.R1040
Contig ID
```

dpv701103344.h1 5'-most EST

24410 Seq. No.

116126 1.R1040 Contig ID taw700659924.h1 5'-most EST BLASTX Method



NCBI GI g2384669
BLAST score 331
E value 3.0e-31
Match length 79
% identity 78

NCBI Description (AF012656) putative potassium transporter AtKT1p

[Arabidopsis thaliana]

Seq. No. 24411

Contig ID 116133\_1.R1040 5'-most EST taw700659806.h1

Method BLASTX
NCBI GI g2894596
BLAST score 234
E value 2.0e-21
Match length 83
% identity 67

NCBI Description (AL021889) putative protein [Arabidopsis thaliana]

Seq. No. 24412

Contig ID 116161\_1.R1040 5'-most EST ary700764304.h1

Seq. No. 24413

Contig ID 116177\_1.R1040

5'-most EST jC-gmro02910034f05d1

Seq. No. 24414

Contig ID 116233\_1.R1040 5'-most EST gsv701044815.h1

Seq. No. 24415

Contig ID 116257\_1.R1040 5'-most EST taw700660001.h1

Method BLASTX
NCBI GI g2583118
BLAST score 154
E value 2.0e-10
Match length 72
% identity 49

NCBI Description (AC002387) hypothetical protein [Arabidopsis thaliana]

Seq. No. 24416

Contig ID 116271\_1.R1040 5'-most EST taw700660018.h1

Seq. No. 24417

Contig ID 116285\_1.R1040 5'-most EST taw700660040.h1

Seq. No. 24418

Contig ID 116301\_1.R1040 5'-most EST kmv700742274.h1

Seq. No. 24419

Contig ID 116308\_1.R1040 5'-most EST bth700844931.h1



Method BLASTX
NCBI GI g1710151
BLAST score 543
E value 1.0e-96
Match length 202
% identity 84

NCBI Description (U72711) proline iminopeptidase [Arabidopsis thaliana]

Seq. No. 24420

Contig ID 116318\_1.R1040 5'-most EST taw700660087.h1

Seq. No. 24421

Contig ID 116331\_1.R1040 5'-most EST vzy700750865.h1

Method BLASTX
NCBI GI g2832682
BLAST score 208
E value 2.0e-16
Match length 101
% identity 45

NCBI Description (AL021712) hypothetical protein [Arabidopsis thaliana]

Seq. No. 24422

Contig ID 116346\_1.R1040 5'-most EST smc700746726.h1

Seq. No. 24423

Contig ID 116348\_1.R1040 5'-most EST gsv701051881.h1

Seq. No. 24424

Contig ID 116358\_1.R1040

5'-most EST uC-gmflminsoy097b09b1

Seq. No. 24425

Contig ID 116360\_1.R1040 5'-most EST taw700660141.h1

Seq. No. 24426

Contig ID 116387\_1.R1040 5'-most EST taw700660175.h1

Seq. No. 24427

Contig ID 116389\_1.R1040 5'-most EST taw700660178.h1

Seq. No. 24428

Contig ID 116398 1.R1040 5'-most EST rca700995963.h1

Method BLASTX
NCBI GI g1001355
BLAST score 466
E value 2.0e-46
Match length 170
% identity 54

NCBI Description (D64006) auxin-induced protein [Synechocystis sp.]



Seq. No. 24429

Contig ID 116400\_1.R1040 5'-most EST taw700660194.h1

Seq. No. 24430

Contig ID 116412 1.R1040 5'-most EST taw700660221.h1

Seq. No. 24431

Contig ID 116417\_1.R1040

5'-most EST g5126602
Method BLASTX
NCBI GI g1935909
BLAST score 211
E value 2.0e-16
Match length 170
% identity 32

NCBI Description (U77345) lethal leaf-spot 1 [Zea mays]

Seq. No. 24432

Contig ID 116431\_1.R1040

5'-most EST jC-gmle01810034c07a2

Method BLASTX
NCBI GI g4371280
BLAST score 233
E value 2.0e-19
Match length 58
% identity 79

NCBI Description (AC006260) hypothetical protein [Arabidopsis thaliana]

Seq. No. 24433

Contig ID 116433 1.R1040 5'-most EST taw700660259.h1

Seq. No. 24434

Contig ID 116484\_1.R1040 5'-most EST smc700747740.h1

Seq. No. 24435

Contig ID 116500\_1.R1040 5'-most EST pcp700989588.h1

Method BLASTX
NCBI GI g4115379
BLAST score 353
E value 2.0e-33
Match length 133
% identity 56

NCBI Description (AC005967) putative carbonyl reductase [Arabidopsis

thaliana]

Seq. No. 24436

Contig ID 116501\_1.R1040 5'-most EST uC-gmropic041f10b1

Seq. No. 24437

Contig ID 116501 2.R1040

3864



5'-most EST taw700660360.h1

Seq. No. 24438

Contig ID 116501\_3.R1040 5'-most EST gsv701045057.h1

Seq. No. 24439

Contig ID 116519\_1.R1040 5'-most EST taw700660391.h1

Seq. No. 24440

Contig ID 116535\_1.R1040

Match length 74 % identity 74

NCBI Description (AL031135) putative protein [Arabidopsis thaliana]

>gi\_3805841\_emb\_CAA21461\_ (AL031986) putative protein

[Arabidopsis thaliana]

Seq. No. 24441

Contig ID 116541\_1.R1040 5'-most EST smc700744480.h1

Method BLASTN
NCBI GI g1407596
BLAST score 158
E value 6.0e-84
Match length 170
% identity 98

NCBI Description Human TSC-22 protein mRNA, complete cds

Seq. No. 24442

Contig ID 116552\_1.R1040 5'-most EST uC-gmronoir044d02b1

Seq. No. 24443

Contig ID 116566\_1.R1040 5'-most EST kl1701211943.h1

Seq. No. 24444

Contig ID 116571\_1.R1040 5'-most EST zhf700957515.h1

Seq. No. 24445

Contig ID 116592 1.R1040 5'-most EST taw700660483.h1

Seq. No. 24446

Contig ID 116601\_1.R1040

5'-most EST jC-gmst02400074e07a1

Method BLASTX
NCBI GI g3395439
BLAST score 331
E value 1.0e-30

3865



Match length 83 % identity 76

NCBI Description (AC004683) hypothetical protein [Arabidopsis thaliana]

Seq. No. 24447

Contig ID 116617\_1.R1040

5'-most EST g4307591

Seq. No. 24448

Contig ID 116627\_1.R1040 5'-most EST taw700660536.h1

Seq. No. 24449

Contig ID 116655\_1.R1040 5'-most EST taw700660577.h1

Seq. No. 24450

Contig ID 116659\_1.R1040

5'-most EST g4303884
Method BLASTX
NCBI GI g3668087
BLAST score 377
E value 5.0e-36
Match length 111
% identity 21

NCBI Description (AC004667) hypothetical protein [Arabidopsis thaliana]

Seq. No. 24451

Contig ID 116667\_1.R1040 5'-most EST taw700660591.h1

Seq. No. 24452

Contig ID 116685\_1.R1040 5'-most EST jsh701065639.h1

Seq. No. 24453

Contig ID 116696 1.R1040

5'-most EST uC-gmflminsoy040b05b1

Seq. No. 24454

Contig ID 116705\_1.R1040 5'-most EST smc700750457.h1

Seq. No. 24455

Contig ID 116724 1.R1040

5'-most EST jC-gmfl02220090e02d1

Seq. No. 24456

Contig ID 116736\_1.R1040 5'-most EST bnc700605512.h2

Method BLASTX
NCBI GI g4006900
BLAST score 320
E value 2.0e-29
Match length 82
% identity 76

NCBI Description (Z99708) hypothetical protein [Arabidopsis thaliana]



```
24457
Seq. No.
                   116754 1.R1040
Contig ID
                   rca701\overline{0}01369.h1
5'-most EST
                   24458
Seq. No.
                   116759 1.R1040
Contig ID
                   eep700868324.hl
5'-most EST
                   BLASTX
Method
                   g3169010
NCBI GI
                   352
BLAST score
                   2.0e-33
E value
                   126
Match length
                   53
% identity
NCBI Description (AJ006412) putative GTP-binding protein [Homo sapiens]
                   24459
Seq. No.
                   116763 1.R1040
Contig ID
5'-most EST
                   bnc700605540.h2
                   BLASTN
Method
                   g4006885
NCBI GI
                   57
BLAST score
                   2.0e-23
E value
                   213
Match length
                   82
% identity
                   Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig
NCBI Description
                   fragment No
                   24460
Seq. No.
                   116767 1.R1040
Contig ID
5'-most EST
                   bnc700605545.h2
                   24461
Seq. No.
                   116773 1.R1040
Contig ID
                   bnc700605551.h2
5'-most EST
Method
                   BLASTX
                   q4508074
NCBI GI
BLAST score
                   205
                   7.0e-16
E value
Match length
                   156
% identity
                  (AC005882) 45341 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   24462
Contig ID
                   116788 1.R1040
5'-most EST
                   zpv700763687.h1
                   24463
Seq. No.
                   116791 1.R1040
Contig ID
                   pcp700995875.hl
5'-most EST
Method
                   BLASTX
```

NCBI GI g4454012 BLAST score 564 E value 4.0e-58 Match length 149 % identity 62

NCBI Description (AL035396) Pollen-specific protein precursor like

5'-most EST

Method



## [Arabidopsis thaliana]

```
24464
Seq. No.
                  116793 1.R1040
Contig ID
5'-most EST
                  bth700846093.h1
Method
                  BLASTX
NCBI GI
                  g1575436
BLAST score
                  168
                  6.0e-12
E value
                  54
Match length
% identity
NCBI Description
                  (U62734) caffeoyl-CoA O-methyltransferase 2 [Nicotiana
                  tabacum]
                  24465
Seq. No.
                  116793 2.R1040
Contig ID
5'-most EST
                  qsv701044408.hl
                  24466
Seq. No.
Contig ID
                  116798 1.R1040
5'-most EST
                  sat701012263.h1
Seq. No.
                   24467
                   116800 1.R1040
Contig ID
5'-most EST
                  uC-qmflminsoy084g04b1
Method
                  BLASTX
NCBI GI
                   q3687231
BLAST score
                   453
                   8.0e-56
E value
Match length
                   134
% identity
                  (AC005169) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   24468
Seq. No.
                   116814_1.R1040
Contig ID
5'-most EST
                   g4293443
                   BLASTX
Method
                   q4454044
NCBI GI
BLAST score
                   366
                   2.0e-34
E value
                   128
Match length
                   62
% identity
                   (AL035394) putative Ap2 domain protein [Arabidopsis
NCBI Description
                   thaliana]
                   24469
Seq. No.
Contig ID
                   116814 2.R1040
                   gsv701051518.hl
5'-most EST
                   24470
Seq. No.
                   116818 1.R1040
Contig ID
5'-most EST
                   awf700838526.h1
                   24471
Seq. No.
Contig ID
                   116828 1.R1040
```

jsh701066017.hl

BLASTX



```
q2655888
NCBI GI
                  1001
BLAST score
                  1.0e-109
E value
                  309
Match length
                  24
% identity
                  (AL009171) 62D9.a [Drosophila melanogaster]
NCBI Description
Seq. No.
                  24472
                  116829 1.R1040
Contig ID
                  bnc700605620.h2
5'-most EST
                  BLASTX
Method
                   g4432846
                   272
```

NCBI GI BLAST score E value 4.0e-24 91 Match length 66 % identity

NCBI Description (AC006283) unknown protein [Arabidopsis thaliana]

Seq. No. 24473 116841 1.R1040 Contig ID bth700849482.h1 5'-most EST BLASTX Method

g3068705 NCBI GI 194 BLAST score E value 7.0e-15 80 Match length 49 % identity

(AF049236) unknown [Arabidopsis thaliana] NCBI Description

24474 Seq. No.

116859 1.R1040 Contig ID  $bnc700\overline{6}05652.h2$ 5'-most EST

BLASTX Method NCBI GI q3063691 494 BLAST score E value 5.0e-50 Match length 138 63 % identity

(AL022537) putative protein [Arabidopsis thaliana] NCBI Description

24475 Seq. No.

116873 1.R1040 Contig ID 5'-most EST jC-gmle01810043h12a1

BLASTN Method NCBI GI g2104678 BLAST score 562 E value 0.0e + 00Match length 927 % identity 92

NCBI Description V.faba mRNA for transcription factor containing HMG-box

24476 Seq. No.

116887 1.R1040 Contig ID pmv700888554.h1 5'-most EST

Method BLASTX g2191179 NCBI GI 176 BLAST score



4.0e-13 E value Match length 63 % identity 63

(AF007270) contains similarity to syntaxin [Arabidopsis NCBI Description

thaliana]

Seq. No. 24477

116902 1.R1040 Contig ID fC-gmst700662109f1 5'-most EST

Seq. No. 24478

116902 2.R1040 Contig ID

uC-qmflminsoy018f08b1 5'-most EST

24479 Seq. No.

116909 1.R1040 Contig ID 5'-most EST ncj700977533.h1

Seq. No. 24480

116923 1.R1040 Contig ID 5'-most EST gsv701055795.h1

Seq. No. 24481

116923 2.R1040 Contig ID rca701000919.hl 5'-most EST

24482 Seq. No.

116924 1.R1040 Contia ID uaw700661085.hl 5'-most EST

BLASTX Method g3426048 NCBI GI 239 BLAST score E value 6.0e-20 Match length 59

83 % identity

(AC005168) putative hydroxymethylglutaryl-CoA lyase NCBI Description

precursor [Arabidopsis thaliana]

24483 Seq. No.

116931 1.R1040 Contig ID 5'-most EST zhf700956511.h1

24484 Seq. No.

116944 1.R1040 Contig ID uaw700660764.hl 5'-most EST

24485 Seq. No.

116954 1.R1040 Contig ID uaw700661512.h1 5'-most EST

24486 Seq. No.

Contig ID 116962 1.R1040 5'-most EST uaw700661380.hl

Seq. No. 24487

Contig ID 116966 1.R1040

5'-most EST jC-gmst02400076c09a1



```
24488
Seq. No.
                    116966 2.R1040
Contig ID
                    zhf700\overline{9}59349.h1
5'-most EST
                    24489
Seq. No.
                    116969 1.R1040
Contig ID
                    r1r700\overline{8}98877.h1
5'-most EST
                    BLASTX
Method
                    q4335773
NCBI GI
BLAST score
                    198
E value
                    2.0e-19
Match length
                    149
                    40
% identity
                   (AC006284) unknown protein [Arabidopsis thaliana]
NCBI Description
                    24490
Seq. No.
                    116974 1.R1040
Contig ID
                    uaw700661742.h1
5'-most EST
                    BLASTX
Method
                    g4204263
NCBI GI
                    140
BLAST score
                    1.0e-08
E value
Match length
                    33
% identity
                    (AC005223) 40409 [Arabidopsis thaliana]
NCBI Description
                    24491
Seq. No.
                    116976 1.R1040
Contig ID
                    uC-gmflminsoy071d09b2
5'-most EST
                    BLASTX
Method
                     g2564679
NCBI GI
                     216
BLAST score
E value
                     2.0e-20
                     182
Match length
 % identity
                     35
                     (AF023484) putative KP78 protein kinase [Drosophila
NCBI Description
                     melanogaster]
                     24492
 Seq. No.
                     116985 1.R1040
 Contia ID
                     zhf700964746.hl
 5'-most EST
                     24493
 Seq. No.
                     116988 1.R1040
 Contig ID
                     uaw700660826.hl
 5'-most EST
                     24494
 Seq. No.
                     117000 1.R1040
 Contig ID
                     \texttt{fC-gms}\overline{\texttt{t}}700660842\texttt{f}1
 5'-most EST
```

Contig ID 117021\_1.R1040 5'-most EST dpv701102005.h1

Method BLASTN
NCBI GI g414180
BLAST score 142



E value 8.0e-74 Match length 326 % identity 88

NCBI Description P.sativum mRNA for pIAA4/5.1

Seq. No. 24496

Contig ID 117023\_1.R1040 5'-most EST uaw700661754.h1

Method BLASTX
NCBI GI 94559330
BLAST score 346
E value 1.0e-37
Match length 111
% identity 73

NCBI Description (AC007087) unknown protein [Arabidopsis thaliana]

Seq. No. 24497

Contig ID 117031\_1.R1040 5'-most EST kmv700739176.h1

Seq. No. 24498

Contig ID 117035\_1.R1040 5'-most EST wvk700686139.h1

Seq. No. 24499

Contig ID 117036\_1.R1040 5'-most EST leu701145951.h1

Seq. No. 24500

Contig ID 117042\_1.R1040 5'-most EST pxt700942147.h1

Method BLASTX
NCBI GI g2244865
BLAST score 376
E value 3.0e-36
Match length 128
% identity 62

NCBI Description (Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No. 24501

Contig ID 117047\_1.R1040 5'-most EST rlr700896710.h1

Method BLASTX
NCBI GI g2459444
BLAST score 564
E value 5.0e-58
Match length 189
% identity 59

NCBI Description (AC002332) hypothetical protein [Arabidopsis thaliana]

Seq. No. 24502

Contig ID 117060\_1.R1040 5'-most EST uaw700660921.h1

Seq. No. 24503

Contig ID 117065\_1.R1040 5'-most EST uaw700660927.h1



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24504
Seq. No.
                  117067 1.R1040
Contig ID
                  zhf700\overline{9}60002.h1
5'-most EST
                  24505
Seq. No.
                  117075 1.R1040
Contig ID
                  uaw700660938.hl
5'-most EST
                   24506
Seq. No.
                   117078 1.R1040
Contig ID
                   uaw700660941.hl
5'-most EST
                   BLASTX
Method
                   g1531758
NCBI GI
BLAST score
                   349
                   3.0e-33
E value
                   98
Match length
                   68
% identity
                   (X98772) AUX1 [Arabidopsis thaliana] >gi_3335360 (AC003028)
NCBI Description
                   unknown protein [Arabidopsis thaliana]
                   24507
Seq. No.
                   117079 1.R1040
Contig ID
                   uaw700660942.h1
5'-most EST
                   24508
Seq. No.
                   117093 1.R1040
Contig ID
                   uaw700660959.h1
5'-most EST
                   24509
Seq. No.
                   117096 1.R1040
Contig ID
                   uaw700660962.hl
5'-most EST
                   BLASTX
Method
                   g1086252
NCBI GI
BLAST score
                   222
                   3.0e-18
E value
                   80
Match length
% identity
                   54
                   sucrose cleavage protein - Potato >gi 707001 bbs 157931
NCBI Description
                   (S74161) sucrolytic enzyme/ferredoxin homolog [Solanum
                   tuberosum=potatoes, cv. Cara, leaf, Peptide, 322 aa]
                   [Solanum tuberosum]
                   24510
Seq. No.
                   117098 1.R1040
Contig ID
                   uaw700660965.h1
5'-most EST
                   24511
Seq. No.
                   117099 1.R1040
Contig ID
```

5'-most EST uC-gmrominsoy091b02b1

Method BLASTX
NCBI GI g3236235
BLAST score 218
E value 1.0e-17
Match length 130
% identity 45

NCBI Description (AC004684) unknown protein [Arabidopsis thaliana]



>gi\_4056501 (AC005896) unknown protein [Arabidopsis
thaliana]

Seq. No. 24512

Contig ID 117103\_1.R1040 5'-most EST uC-gmropic063d03b1

Method BLASTX
NCBI GI g3201625
BLAST score 604
E value 9.0e-63
Match length 151
% identity 78

NCBI Description (AC004669) hypothetical protein [Arabidopsis thaliana]

Seq. No. 24513

Contig ID 117130\_1.R1040 5'-most EST uaw700661006.h1

Seq. No. 24514

Contig ID 117145\_1.R1040 5'-most EST uaw700661022.h1

Seq. No. 24515

Contig ID 117149\_1.R1040 5'-most EST uaw700661026.h1

Method BLASTX
NCBI GI 94455275
BLAST score 171
E value 4.0e-12
Match length 158
% identity 22

NCBI Description (AL035527) putative protein [Arabidopsis thaliana]

Seq. No. 24516

Contig ID 117164\_1.R1040 5'-most EST uaw700661044.h1

Method BLASTX
NCBI GI g4559327
BLAST score 167
E value 1.0e-17
Match length 130
% identity 45

NCBI Description (AC007087) hypothetical protein [Arabidopsis thaliana]

Seq. No. 24517

Contig ID 117191\_1.R1040 5'-most EST uaw700661092.h1

Seq. No. 24518

Contig ID 117192\_1.R1040 5'-most EST zhf700952913.h1

Method BLASTX
NCBI GI g3451473
BLAST score 217
E value 1.0e-17
Match length 91
% identity 42



```
NCBI Description
                   (AL031349) 4-nitrophenylphosphatase [Schizosaccharomyces
                   pombe]
Seq. No.
                   24519
Contig ID
                   117203 1.R1040
5'-most EST
                   uaw700661090.hl
Method
                   BLASTX
NCBI GI
                   q4512263
BLAST score
                   429
                   1.0e-44
E value
                   137
Match length
% identity
                   79
                  (AB018526) H+/Ca2+ exchanger 2 [Ipomoea nil]
NCBI Description
Seq. No.
                   24520
Contig ID
                   117203 2.R1040
5'-most EST
                   sat701013709.h1
Method
                   BLASTX
NCBI GI
                   q4512263
BLAST score
                   600
E value
                   2.0e-62
Match length
                   159
% identity
                   74
                  (AB018526) H+/Ca2+ exchanger 2 [Ipomoea nil]
NCBI Description
                   24521
Seq. No.
                   117204 1.R1040
Contig ID
5'-most EST
                   uaw700661091.hl
Method
                   BLASTN
                   g1620985
NCBI GI
BLAST score
                   34
E value
                   1.0e-09
                   90
Match length
                   84
% identity
NCBI Description N.plumbaginifolia mRNA for 40S ribosomal protein S17
                   24522
Seq. No.
Contig ID
                   117207 1.R1040
5'-most EST
                   q43053\overline{2}8
Method
                   BLASTN
NCBI GI
                   g762924
BLAST score
                   69
E value
                   3.0e-30
Match length
                   73
                   99
% identity
NCBI Description
                  D.melanogaster mRNA for elastin-like protein
Seq. No.
                   24523
Contig ID
                   117224 1.R1040
5'-most EST
                   asn701141481.h1
Method
                   BLASTX
                   g3924594
NCBI GI
BLAST score
                   535
E value
                   1.0e-54
Match length
                   119
% identity
```

NCBI Description (AF069442) putative ribonucleoprotein [Arabidopsis



thaliana] >gi\_4262139\_gb\_AAD14439\_ (AC005275) putative ribonucleoprotein [Arabidopsis thaliana]

Seq. No. 24524

Contig ID 117225\_1.R1040

5'-most EST uC-gmrominsoy109h11b1

Seq. No. 24525

Contig ID 117248\_1.R1040 5'-most EST uaw700662743.h1

Seq. No. 24526

Contig ID 117249\_1.R1040 5'-most EST leu701150553.h1

Method BLASTX
NCBI GI 94335735
BLAST score 223
E value 3.0e-36
Match length 140
% identity 54

NCBI Description (AC006248) hypothetical protein [Arabidopsis thaliana]

Seq. No. 24527

Contig ID 117262\_1.R1040 5'-most EST uaw700661173.h1

Seq. No. 24528

Contig ID 117265\_1.R1040 5'-most EST zhf700961211.h1

Method BLASTX
NCBI GI g2245020
BLAST score 150
E value 1.0e-09
Match length 113
% identity 31

NCBI Description (Z97341) growth regulator homolog [Arabidopsis thaliana]

Seq. No. 24529

Contig ID 117268\_1.R1040 5'-most EST fC-gmse700670424f2

Seq. No. 24530

Contig ID 117270\_1.R1040 5'-most EST gsv701046661.h1

Method BLASTX
NCBI GI g2342686
BLAST score 513
E value 3.0e-52
Match length 136
% identity 71

NCBI Description (AC000106) Similar to Saccharomyces hypothetical protein YDR051c (gb\_Z49209). ESTs gb\_T44436,gb\_42252 come from this

gene. [Arabidopsis thaliana]

Seq. No. 24531

Contig ID 117276\_1.R1040 5'-most EST g5677335

\_



 Seq. No.
 24532

 Contig ID
 117278\_1.R1040

 5'-most EST
 uaw700661194.h1

 Method
 BLASTX

NCBI GI g3157938
BLAST score 467
E value 5.0e-47
Match length 112
% identity 81

NCBI Description (AC002131) Similar to seryl-tRNA synthetase gb\_U10400 from

S cerevisiae. EST gb\_N96627 comes from this gene.

[Arabidopsis thaliana]

Seq. No. 24533

Contig ID 117279\_1.R1040 5'-most EST awf700840924.h1

Seq. No. 24534

Contig ID 117287\_1.R1040 5'-most EST uaw700661248.h1

Seq. No. 24535

Contig ID 117294\_1.R1040 5'-most EST fC-gmst700661229f1

Method BLASTX
NCBI GI g2129899
BLAST score 231
E value 4.0e-19
Match length 66
% identity 62

NCBI Description chalcone reductase homolog - Sesbania rostrata (fragment)

>gi\_899483\_emb\_CAA88591\_ (Z48672) chalcone reductase

homologue [Sesbania rostrata]

Seq. No. 24536

Contig ID 117302\_1.R1040

5'-most EST g5606350

Seq. No. 24537

Contig ID 117322\_1.R1040 5'-most EST uC-gmropic075c07b1

Method BLASTX
NCBI GI g3834322
BLAST score 251
E value 2.0e-33
Match length 83
% identity 86

NCBI Description (AC005679) EST gb R30300 comes from this gene. [Arabidopsis

thaliana]

Seq. No. 24538

Contig ID 117323\_1.R1040 5'-most EST uaw700663663.h1

Seq. No. 24539

Contig ID 117347 1.R1040



5'-most EST uaw700661324.h1

Method BLASTX
NCBI GI g4415933
BLAST score 384
E value 1.0e-53
Match length 140
% identity 76

NCBI Description (AC006418) putative cellular apoptosis susceptibility

protein [Arabidopsis thaliana]

>gi\_4559390\_gb\_AAD23050.1\_AC006526\_15 (AC006526) putative
cellular apoptosis susceptibility protein [Arabidopsis

thaliana]

Seq. No. 24540

Contig ID 117358\_1.R1040 5'-most EST uaw700662305.h1

Method BLASTX
NCBI GI g2244996
BLAST score 307
E value 3.0e-28
Match length 106
% identity 21

NCBI Description (Z97341) similarity to a membrane-associated salt-inducible

protein [Arabidopsis thaliana]

Seq. No. 24541

Contig ID 117372\_1.R1040 5'-most EST uxk700672463.h1

Method BLASTX
NCBI GI g4388731
BLAST score 401
E value 4.0e-39
Match length 112
% identity 71

NCBI Description (AC006413) hypothetical protein [Arabidopsis thaliana]

Seq. No. 24542

Contig ID 117373\_1.R1040 5'-most EST fC-qmst700661354f1

Method BLASTN
NCBI GI g2262200
BLAST score 256
E value 1.0e-142
Match length 418
% identity 90

NCBI Description Phaseolus vulgaris gibberellin 20-oxidase mRNA, complete

cds

Seq. No. 24543

Contig ID 117389 1.R1040 5'-most EST uaw700661372.h1

Seq. No. 24544

Contig ID 117404\_1.R1040 5'-most EST uaw700661388.h1

Seq. No. 24545



Contig ID 117417 1.R1040 5'-most EST uaw700661405.h1 24546 Seq. No. 117468 1.R1040 Contig ID hrw701056953.hl 5'-most EST Seq. No. 24547 117472 1.R1040 Contig ID uaw700661470.h1 5'-most EST 24548 Seq. No. Contig ID 117475 1.R1040  $epx701\overline{1}07827.h1$ 5'-most EST BLASTX Method NCBI GI g2842490 BLAST score 390 E value 6.0e-38

83 % identity NCBI Description (AL021749) heat-shock protein [Arabidopsis thaliana]

24549 Seq. No. Contig ID 117477 1.R1040 uaw700661475.h1 5'-most EST Method BLASTX g3445208 NCBI GI 405 BLAST score

83

E value 1.0e-39 122 Match length % identity 72

(AC004786) putative amino-acid acetyltransferase NCBI Description

[Arabidopsis thaliana]

24550 Seq. No. Contig ID

117481 1.R1040 5'-most EST uaw700661479.hl

Seq. No. Contig ID

Match length

117487 1.R1040

5'-most EST

uC-gmflminsoy064b07b1

Seq. No.

24552

24551

Contig ID 5'-most EST 117488 1.R1040 uaw700661486.h1

BLASTX Method NCBI GI g4335773 BLAST score 268 2.0e-23 E value 85 Match length % identity 68

(AC006284) unknown protein [Arabidopsis thaliana] NCBI Description

Seq. No.

24553

Contig ID 5'-most EST 117496\_1.R1040 leu701146511.h1



Contig ID 117496 2.R1040 5'-most EST epx701105496.hl

Seq. No. 24555

Contig ID 117505 1.R1040

5'-most EST g5752532 Method BLASTN g4220635 NCBI GI BLAST score 34 1.0e-09

E value Match length 86 % identity 85

Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: NCBI Description

MDB19, complete sequence [Arabidopsis thaliana]

24556 Seq. No.

Contig ID 117525 1.R1040 5'-most EST uaw700662009.h1

Method BLASTX NCBI GI g3337361 BLAST score 344 E value 1.0e-32 Match length 100 % identity 61

NCBI Description (AC004481) ankyrin-like protein [Arabidopsis thaliana]

24557 Seq. No.

Contig ID 117530 1.R1040 5'-most EST uaw700661538.hl

24558 Seq. No.

117534 1.R1040 Contig ID 5'-most EST dpv701103445.h1

Method BLASTX NCBI GI q2274993 BLAST score 428 E value 3.0e-42Match length 104 % identity 76

NCBI Description (AJ000230) unnamed protein product [Hordeum vulgare]

Seq. No.

24559 117542 1.R1040 Contig ID 5'-most EST  $uaw700\overline{6}61552.h1$ 

Seq. No.

24560

117549 1.R1040 Contig ID 5'-most EST gsv701053766.hl

24561 Seq. No.

117554 2.R1040 Contig ID 5'-most EST pxt700944670.hl

Seq. No.

24562

Contig ID 117556 1.R1040 5'-most EST uaw700661568.h1



Contig ID 117577\_1.R1040 5'-most EST gsv701055758.h1

Method BLASTX
NCBI GI g2459433
BLAST score 227
E value 2.0e-18
Match length 63
% identity 68

NCBI Description (AC002332) hypothetical protein [Arabidopsis thaliana]

Seq. No. 24564

Contig ID 117594\_1.R1040 5'-most EST uaw700661713.h1

Seq. No. 24565

Contig ID 117595\_1.R1040

5'-most EST jC-gmro02910013a09a1

Method BLASTN
NCBI GI g2564044
BLAST score 38
E value 8.0e-12
Match length 81
% identity 95

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K19P17, complete sequence [Arabidopsis thaliana]

Seq. No. 24566

Contig ID 117595\_2.R1040 5'-most EST zhf700961001.h1

Seq. No. 24567

Contig ID 117596\_1.R1040 5'-most EST pmv700890487.h1

Seq. No. 24568

Contig ID 117597\_1.R1040 5'-most EST wvk700680781.h1

Seq. No. 24569

Contig ID 117614 1.R1040

5'-most EST jC-gmst02400029e06d1

Seq. No. 24570

Contig ID 117618\_1.R1040 5'-most EST uaw700661741.h1

Method BLASTX
NCBI GI g2982452
BLAST score 247
E value 8.0e-29
Match length 107
% identity 59

NCBI Description (AL022223) receptor protein kinase-like protein

[Arabidopsis thaliana]

Seq. No. 24571



Contig ID 117623\_1.R1040 5'-most EST kmv700741073.h1

Method BLASTX
NCBI GI g3738232
BLAST score 353
E value 4.0e-33
Match length 172
% identity 44

NCBI Description (AB007791) DREB2B [Arabidopsis thaliana]

>gi\_4126708\_dbj\_BAA36706\_ (AB016571) DREB2B [Arabidopsis

thaliana]

Seq. No. 24572

Contig ID 117626\_1.R1040 5'-most EST uaw700662117.h1

Seq. No. 24573

Contig ID 117634\_1.R1040 5'-most EST uaw700661761.h1

Method BLASTX
NCBI GI g710465
BLAST score 287
E value 9.0e-26
Match length 137
% identity 47

NCBI Description OEP86-outer envelope protein [Peas, Peptide Chloroplast,

878 aa]

Seq. No. 24574

Contig ID 117635\_1.R1040 5'-most EST fua701038753.h1

Method BLASTX
NCBI GI g3850583
BLAST score 288
E value 8.0e-26
Match length 139
% identity 51

NCBI Description (AC005278) Contains similarity to transcription initiation

factor IIE, alpha subunit gb X63468 from Homo sapiens.

[Arabidopsis thaliana]

Seq. No. 24575

Contig ID 117653\_1.R1040 5'-most EST gsv701044929.h1

Method BLASTX
NCBI GI g2459416
BLAST score 270
E value 1.0e-23
Match length 115
% identity 36

NCBI Description (AC002332) unknown protein [Arabidopsis thaliana]

Seq. No. 24576

Contig ID 117655\_1.R1040 5'-most EST fC-gmst700662075f5

Method BLASTX NCBI GI g2827715



BLAST score E value 2.0e-18 153 Match length 35 % identity

(AL021684) receptor protein kinase - like protein NCBI Description

[Arabidopsis thaliana]

24577 Seq. No.

117656 2.R1040 Contig ID dpv701102809.h1 5'-most EST

Method BLASTX NCBI GI q2498864 BLAST score 411 6.0e-40 E value 182 Match length % identity 44

RRP5 PROTEIN HOMOLOG (KIAA0185) >gi 1136430 dbj BAA11502 NCBI Description

(D80007) similar to hypothetical protein YM9959.11C of

S.cerevisiae. [Homo sapiens]

24578 Seq. No.

117660 1.R1040 Contig ID 5'-most EST bth700849358.h1

Method BLASTX q1172923 NCBI GI 141 BLAST score 1.0e-08 E value 137 Match length % identity 26

RAN GTPASE ACTIVATING PROTEIN 1 >gi\_1083497\_pir\_\_A36983 NCBI Description

RNA1 homolog fug1 - mouse >gi 472852 (U08110) homolog of yeast RNA1, RNA production and processing protein, Swiss

Prot Accession Number P11745 [Mus musculus]

Seq. No. 24579

117677 1.R1040 Contig ID

uC-gmrominsoy070a10b1 5'-most EST

BLASTX Method NCBI GI q417592 277 BLAST score 2.0e-24 E value 147 Match length 43 % identity

RIBONUCLEIC ACID TRAFFICKING PROTEIN 1 (5'-3' NCBI Description

EXORIBONUCLEASE) (P116) >gi\_83014\_pir\_\_S20126

exoribonuclease RAT1 (EC 3.1.11.-) - yeast (Saccharomyces cerevisiae) >gi 172365 (M95626) Rat1p [Saccharomyces cerevisiae] >gi 386005 bbs 132577 (S61567) transcription activator=TAP1/RAT1 [Saccharomyces cerevisiae=yeast,

Peptide, 1006 aa] [Saccharomyces cerevisiae] >gi 1420179 emb CAA99240 (Z74956) ORF YOR048c

[Saccharomyces cerevisiae]

24580 Seq. No.

117684\_1.R1040 Contig ID 5'-most EST fC-qmst700661823f1

BLASTX Method



NCBI GI g3810598 BLAST score 1189 E value 1.0e-131 Match length 292 % identity 72

NCBI Description (AC005398) putative endo-xyloglucan transferase

[Arabidopsis thaliana]

Seq. No. 24581

Contig ID 117699\_1.R1040

5'-most EST jC-gmro02910038c02a1

Method BLASTX
NCBI GI g2950478
BLAST score 175
E value 2.0e-12
Match length 82
% identity 44

NCBI Description (AL022070) hypothetical protein [Schizosaccharomyces pombe]

Seq. No. 24582

Contig ID 117699 2.R1040 5'-most EST wvk700684689.h1

Seq. No. 24583

Contig ID 117720\_1.R1040 5'-most EST zhf700955535.h1

Method BLASTX
NCBI GI 94508069
BLAST score 1025
E value 1.0e-130
Match length 345
% identity 67

NCBI Description (AC005882) 12246 [Arabidopsis thaliana]

Seq. No. 24584

Contig ID 117726\_1.R1040

5'-most EST jC-gmle01810073a12a1

Seq. No. 24585

Contig ID 117744\_1.R1040 5'-most EST sat701012787.h1

Method BLASTX
NCBI GI g2244979
BLAST score 547
E value 5.0e-56
Match length 140
% identity 76

NCBI Description (Z97340) similarity to enoyl-CoA hydratase [Arabidopsis

thaliana]

Seq. No. 24586

Contig ID 117746 1.R1040

5'-most EST jC-gmro02910061a04d1

Seq. No. 24587

Contig ID 117749\_1.R1040 5'-most EST uaw700661905.h1



Contig ID 117784\_1.R1040 5'-most EST zpv700758569.h1

Seq. No. 24589

Contig ID 117787 1.R1040

5'-most EST jC-gmro02910023a05d1

Method BLASTX
NCBI GI g3183237
BLAST score 169
E value 9.0e-12
Match length 136
% identity 29

NCBI Description HYPOTHETICAL 103.4 KD TRP-ASP REPEATS CONTAINING PROTEIN

C3D6.12 IN CHROMOSOME II >gi\_2117308\_emb\_CAB09121\_ (Z95620)

trp asp repeat protein [Schizosaccharomyces pombe]

Seq. No. 24590

Contig ID 117824 1.R1040 5'-most EST wvk700680847.h1

Seq. No. 24591

Contig ID 117834\_1.R1040 5'-most EST xpa700795246.h1

Seq. No. 24592

Contig ID 117836 1.R1040

5'-most EST g4292261

Seq. No. 24593

Contig ID 117865\_1.R1040 5'-most EST uaw700662131.h1

Seq. No. 24594

Contig ID 117877\_1.R1040 5'-most EST kmv700739964.h1

Seq. No. 24595

Contig ID 117897\_1.R1040 5'-most EST zsg701120161.h1

Method BLASTX
NCBI GI g1335862
BLAST score 502
E value 8.0e-51
Match length 135
% identity 75

NCBI Description (U42608) clathrin heavy chain [Glycine max]

Seq. No. 24596

Contig ID 117902\_1.R1040 5'-most EST uaw700662201.h1

Method BLASTN
NCBI GI g2244788
BLAST score 59
E value 1.0e-24
Match length 179



% identity 83
NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No. 24597

Contig ID 117919\_1.R1040 5'-most EST asn701139901.h1

Seq. No. 24598

Contig ID 117925 1.R1040

5'-most EST uC-gmflminsoy003d07b1

Method BLASTN
NCBI GI g3821780
BLAST score 33
E value 9.0e-09
Match length 33
% identity 58

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 24599

Contig ID 117927\_1.R1040 5'-most EST uaw700662232.h1

Method BLASTX
NCBI GI g3776007
BLAST score 240
E value 5.0e-20
Match length 78
% identity 63

NCBI Description (AJ010467) RNA helicase [Arabidopsis thaliana]

Seq. No. 24600

Contig ID 117929\_1.R1040 5'-most EST sat701013107.h1

Method BLASTX
NCBI GI g2961380
BLAST score 245
E value 1.0e-25
Match length 80
% identity 71

NCBI Description (AL022141) putative protein [Arabidopsis thaliana]

Seq. No. 24601

Contig ID 117932\_1.R1040

5'-most EST uC-gmrominsoy182d06b1

Method BLASTX
NCBI GI g3080390
BLAST score 127
E value 5.0e-16
Match length 97
% identity 53

NCBI Description (AL022603) putative protein [Arabidopsis thaliana]

Seq. No. 24602

Contig ID 117933\_1.R1040 5'-most EST gsv701053803.h1

Method BLASTX NCBI GI g4415921



BLAST score 960 E value 1.0e-107 Match length 337 % identity 56

NCBI Description (AC006282) putative glucosyl transferase [Arabidopsis

thaliana]

Seq. No. 24603

Contig ID 117942 1.R1040 5'-most EST uaw700662264.h1

Seq. No. 24604

Contig ID 117948\_1.R1040 5'-most EST gsv701051128.h1

Method BLASTX
NCBI GI g2500537
BLAST score 245
E value 1.0e-20
Match length 154
% identity 42

NCBI Description PROBABLE ATP-DEPENDENT RNA HELICASE HAS1

>gi\_626265\_pir\_\_S47451 hypothetical protein YMR290c - yeast

(Saccharomyces cerevisiae) >gi\_530347\_emb\_CAA56799\_ (X80836) RNA helicase [Saccharomyces cerevisiae]

Seq. No. 24605

Contig ID 117974\_1.R1040 5'-most EST xpa700796440.h1

Seq. No. 24606

Contig ID 117978\_1.R1040 5'-most EST gsv701053283.h1

Method BLASTX
NCBI GI g2829868
BLAST score 192
E value 1.0e-14
Match length 66
% identity 61

NCBI Description (AC002396) Unknown protein [Arabidopsis thaliana]

Seq. No. 24607

Contig ID 118008\_1.R1040 5'-most EST zhf700956337.h1

Seq. No. 24608

Contig ID 118015\_1.R1040

5'-most EST jC-gmle01810007b03a1

Method BLASTX
NCBI GI g3063708
BLAST score 516
E value 2.0e-52
Match length 166
% identity 59

NCBI Description (AL022537) putative protein [Arabidopsis thaliana]

Seq. No. 24609

Contig ID 118018\_1.R1040



5'-most EST uC-gmropic028c09b1 Method BLASTX NCBI GI q3335375 BLAST score 655 E value 7.0e-69 Match length 139 % identity 86 (AC003028) putative amidase [Arabidopsis thaliana] NCBI Description 24610 Seq. No. 118038 1.R1040

Contig ID 5'-most EST bth700847613.h1

Seq. No. 24611

118045 1.R1040 Contig ID 5'-most EST qsv701047060.hl

Seq. No. 24612

118045 2.R1040 Contig ID 5'-most EST sat701014352.h1

24613 Seq. No.

Contig ID 118055 1.R1040 5'-most EST fde700873161.hl

BLASTX Method NCBI GI q1345933 BLAST score 439 E value 2.0e-55 Match length 164 72 % identity

NCBI Description

CITRATE SYNTHASE, GLYOXYSOMAL PRECURSOR (GCS) >gi\_1084323\_pir\_\_S53007 citrate synthase - cucurbit 975633\_dbj\_BAA07328\_ (D38132) glyoxysomal citrate

synthase [Cucurbita sp.]

24614 Seq. No.

118058 1.R1040 Contig ID uaw700662704.h1 5'-most EST

Method BLASTX g3928093 NCBI GI BLAST score 264 8.0e-23 E value Match length 66 74 % identity

NCBI Description (AC005770) IVR-like protein [Arabidopsis thaliana]

24615 Seq. No.

118080 1.R1040 Contig ID

5'-most EST g4314115 BLASTX Method NCBI GI g3150408 BLAST score 360 E value 6.0e - 34Match length 158 45 % identity

NCBI Description (AC004165) hypothetical protein [Arabidopsis thaliana]



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Seq. No.
                   118083 1.R1040
Contig ID
5'-most EST
                   sat701007593.h1
                   BLASTX
Method
                   g4006909
NCBI GI
BLAST score
                   270
                   2.0e-23
E value
Match length
                   78
% identity
                   71
NCBI Description
                   (Z99708) putative protein [Arabidopsis thaliana]
Seq. No.
                   24617
                   118101 1.R1040
Contig ID
5'-most EST
                   uaw700662755.h1
                   24618
Seq. No.
                   118149 1.R1040
-Contig ID
                   zlv700807693.h1
5'-most EST
                   24619
Seq. No.
                   118156 1.R1040
Contig ID
5'-most EST
                   leu701154865.hl
Method
                   BLASTN
NCBI GI
                   q4106527
BLAST score
                   78
                   9.0e-36
E value
Match length
                   82
% identity
                   99
NCBI Description Mus musculus Pontin52 mRNA, complete cds
                   24620
Seq. No.
Contig ID
                   118158 1.R1040
                   dkc700\overline{9}67932.h1
5'-most EST
Method
                   BLASTX
                   q3402711
NCBI GI
BLAST score
                   160
                   1.0e-10
E value
                   84
Match length
% identity
                   (AC004261) putative RNA-binding protein [Arabidopsis
NCBI Description
                   thaliana]
                   24621
Seq. No.
Contig ID
                   118169 1.R1040
5'-most EST
                   uC-gmflminsoy074d07b1
Method
                   BLASTX
NCBI GI
                   g4522009
```

BLAST score 164 4.0e-11 E value

Match length 71 % identity

NCBI Description (AC007069) unknown protein [Arabidopsis thaliana]

Seq. No. 24622

Contig ID 118169 4.R1040 5'-most EST zhf700963618.h1



Contig ID 118170\_1.R1040 5'-most EST uaw700662955.h1

Seq. No. 24624

Contig ID 118193\_1.R1040

5'-most EST g5057635

Method BLASTX

NCBI GI g2708314

BLAST score 574

E value 1.0e-58

Match length 307

% identity 32

NCBI Description (AF027727) protein disulfide isomerase RB60 [Chlamydomonas

reinhardtii] >gi\_4104541 (AF036939) protein disulfide

isomerase [Chlamydomonas reinhardtii]

Seq. No. 24625

Contig ID 118207\_2.R1040 5'-most EST epx701109832.h1

Seq. No. 24626

Contig ID 118212 1.R1040 5'-most EST uaw700663116.h1

Seq. No. 24627

Contig ID 118230\_1.R1040

5'-most EST jC-gmst02400063h04d1

Seq. No. 24628

Contig ID 118231\_1.R1040

5'-most EST  $g57536\overline{2}8$ 

Seq. No. 24629

Contig ID 118231\_4.R1040 5'-most EST epx701106665.h1

Seq. No. 24630

Contig ID 118259 1.R1040 5'-most EST asn701141232.h1

Method BLASTX
NCBI GI g927428
BLAST score 891
E value 3.0e-96
Match length 203
% identity 81

NCBI Description (X86733) fis1 [Linum usitatissimum]

Seq. No. 24631

Contig ID 118259\_2.R1040

5'-most EST jC-gmf\(\bar{1}\)02220052a03d1

Method BLASTX
NCBI GI g927428
BLAST score 205
E value 4.0e-16
Match length 42
% identity 86



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NCBI Description
                  (X86733) fis1 [Linum usitatissimum]
                   24632
Seq. No.
                   118266 1.R1040
Contig ID
5'-most EST
                   uaw700665779.h1
Method
                   BLASTN
NCBI GI
                   q3021347
BLAST score
                   44
                   1.0e-15
E value
                   72
Match length
% identity
                   90
NCBI Description Cicer arietinum mRNA for cytoplasmic ribosomal protein L18
Seq. No.
                   24633
                   118287 1.R1040
Contig ID
                   a5752980
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4107276
BLAST score
                   415
E value
                   2.0e-40
Match length
                   92
                   87
% identity
                  (X98506) acetyl-CoA synthetase [Solanum tuberosum]
NCBI Description
                   24634
Seq. No.
Contig ID
                   118297 1.R1040
5'-most EST
                   uaw700663319.hl
Method
                   BLASTX
NCBI GI
                   g3335378
                   325
BLAST score
                   3.0e-30
E value
Match length
                   86
% identity
                   70
                   (AC003028) Myb-related transcription activator [Arabidopsis
NCBI Description
                   thaliana]
                   24635
Seq. No.
                   118298 1.R1040
Contig ID
                   rca701002040.hl
5'-most EST
                   24636
Seq. No.
                   118300 1.R1040
Contig ID
5'-most EST
                   uaw700663324.h1
                   24637
Seq. No.
                   118305 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy307b01b1
                   BLASTX
Method
                   g3885340
NCBI GI
BLAST score
                   259
E value
                   2.0e-22
                   79
Match length
% identity
```

NCBI Description

Contig ID 118308\_1.R1040

(AC005623) unknown protein [Arabidopsis thaliana]



5'-most EST jC-gmst02400043b06d1

Seq. No. 24639

Contig ID 118323 1.R1040

5'-most EST jC-gmle01810061c02a1

Seq. No. 24640

Contig ID 118323\_2.R1040 5'-most EST uaw700663350.h1

Seq. No. 24641

Contig ID 118332 1.R1040

5'-most EST g4397347

Seq. No. 24642

Contig ID 118335 1.R1040

5'-most EST jC-gmro02910064g04a1

Seq. No. 24643

Contig ID 118335\_2.R1040 5'-most EST uaw700663362.h1

Seq. No. 24644

Contig ID 118354\_1.R1040 5'-most EST sat701011567.h1

Method BLASTN
NCBI GI g20834
BLAST score 440
E value 0.0e+00
Match length 808
% identity 89

NCBI Description P.sativum PHSP1 mRNA for HSP70

Seq. No. 24645

Contig ID 118369\_1.R1040 5'-most EST wrg700787182.h2

Method BLASTN
NCBI GI g18735
BLAST score 220
E value 1.0e-120
Match length 371
% identity 91

NCBI Description Soybean RPB1-C gene for largest subunit of RNA polymerase

ΤT

Seq. No. 24646

Contig ID 118373\_1.R1040 5'-most EST zhf700955942.h1

Method BLASTX
NCBI GI g3249070
BLAST score 171
E value 6.0e-12
Match length 107
% identity 42

NCBI Description (AC004473) Contains similarity to siah binding protein 1 (SiahBP1) gb U51586 from Homo sapiens. ESTs gb T43314,

gb\_T43315 and gb R90521, gb T75905 [Arabidopsis thaliana]



Contig ID 118384 1.R1040 5'-most EST leu701155193.h1

Seq. No. 24648

Contig ID 118409 1.R1040 5'-most EST uaw700663582.h1

Seq. No. 24649

Contig ID 118415\_1.R1040 5'-most EST uC-gmropic070e05b1

Method BLASTX
NCBI GI g4220527
BLAST score 460
E value 1.0e-45
Match length 185
% identity 50

NCBI Description (AL035356) putative protein [Arabidopsis thaliana]

Seq. No. 24650

Contig ID 118438\_1.R1040 5'-most EST yz1700967071.h1

Method BLASTX
NCBI GI g1091678
BLAST score 190
E value 2.0e-14
Match length 115
% identity 37

NCBI Description activator-like transposable element [Pennisetum glaucum]

Seq. No. 24651

Contig ID 118452\_1.R1040 5'-most EST uaw700663637.h1

Seq. No. 24652

Contig ID 118454\_1.R1040 5'-most EST uaw700663639.h1

Seq. No. 24653

Contig ID 118457\_1.R1040 5'-most EST uC-gmronoir073e04b1

Method BLASTX
NCBI GI g2735841
BLAST score 274
E value 6.0e-24
Match length 137
% identity 44

NCBI Description (AF010283) No definition line found [Sorghum bicolor]

Seq. No. 24654

Contig ID 118486\_1.R1040 5'-most EST uC-gmropic045g12b1

Seq. No. 24655

Contig ID 118492\_1.R1040 5'-most EST uaw700663678.h1



Method BLASTX
NCBI GI g4539330
BLAST score 1121
E value 1.0e-123
Match length 346
% identity 63

NCBI Description (AL035679) putative receptor-like protein kinase (fragment)

[Arabidopsis thaliana]

Seq. No. 24657

Contig ID 118505\_2.R1040 5'-most EST fC-gmst700663791r4

Method BLASTX
NCBI GI 94539330
BLAST score 180
E value 6.0e-13
Match length 69
% identity 55

NCBI Description (AL035679) putative receptor-like protein kinase (fragment)

[Arabidopsis thaliana]

Seq. No. 24658

Contig ID 118512\_1.R1040 5'-most EST eep700865890.h1

Method BLASTN
NCBI GI g3402671
BLAST score 37
E value 2.0e-11
Match length 73
% identity 88

NCBI Description Arabidopsis thaliana chromosome II BAC T16B24 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 24659

Contig ID 118513\_1.R1040 5'-most EST jex700903558.h1

Seq. No. 24660

Contig ID 118539 1.R1040 5'-most EST gsv701044503.h1

Method BLASTX
NCBI GI g2191172
BLAST score 188
E value 2.0e-14
Match length 51
% identity 69

NCBI Description (AF007270) contains similarity to GATA-type zinc fingers

(PS:PS00344) [Arabidopsis thaliana]

Seq. No. 24661

Contig ID 118555 1.R1040 5'-most EST wvk700683214.h1



118556 1.R1040 Contig ID

5'-most EST uC-gmrominsoy044b07b1

Method BLASTX NCBI GI g1084780 **1**75 BLAST score 1.0e-12 E value Match length 112 % identity 35

NCBI Description

probable membrane protein YPR048w - yeast (Saccharomyces cerevisiae) >gi\_805031\_emb\_CAA89168\_ (Z49219) unknown [Saccharomyces cerevisiae] >gi\_1314119\_emb\_CAA94995\_

(Z71255) unknown [Saccharomyces cerevisiae]

24663 Seq. No.

118563 1.R1040 Contig ID 5'-most EST fC-gms\u00e4700663766f3

Method BLASTX NCBI GI g4335745 BLAST score 152 E value 4.0e-10 Match length 98 % identity 36

NCBI Description (AC006284) putative hydrolase (contains an

esterase/lipase/thioesterase active site serine domain

(prosite: PS50187) [Arabidopsis thaliana]

Seq. No. 24664

118566 1.R1040 Contig ID 5'-most EST k11701213959.h1

Method BLASTX NCBI GI g2827637 BLAST score 143 E value 7.0e-09 Match length 52

% identity 56

NCBI Description (AL021636) putative protein [Arabidopsis thaliana]

Seq. No. 24665

Contig ID 118569 1.R1040 5'-most EST uxk700667627.h1

Seq. No. 24666

Contig ID 118579 1.R1040 5'-most EST uaw700663782.h1

Seq. No. 24667

Contig ID 118586 1.R1040 5'-most EST uaw700663792.h1

Seq. No. 24668

Contig ID 118589 1.R1040

5'-most EST uC-gmflminsoy037a05b1

24669 Seq. No.

Contig ID 118597 1.R1040 5'-most EST uaw700663808.hl



Method BLASTX
NCBI GI g3582340
BLAST score 197
E value 3.0e-15
Match length 86
% identity 47

NCBI Description (AC005496) unknown protein [Arabidopsis thaliana]

Seq. No. 24670

Contig ID 118599\_1.R1040 5'-most EST kmv700741520.h1

Seq. No. 24671

Contig ID 118611\_1.R1040 5'-most EST uaw700663833.h1

Seq. No. 24672

Contig ID 118625\_1.R1040 5'-most EST uaw700663854.h1

Method BLASTX
NCBI GI g3367522
BLAST score 235
E value 7.0e-20
Match length 101
% identity 50

NCBI Description (AC004392) EST gb T04691 comes from this gene. [Arabidopsis

thaliana]

Seq. No. 24673

Contig ID 118643 1.R1040 5'-most EST uaw700663878.h1

Method BLASTX
NCBI GI g3033375
BLAST score 508
E value 2.0e-51
Match length 170
% identity 57

NCBI Description (AC004238) putative berberine bridge enzyme [Arabidopsis

thaliana]

Seq. No. 24674

Contig ID 118662 1.R1040 5'-most EST awf700841118.h1

Seq. No. 24675

Contig ID 118674\_1.R1040 5'-most EST uaw700664222.h1

Method BLASTN
NCBI GI g1066858
BLAST score 582
E value 0.0e+00
Match length 793
% identity 94

NCBI Description Glycine max (clone 91) acetyl-CoA-carboxylase (ACCase-A)

mRNA, 3' end of cds

Seq. No. 24676



```
Contig ID
                   118684 1.R1040
5'-most EST
                   leu701151065.hl
Method
                   BLASTX
NCBI GI
                   q4091008
BLAST score
                   397
E value
                   9.0e-39
Match length
                   119
% identity
                   64
NCBI Description
                  (AF040700) methionyl-tRNA synthetase [Oryza sativa]
Seq. No.
Contig ID
                   118690 1.R1040
5'-most EST
                   kl1701205187.h1
Seq. No.
                   24678
                   118696 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy074g03b1
Method
                   BLASTX
NCBI GI
                   q2088651
BLAST score
                   179
E value
                   4.0e-13
Match length
                   116
% identity
                   41
                   (AF002109) hypersensitivity-related gene 201 isolog
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   24679
Contig ID
                   118739 1.R1040
5'-most EST
                   jC-gmro02910010c05a1
Method
                   BLASTX
NCBI GI
                   g3522937
BLAST score
                   258
E value
                   7.0e-22
Match length
                   309
% identity
                   28
NCBI Description
                  (AC004411) unknown protein [Arabidopsis thaliana]
Seq. No.
                  24680
                  118742 1.R1040
Contig ID
5'-most EST
                  uaw700664605.h1
Method
                  BLASTX
NCBI GI
                  g2500036
BLAST score
                  155
E value
                  2.0e-10
Match length
                  51
% identity
                  61
NCBI Description
                  DIHYDROOROTASE PRECURSOR (DHOASE) >gi 2121273 (AF000146)
                  dihydroorotase [Arabidopsis thaliana]
                  >gi_3292818_emb_CAA19808_ (AL031018) dihydroorotase
                   [Arabidopsis thaliana]
```

Contig ID 118763\_1.R1040 5'-most EST pmv700894093.h1

Method BLASTX
NCBI GI g2739386
BLAST score 178



E value 6.0e-13 Match length 81 % identity 47

NCBI Description (AC002505) unknown protein [Arabidopsis thaliana]

Seq. No. 24682

Contig ID 118766\_1.R1040 5'-most EST zhf700954595.h1

Method BLASTX
NCBI GI g1174862
BLAST score 144
E value 3.0e-09
Match length 60
% identity 37

NCBI Description PUTATIVE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE C13A11.04C

(UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING

PROTEASE) (DEUBIQUITINATING ENZYME)

>gi 984225 emb CAA90805 (Z54096) unknown

[Schizosaccharomyces pombe]

Seq. No. 24683

Contig ID 118772 1.R1040 5'-most EST hrw701062193.h1

Method BLASTX
NCBI GI g2791278
BLAST score 232
E value 3.0e-19
Match length 139
% identity 39

NCBI Description (Z69257) beta-xylosidase [Hypocrea jecorina]

Seq. No. 24684

Contig ID 118774\_1.R1040 5'-most EST uaw700666952.h1

Seq. No. 24685

Contig ID 118803\_1.R1040 5'-most EST jC-gmle01810010c12a1

Seq. No. 24686

Contig ID 118810\_1.R1040 5'-most EST eep700868507.h1

Method BLASTX
NCBI GI g3953457
BLAST score 147
E value 7.0e-09
Match length 98
% identity 37

NCBI Description (AC002328) F20N2.2 [Arabidopsis thaliana]

Seq. No. 24687

Contig ID 118813\_1.R1040 5'-most EST fC-gmse700671180a1

Method BLASTX
NCBI GI g2961358
BLAST score 1350
E value 1.0e-150



Match length 300 % identity 85

NCBI Description (AL022140) serine/threonine protein kinase like protein

[Arabidopsis thaliana]

Seq. No. 24688

Contig ID 118813\_2.R1040 5'-most EST jC-gmst02400066h11d1

Method BLASTX
NCBI GI g2961358
BLAST score 206
E value 3.0e-16
Match length 51
% identity 75

NCBI Description (AL022140) serine/threonine protein kinase like protein

[Arabidopsis thaliana]

Seq. No. 24689

Contig ID 118832\_1.R1040 5'-most EST uaw700664412.h1

Method BLASTX
NCBI GI g3328101
BLAST score 288
E value 3.0e-26
Match length 78
% identity 64

NCBI Description (AF073995) beta-galactosidase [synthetic construct]

Seq. No. 24690

Contig ID 118835\_1.R1040 5'-most EST leu701154262.h1

Method BLASTX
NCBI GI g3935183
BLAST score 273
E value 6.0e-25
Match length 138
% identity 52

NCBI Description (AC004557) F17L21.26 [Arabidopsis thaliana]

Seq. No. 24691

Contig ID 118837\_1.R1040 5'-most EST crh700854135.h1

Method BLASTX
NCBI GI g3132471
BLAST score 333
E value 3.0e-33
Match length 118
% identity 61

NCBI Description (AC003096) putative protein phosphatase 2C [Arabidopsis

thaliana]

Seq. No. 24692

Contig ID 118853\_1.R1040 5'-most EST awf700839191.h1

Seq. No. 24693

Contig ID 118854 1.R1040



5'-most EST g4397574
Method BLASTN
NCBI GI g400531
BLAST score 269
E value 1.0e-149
Match length 713
% identity 84

NCBI Description V.sativa mRNA for NADPH-ferrihemoprotein reductase

Seq. No. 24694

Contig ID 118855\_1.R1040

5'-most EST uC-gmrominsoy142c02b1

Seq. No. 24695

Contig ID 118856\_1.R1040 5'-most EST uC-gmropic045h11b1

Seq. No. 24696

Contig ID 118856\_2.R1040 5'-most EST epx701106004.h1

Seq. No. 24697

Contig ID 118856\_3.R1040 5'-most EST wrg700789707.h1

Seq. No. 24698

Contig ID 118859\_1.R1040 5'-most EST crh700853408.h1

Method BLASTX
NCBI GI g3738230
BLAST score 289
E value 1.0e-25
Match length 137
% identity 45

NCBI Description (AB007790) DREB2A [Arabidopsis thaliana]

>gi 4126706\_dbj\_BAA36705\_ (AB016570) DREB2A [Arabidopsis

thaliana]

Seq. No. 24699

Contig ID 118859\_2.R1040 5'-most EST epx701109895.h1

Seq. No. 24700

Contig ID 118861\_1.R1040 5'-most EST jC-gmle01810088f12a1

Method BLASTX
NCBI GI g2104951
BLAST score 366
E value 8.0e-35
Match length 180
% identity 53

NCBI Description (U96717) MAP kinase-like protein [Selaginella lepidophylla]

Seq. No. 24701

Contig ID 118867 1.R1040

5'-most EST uC-gmrominsoy039h06b1

Method BLASTX



NCBI GI g3337361 BLAST score 417 E value 8.0e-41 Match length 173 % identity 49

NCBI Description (AC004481) ankyrin-like protein [Arabidopsis thaliana]

Seq. No. 24702

Contig ID 118872\_1.R1040 5'-most EST uaw700664456.h1

Seq. No. 24703

Contig ID 118886\_1.R1040 5'-most EST uaw700664473.h1

Seq. No. 24704

Contig ID 118887\_1.R1040 5'-most EST zhf700965219.h1

Seq. No. 24705

Contig ID 118899\_1.R1040 5'-most EST hyd700727966.h1

Seq. No. 24706

Contig ID 118901\_1.R1040

5'-most EST uC-gmrominsoy030g10b1

Method BLASTX
NCBI GI g2281105
BLAST score 259
E value 2.0e-22
Match length 122
% identity 46

NCBI Description (AC002333) unknown protein [Arabidopsis thaliana]

Seq. No. 24707

Contig ID 118903\_1.R1040

5'-most EST jC-gmle01810009a06d1

Seq. No. 24708

Contig ID 118911\_1.R1040 5'-most EST fC-gmst700667018f2

Method BLASTX
NCBI GI 94204575
BLAST score 421
E value 3.0e-41
Match length 135
% identity 64

NCBI Description (AF098510) cytochrome b5 DIF-F [Petunia x hybrida]

Seq. No. 24709

Contig ID 118929\_1.R1040 5'-most EST wvk700685911.h1

Method BLASTX
NCBI GI g3668089
BLAST score 847
E value 4.0e-91
Match length 178



% identity (AC004667) unknown protein [Arabidopsis thaliana] NCBI Description 24710 Seq. No. 118941 1.R1040 Contig ID uaw700664541.hl

24711 Seq. No.

5'-most EST

118948 1.R1040 Contig ID 5'-most EST fC-qmle7000743383f1

Seq. No. 24712

118950 1.R1040 Contig ID 5'-most EST jC-gmle01810060f04a1

24713 Seq. No.

118952 1.R1040 Contig ID awf700842458.hl 5'-most EST

24714 Seq. No.

118959 1.R1040 Contig ID 5'-most EST uaw700664561.hl

Seq. No. 24715

118961 1.R1040 Contig ID uC-gmropic069h11b1 5'-most EST

BLASTX Method a3132889 NCBI GI BLAST score 194 1.0e-14 E value Match length 152 31 % identity

(AF026386) WaaA [Salmonella typhimurium] NCBI Description

24716 Seq. No.

118969 1.R1040 Contig ID zhf700958206.hl 5'-most EST

24717 Seq. No.

118977 1.R1040 Contig ID uaw700664583.h1 5'-most EST

24718 Seq. No.

118998 1.R1040 Contig ID uaw700664611.h1 5'-most EST

24719 Seq. No.

119004 1.R1040 Contig ID leu701155824.h1 5'-most EST

BLASTX Method NCBI GI g2197127 BLAST score 205 E value 1.0e-15 152 Match length 32 % identity

(AF003907) swelling-induced chloride conductance regulatory NCBI Description

protein pIcIn [Oryctolagus cuniculus]



```
24720
Seq. No.
                  119013 1.R1040
Contig ID
                  jC-qmro02910016b09a1
5'-most EST
                  BLASTX
Method
                  g1724110
NCBI GI
BLAST score
                  1051
                  1.0e-114
E value
                  346
Match length
                  56
% identity
                   (U79770) cinnamyl-alcohol dehydrogenase Eli3
NCBI Description
                   [Mesembryanthemum crystallinum]
                  24721
Seq. No.
                  119025 1.R1040
Contig ID
                  uaw700664643.hl
5'-most EST
                  BLASTX
Method
NCBI GI
                   q3242715
                   260
BLAST score
                   6.0e-23
E value
Match length
                   83
                   58
% identity
                  (AC003040) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   24722
Seq. No.
                   119028 1.R1040
Contig ID
                   uaw700664646.hl
5'-most EST
Seq. No.
                   24723
                   119041 1.R1040
Contig ID
                   uaw700664664.hl
5'-most EST
                   24724
Seq. No.
                   119043 1.R1040
Contig ID
5'-most EST
                   uaw700665139.h1
Seq. No.
                   24725
                   119058 1.R1040
Contig ID
                   uaw700664686.hl
5'-most EST
                   BLASTX
Method
                   q4176420
NCBI GI
                   397
BLAST score
                   2.0e-38
E value
                   115
Match length
                   63
% identity
                  (AB008097) cytochrome P450 [Arabidopsis thaliana]
NCBI Description
                   24726
Seq. No.
                   119066 1.R1040
Contig ID
5'-most EST
                   uaw700664696.hl
```

Contig ID 119073 1.R1040 5'-most EST uaw700664708.h1

Method BLASTX NCBI GI g3193284 BLAST score 165



```
8.0e-12
E value
Match length
                   41
                   76
% identity
                   (AF069298) No definition line found [Arabidopsis thaliana]
NCBI Description
                   24728
Seq. No.
                   119095 1.R1040
Contig ID
                   leu701155727.h1
5'-most EST
                   BLASTX
Method
                   g2827637
NCBI GI
                   147
BLAST score
                   3.0e-09
E value
                   127
Match length
                   31
% identity
                  (AL021636) putative protein [Arabidopsis thaliana]
NCBI Description
                   24729
Seq. No.
                   119101 1.R1040
Contig ID
                   uaw700664738.hl
5'-most EST
                   BLASTX
Method
                   g3269285
NCBI GI
                   161
BLAST score
                   4.0e-19
E value
                   109
Match length
                   47
% identity
                   (AL030978) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   24730
Seq. No.
                   119105 1.R1040
Contig ID
                   gsv701\overline{0}44730.h1
5'-most EST
                   24731
Seq. No.
                   119107 1.R1040
Contig ID
                   uaw700664744.hl
5'-most EST
                   BLASTX
Method
                   q3298544
NCBI GI
BLAST score
                   331
                   3.0e - 31
E value
                   72
Match length
                   83
% identity
                   (AC004681) unknown protein [Arabidopsis thaliana]
NCBI Description
                   24732
Seq. No.
                   119113 1.R1040
Contig ID
                   awf700837140.h1
5'-most EST
                   BLASTX
Method
                   g2505879
NCBI GI
BLAST score
                   213
                   2.0e-17
E value
Match length
                   74
% identity
                   (Y12776) hypothetical protein [Arabidopsis thaliana]
NCBI Description
```

Contig ID 119118\_1.R1040 5'-most EST jex700907868.h1

Method BLASTX

g2529673 NCBI GI 164 BLAST score 1.0e-11 E value 74 Match length 46 % identity NCBI Description (AC002535) hypothetical protein [Arabidopsis thaliana] 24734 Seq. No. 119129 1.R1040 Contig ID úaw700666245.h1 5'-most EST BLASTX Method g3193297 NCBI GI 436 BLAST score 6.0e-43E value 100 Match length % identity (AF069298) similar to epoxide hydrolases [Arabidopsis NCBI Description thaliana] 24735 Seq. No. 119136 1.R1040 Contig ID  $uaw700\overline{6}65150.h1$ 5'-most EST 24736 Seq. No. 119153 1.R1040 Contig ID uC-gmrominsoy040f07b1 5'-most EST BLASTX Method

g2829894 NCBI GI

639 BLAST score 1.0e-66 E value 207 Match length 62 % identity

NCBI Description (AC002311) Unknown protein [Arabidopsis thaliana]

24737 Seq. No.

119163 1.R1040 Contig ID uaw700665257.h1 5'-most EST

24738 Seq. No.

119164 1.R1040 Contig ID sat701014089.hl 5'-most EST

24739 Seq. No.

119171 1.R1040 Contig ID zpv700759827.h1 5'-most EST

BLASTX Method NCBI GI q123538 BLAST score 412 2.0e-40 E value Match length 106 68 % identity

17.5 KD CLASS I HEAT SHOCK PROTEIN (HSP 17.5-M) >gi 169983 NCBI Description (M11318) 17.5 kd heat shock protein Gmhsp17.6L [Glycine

max]

24740 Seq. No.

119176\_1.R1040 Contig ID



5'-most EST uaw700664829.hl

Seq. No. 24741

Contig ID 119177\_1.R1040 5'-most EST uaw700664830.h1

Seq. No. 24742

Contig ID 119190 1.R1040

5'-most EST jC-gmr002800025a01a1

Seq. No. 24743

Contig ID 119190 2.R1040

5'-most EST g5688440

Seq. No. 24744

Contig ID 119200\_1.R1040 5'-most EST zsg701130383.h1

Method BLASTX
NCBI GI g4406774
BLAST score 285
E value 2.0e-25
Match length 93
% identity 61

NCBI Description (AC006836) putative nonsense-mediated mRNA decay protein,

5' partial [Arabidopsis thaliana]

Seq. No. 24745

Contig ID 119203\_1.R1040 5'-most EST leu701156369.h1

Seq. No. 24746

Contig ID 119203\_2.R1040 5'-most EST zpv700757790.h1

Seq. No. 24747

Contig ID 119223\_1.R1040 5'-most EST uaw700664888.h1

Seq. No. 24748

Contig ID 119225 1.R1040 5'-most EST uaw700664891.h1

Method BLASTX
NCBI GI 94388717
BLAST score 404
E value 1.0e-39
Match length 106
% identity 73

NCBI Description (AC006413) putative nuclear phosphoprotein (contains multiple TPR repeats prosite:QDOC50005) [Arabidopsis

thaliana]

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Seq. No. 24749 Contig ID 11925

Contig ID 119258 1.R1040 5'-most EST uaw700664933.h1

Seq. No. 24750

Contig ID 119260\_1.R1040



5'-most EST uaw700664936.hl

Seq. No. 24751

Contig ID 119262\_1.R1040 5'-most EST sat701009338.h1

Seq. No. 24752

Contig ID 119262\_2.R1040 5'-most EST uaw700665195.h1

Seq. No. 24753

Contig ID 119277\_1.R1040

5'-most EST uC-gmrominsoy183c08b1

Method BLASTN
NCBI GI g166411
BLAST score 281
E value 1.0e-156
Match length 668
% identity 87

NCBI Description Medicago sativa NADH-glutamate synthase mRNA, comlete cds

Seq. No. 24754

Contig ID 119281\_1.R1040 5'-most EST vwf700677857.h1

Seq. No. 24755

Contig ID 119327\_1.R1040 5'-most EST uaw700665023.h1

Seq. No. 24756

Contig ID 119328\_1.R1040 5'-most EST xpa700794756.h1

Seq. No. 24757

Contig ID 119338\_1.R1040 5'-most EST uaw700665036.h1

Method BLASTX
NCBI GI g3236261
BLAST score 585
E value 2.0e-60
Match length 187
% identity 58

NCBI Description (AC004684) putative zinc finger protein [Arabidopsis

thaliana]

Seq. No. 24758

Contig ID 119353 1.R1040

5'-most EST uC-gmrominsoy204g09b1

Seq. No. 24759

Contig ID 119370\_1.R1040 5'-most EST zsg701122585.h1

Method BLASTX
NCBI GI g2274988
BLAST score 279
E value 8.0e-25
Match length 99

3907



% identity 61
NCBI Description (AJ000226) partial sequence, homology to serine
hydroxymethyltransferases [Hordeum vulgare]

Seq. No. 24760

Contig ID 119373\_1.R1040 5'-most EST uaw700665076.h1

Method BLASTN
NCBI GI g2654107
BLAST score 138
E value 7.0e-72
Match length 222
% identity 91

NCBI Description Pisum sativum cytosine-5 DNA methyltransferase mRNA,

complete cds

Seq. No. 24761

Contig ID 119384\_1.R1040 5'-most EST uaw700665087.h1

Seq. No. 24762

Contig ID 119386\_1.R1040 5'-most EST uaw700665089.h1

Seq. No. 24763

Contig ID 119389\_1.R1040 5'-most EST uaw700665141.h1

Seq. No. 24764

Contig ID 119391\_1.R1040

5'-most EST g4295450

Seq. No. 24765

Contig ID 119409\_1.R1040 5'-most EST fua701041589.h1

Seq. No. 24766

Contig ID 119410\_1.R1040 5'-most EST uaw700665121.h1

Seq. No. 24767

Contig ID 119414\_1.R1040 5'-most EST uaw700665126.h1

Seq. No. 24768

Contig ID 119425\_1.R1040 5'-most EST uaw700666183.h1

Seq. No. 24769

Contig ID 119439\_1.R1040 5'-most EST uC-gmropic066d08b1

Method BLASTX
NCBI GI g3858937
BLAST score 412
E value 2.0e-40
Match length 128
% identity 65

3908



NCBI Description (AL021636) putative protein [Arabidopsis thaliana]

Seq. No. 24770

Contig ID 119446 1.R1040

5'-most EST jC-gmro02910039b12a1

Method BLASTX
NCBI GI g3136048
BLAST score 319
E value 2.0e-29
Match length 141
% identity 45

NCBI Description (AL023592) putative helicase [Schizosaccharomyces pombe]

Seq. No. 24771

Contig ID 119452 1.R1040 5'-most EST sat701009814.h1

Seq. No. 24772

Contig ID 119457 1.R1040 5'-most EST zpv700760805.h1

Seq. No. 24773

Contig ID 119458\_1.R1040 5'-most EST uaw700665196.h1

Seq. No. 24774

Contig ID 119467\_1.R1040

Match length 35 % identity 77

NCBI Description (AC006929) hypothetical protein [Arabidopsis thaliana]

Seq. No. 24775

Contig ID 119471\_1.R1040 5'-most EST uaw700665726.h1

Seq. No. 24776

Contig ID 119483\_1.R1040

5'-most EST jC-gmr002910068b07a1

Method BLASTN
NCBI GI g295447
BLAST score 573
E value 0.0e+00
Match length 959
% identity 90

NCBI Description Vigna radiata NADPH cytochrome P450 mRNA, complete cds

Seq. No. 24777

Contig ID 119487\_1.R1040 5'-most EST uaw700665207.h1

Seq. No. 24778

Contig ID 119492\_1.R1040



5'-most EST epx701106335.h1

Seq. No. 24779

Contig ID 119507\_1.R1040 5'-most EST zsg701122976.h1

Seq. No. 24780

Contig ID 119513\_1.R1040 5'-most EST uC-gmropic055a04b1

Method BLASTX
NCBI GI g3377805
BLAST score 488
E value 5.0e-49
Match length 124
% identity 69

NCBI Description (AF075597) contains similarity to several apoptosis or

programmed cell death proteins such as rat apoptosis

protein RP-8 (GB:M80601) [Arabidopsis thaliana]

>gi\_3912928\_gb\_AAC78712.1\_ (AF001308) putative zinc finger

protein [Arabidopsis thaliana]

Seq. No. 24781

Contig ID 119513 2.R1040

5'-most EST jC-gmro02910072a04a1

Seq. No. 24782

Contig ID 119526\_1.R1040 5'-most EST uaw700665250.h1

Method BLASTX
NCBI GI g1351662
BLAST score 140
E value 1.0e-08
Match length 86
% identity 41

NCBI Description HYPOTHETICAL 74.4 KD PROTEIN C30D11.09 IN CHROMOSOME I

>gi\_2130408\_pir\_\_S62567 hypothetical protein SPAC30D11.09 -

fission yeast (Schizosaccharomyces pombe)

>gi 1065896 emb CAA91895 (Z67961) hypothetical protein

[Schizosaccharomyces pombe]

Seq. No. 24783

Contig ID 119529 1.R1040 5'-most EST rca700998590.h1

Method BLASTX
NCBI GI g3201680
BLAST score 290
E value 3.0e-26
Match length 101
% identity 57

NCBI Description (AF060941) extra-large G-protein [Arabidopsis thaliana]

Seq. No. 24784

Contig ID 119545\_1.R1040 5'-most EST gsv701051176.h1

Seq. No. 24785

Contig ID 119579 1.R1040

NCBI Description



```
5'-most EST
                  uaw700665311.h1
Seq. No.
                  24786
Contig ID
                  119585 1.R1040
5'-most EST
                  uaw700665318.hl
                  24787
Seq. No.
Contig ID
                  119588 1.R1040
5'-most EST
                  gsv701049666.hl
Method
                  BLASTX
                  g3522952
NCBI GI
BLAST score
                  884
E value
                  3.0e-95
Match length
                  251
% identity
                  66
NCBI Description
                  (AC004411) putative alcohol dehydrogenase [Arabidopsis
                  thalianal
                  24788
Seq. No.
Contig ID
                  119595 1.R1040
5'-most EST
                  hrw701061756.h1
Method
                  BLASTN
NCBI GI
                  q3204107
BLAST score
                  75
                  5.0e-34
E value
Match length
                  155
% identity
                  87
NCBI Description
                  Cicer arietinum mRNA for putative cytidine or
                  deoxycytidylate deaminase, partial
Seq. No.
                  24789
                  119622 1.R1040
Contig ID
5'-most EST
                  uaw700665358.h1
Method
                  BLASTX
NCBI GI
                  a3399777
BLAST score
                  165
E value
                  3.0e-11
Match length
                  63
% identity
                  51
NCBI Description
                  (AF069738) symbiotic ammonium transporter; nodulin [Glycine
                  max]
                  24790
Seq. No.
Contig ID
                  119631 1.R1040
5'-most EST
                  uaw700665369.h1
                  24791
Seq. No.
Contig ID
                  119638 1.R1040
5'-most EST
                  zhf700958411.h1
Method
                  BLASTX
                  g3152568
NCBI GI
BLAST score
                  631
E value
                  6.0e-66
Match length
                  168
% identity
                  73
```

(AC002986) Similar to hypothetical protein product

gb\_Z97337 from A. thaliana. EST gb H76597 comes from this



## gene. [Arabidopsis thaliana]

```
24792
Seq. No.
                  119640 1.R1040
Contig ID
                  uC-qmflminsoy077e04b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2529685
BLAST score
                  201
                  1.0e-25
E value
                   69
Match length
                   85
% identity
                   (AC002535) putative dimethyladenosine transferase
NCBI Description
                   [Arabidopsis thaliana]
                   24793
Seq. No.
                   119659 1.R1040
Contig ID
                   asn701140101.h1
5'-most EST
                   24794
Seq. No.
                   119659 2.R1040
Contig ID
                   fua701043662.h1
5'-most EST
```

24795 Seq. No.

Contig ID 119664 1.R1040 ncj700978465.hl 5'-most EST

24796 Seq. No.

119677 1.R1040 Contig ID fC-gmro700873447d1 5'-most EST

BLASTX Method g2894592 NCBI GI BLAST score 337 2.0e-31 E value 75 Match length % identity

(AL021889) predicted protein [Arabidopsis thaliana] NCBI Description

24797 Seq. No.

119682 1.R1040 Contig ID

 $\verb|jC-gmr| \overline{o} 02910009a04a1$ 5'-most EST

24798 Seq. No.

119685 1.R1040 Contig ID gsv701046043.hl 5'-most EST

BLASTXMethod g4510340 NCBI GI 168 BLAST score 4.0e-12 E value 55 Match length 64 % identity

NCBI Description (AC006921) hypothetical protein [Arabidopsis thaliana]

24799 Seq. No.

119699 1.R1040 Contig ID 5'-most EST leu701147294.h1

BLASTX Method q3738295 NCBI GI



BLAST score 5.0e-44 E value 176 Match length 55 % identity NCBI Description (AC005309) unknown protein [Arabidopsis thaliana] 24800 Seq. No. 119700 1.R1040 Contig ID pmv700891664.h1 5'-most EST BLASTX Method

g4538913 NCBI GI 461 BLAST score 6.0e-46 E value Match length 165 % identity

(AL049482) putative protein [Arabidopsis thaliana] NCBI Description

24801 Seq. No.

119702 1.R1040 Contig ID jC-gmro02910047e10a1 5'-most EST

24802 Seq. No.

119717 1.R1040 Contig ID 5'-most EST uaw700665494.hl

Method BLASTN g170293 NCBI GI 124 BLAST score 2.0e-63 E value 236 Match length % identity

Nicotiana plumbaginifolia plasma-membrane H+ ATPase (pma3) NCBI Description

mRNA, complete cds

24803 Seq. No.

119719 1.R1040 Contig ID fC-gmse700672974y1 5'-most EST

Method BLASTX q4580456 NCBI GI BLAST score 570 4.0e-58 E value 347 Match length 48 % identity

(AC006081) unknown protein [Arabidopsis thaliana] NCBI Description

24804 Seq. No.

119748 1.R1040 Contig ID 5'-most EST dpv701099035.hl

Seq. No. 24805

119791 1.R1040 Contig ID uaw700665609.h1 5'-most EST

24806 Seq. No.

119800 1.R1040 Contig ID zzp700834324.hl 5'-most EST

BLASTX Method g2245069 NCBI GI



```
BLAST score 360
E value 2.0e-34
Match length 105
% identity 68
```

NCBI Description (Z97342) hypothetical protein [Arabidopsis thaliana]

Seq. No. 24807

Contig ID 119806\_1.R1040 5'-most EST uaw700665636.h1

Method BLASTN
NCBI GI g349158
BLAST score 203
E value 1.0e-110
Match length 389
% identity 89

NCBI Description Vigna aconitifolia AIR carboxylase (purE) mRNA, partial cds

Seq. No. 24808

Contig ID 119835\_1.R1040 5'-most EST uaw700665722.h1

Seq. No. 24809

Contig ID 119837\_1.R1040 5'-most EST uC-gmropic091e06b1

Method BLASTN
NCBI GI g4006847
BLAST score 192
E value 1.0e-103
Match length 456
% identity 86

NCBI Description Astragalus bisulcatus mRNA for selenocysteine

methyltransferase

Seq. No. 24810

Contig ID 119838 1.R1040

5'-most EST jC-gmle01810017b07a2

Method BLASTX
NCBI GI g3873837
BLAST score 224
E value 2.0e-18
Match length 139
% identity 36

NCBI Description (Z81029) Similarity to S.pombe hypothetical protein

C1D4.09C (SW:Q10154); cDNA EST EMBL:T00543 comes from this gene; cDNA EST EMBL:T01062 comes from this gene; cDNA EST EMBL:T01321 comes from this gene; cDNA EST EMBL:T02288 com

Seq. No. 24811

Contig ID 119853\_1.R1040 5'-most EST uC-gmropic056f03b1

Method BLASTN
NCBI GI g170030
BLAST score 388
E value 0.0e+00
Match length 416
% identity 99

NCBI Description Soybean nodulin-35 (N-35) gene encoding a subunit of



## uricase II, complete cds

Seq. No. 24812 Contig ID 119862 1.R1040

Contig ID 119862\_1.R1040 5'-most EST uaw700665709.h1 Method BLASTX

NCBI GI g2062169
BLAST score 493
E value 4.0e-50
Match length 103
% identity 55

NCBI Description (AC001645) ABC transporter (PDR5-like) isolog [Arabidopsis

thaliana]

Seq. No. 24813

Contig ID 119882\_1.R1040 5'-most EST jC-gmst02400075d06a1

Seq. No. 24814

Contig ID 119891\_1.R1040 5'-most EST zhf700960261.h1

Method BLASTX
NCBI GI g3004555
BLAST score 396
E value 2.0e-38
Match length 166
% identity 5

NCBI Description (AC003673) similar to salt inducible protein [Arabidopsis

thaliana]

Seq. No. 24815

Contig ID 119895\_1.R1040 5'-most EST eep700866682.h1

Seq. No. 24816

Contig ID 119899\_1.R1040 5'-most EST fua701042104.h1

Method BLASTX
NCBI GI g4191778
BLAST score 287
E value 6.0e-26
Match length 73
% identity 75

NCBI Description (AC005917) putative nucleosome assembly protein I

[Arabidopsis thaliana]

Seq. No. 24817

Contig ID 119905\_1.R1040 5'-most EST fC-gmse700673065a1

Method BLASTX
NCBI GI g3176715
BLAST score 657
E value 1.0e-68
Match length 240
% identity 53

NCBI Description (AC002392) putative receptor-like protein kinase

[Arabidopsis thaliana]



24818 Seq. No.

119925 1.R1040 Contig ID uaw700665780.h1 5'-most EST

24819 Seq. No.

Contig ID 119926 1.R1040 hyd700728280.hl 5'-most EST

24820 Seq. No.

119936\_1.R1040 Contig ID  $k11701\overline{2}04559.h2$ 5'-most EST

BLASTX Method g3953479 NCBI GI 195 BLAST score 1.0e-14 E value 86 Match length 48 % identity

NCBI Description (AC002328) F2202.24 [Arabidopsis thaliana]

24821 Seq. No.

119943 1.R1040 Contig ID uaw700665806.hl 5'-most EST

BLASTX Method g4056467 NCBI GI BLAST score 113 7.0e-11 E value 124 Match length 35 % identity

(AC005990) Strong similarity to gb AB006693 spermidine NCBI Description synthase from Arabidopsis thaliana. ESTs gb\_AA389822,

gb\_T41794, gb\_N38455, gb\_AI100106, gb\_F14442 and gb\_F14256 come from this gene. [Arabidopsis thaliana]

24822 Seq. No.

Contig ID 119961 1.R1040 5'-most EST zpv700762351.hl

24823 Seq. No.

119963 1.R1040 Contig ID 5'-most EST asn701138119.hl

BLASTX Method q4454480 NCBI GI BLAST score 449 E value 1.0e-55 Match length 137 75 % identity

(AC006234) putative (1-4)-beta-mannan endohydrolase NCBI Description

[Arabidopsis thaliana]

24824 Seq. No.

119986 1.R1040 Contig ID uaw700665859.h1 5'-most EST

24825 Seq. No.

119992 1.R1040 Contig ID sat701004817.hl 5'-most EST



BLASTX Method g2894378 NCBI GI BLAST score 278 5.0e-25 E value 88 Match length 62 % identity

(Y14573) putative ribophorin I homologue [Hordeum vulgare] NCBI Description

24826 Seq. No.

119993 1.R1040 Contig ID jC-gmle01810085c05a1 5'-most EST

24827 Seq. No.

120001 1.R1040 Contig ID uaw700665876.h1 5'-most EST

BLASTX Method q4033414 NCBI GI 154 BLAST score 3.0e-10 E value 109 Match length 30 % identity

PUTATIVE IMPORTIN BETA-4 SUBUNIT (KARYOPHERIN BETA-4 NCBI Description SUBUNIT) >gi\_3184106\_emb\_CAA19321\_ (AL023780) putative

importin beta-4 subunit [Schizosaccharomyces pombe]

24828 Seq. No.

120026 1.R1040 Contig ID sat701009713.h1 5'-most EST

BLASTX Method g1346790 NCBI GI 321 BLAST score 3.0e-29 E value 123 Match length 50 % identity

PATHOGENESIS-RELATED HOMEODOMAIN PROTEIN (PRHA) >gi\_507220 NCBI Description

(L21991) homeodomain protein [Arabidopsis thaliana] >qi 2501810 (U48864) PRHA [Arabidopsis thaliana]

24829 Seq. No.

120032 1.R1040 Contig ID fC-qmst700661747d4 5'-most EST

BLASTN Method NCBI GI g1046277 BLAST score 249 1.0e-137 E value Match length 518 89 % identity

Phaseolus vulgaris embryo-specific acidic transcriptional NCBI Description

activator PvAlf mRNA, complete cds

24830 Seq. No.

120036 1.R1040 Contig ID rca701000593.hl 5'-most EST

BLASTX Method g1572819 NCBI GI 360 BLAST score 3.0e - 34E value



Match length 157
% identity 48
NCBI Description (U70855) similar to the RAS gene family [Caenorhabditis elegans]

Seq. No. 24831

Contig ID 120038\_1.R1040 5'-most EST uaw700665927.h1

Seq. No. 24832

Contig ID 120048\_1.R1040

5'-most EST jC-gmle01810050c03a1

Method BLASTX
NCBI GI g2129717
BLAST score 378
E value 1.0e-36
Match length 84
% identity 83

NCBI Description ribonucleoprotein - Arabidopsis thaliana >gi\_166844 (M98340) ribonucleoprotein [Arabidopsis thaliana]

>gi\_1582992\_prf\_\_2119375A Ser/Arg-rich protein [Arabidopsis

thaliana]

Seq. No. 24833

Contig ID 120049 1.R1040

5'-most EST  $g56060\overline{1}5$ 

Seq. No. 24834

Contig ID 120085\_1.R1040 5'-most EST fC-gmse700673810a1

Method BLASTX
NCBI GI g115009
BLAST score 423
E value 4.0e-41
Match length 255
% identity 39

NCBI Description 8-AMINO-7-OXONONANOATE SYNTHASE (7-KETO-8-AMINO-PELARGONIC ACID SYNTHETASE) (7-KAP SYNTHETASE) (L-ALANINE--PIMELYL COA

LIGASE) >gi\_98180\_pir\_\_JQ0512 8-amino-7-oxononanoate synthase (EC 2.3.1.47) - Bacillus sphaericus >gi\_142595 (M29291) 7-keto-8-aminopelargonic acid synthetase (bioF)

[Bacillus sphaericus]

Seq. No. 24835

Contig ID 120096\_1.R1040 5'-most EST jsh701065131.h1

Method BLASTX
NCBI GI g3426043
BLAST score 473
E value 3.0e-47
Match length 126
% identity 61

NCBI Description (AC005168) putative choline kinase [Arabidopsis thaliana]

Seq. No. 24836

Contig ID 120112 1.R1040 5'-most EST wvk700684577.h1



```
24837
Seq. No.
                  120115 1.R1040
Contig ID
                  uxk700670294.hl
5'-most EST
```

Method BLASTX q2760835 NCBI GI 448 BLAST score 2.0e-45 E value 126 Match length 75 % identity

NCBI Description (AC003105) unknown protein [Arabidopsis thaliana]

24838 Seq. No.

120118 1.R1040 Contig ID 5'-most EST uaw700666026.h1

Seq. No. 24839

120122 1.R1040 Contig ID asn701133433.h1 5'-most EST

BLASTX Method g2739382 NCBI GI 278 BLAST score 8.0e-25 E value 116 Match length 53 % identity

(AC002505) myosin heavy chain-like protein [Arabidopsis NCBI Description

thaliana]

24840 Seq. No.

120127 1.R1040 Contig ID uaw700666039.hl 5'-most EST

Seq. No.

24841 120130 1.R1040 Contig ID sat701007288.h2 5'-most EST

24842 Seq. No.

120140 1.R1040 Contig ID uaw700666053.hl 5'-most EST

24843 Seq. No.

120151 1.R1040 Contig ID gsv701051927.hl 5'-most EST

BLASTN Method g4530125 NCBI GI 82 BLAST score 2.0e-38 E value 145 Match length 90 % identity

Phaseolus vulgaris receptor-like protein kinase homolog NCBI Description

RK20-1 mRNA, complete cds

24844 Seq. No.

120163 1.R1040 Contig ID jC-gmst02400072g03a1 5'-most EST

Method BLASTX NCBI GI g4049346



BLAST score E value 2.0e-13 52 Match length % identity 69

NCBI Description (AL034567) putative protein [Arabidopsis thaliana]

24845 Seq. No.

120177 1.R1040 Contig ID 5'-most EST sat701011971.hl

BLASTX Method g2829910 NCBI GI BLAST score 535 E value 7.0e-55 Match length 130 19 % identity

(AC002291) Unknown protein, contains regulator of NCBI Description chromosome condensation motifs [Arabidopsis thaliana]

24846 Seq. No.

120178 1.R1040 Contig ID 5'-most EST uaw700666914.h1

BLASTN Method NCBI GI g2244991 BLAST score 42 E value 2.0e-14 150 Match length 82 % identity

Arabidopsis thaliana DNA chromosome 4, ESSA I contig NCBI Description

fragment No

24847 Seq. No.

120180 1.R1040 Contig ID 5'-most EST uaw700666102.h1

Seq. No. 24848

120201 1.R1040 Contig ID uaw700666127.h1 5'-most EST

Seq. No. 24849

120207 1.R1040 Contig ID uaw700666133.h1 5'-most EST

Seq. No.

24850 120227 1.R1040

Contig ID  $k11701\overline{2}13649.h1$ 5'-most EST

BLASTN Method NCBI GI g862479 100 BLAST score 4.0e-49 E value 244 Match length 85

% identity

NCBI Description Glycine max valosin-containing protein mRNA, complete cds

Seq. No. 24851

120233 1.R1040 Contig ID uaw700666162.h1 5'-most EST

3920



Seq. No. 24852

Contig ID 120247\_1.R1040 5'-most EST uaw700666201.h1

Seq. No. 24853

Contig ID 120261\_1.R1040 5'-most EST dpv701099964.h1

Method BLASTX
NCBI GI g3337361
BLAST score 617
E value 2.0e-64
Match length 133
% identity 82

NCBI Description (AC004481) ankyrin-like protein [Arabidopsis thaliana]

Seq. No. 24854

Contig ID 120266\_1.R1040 5'-most EST uaw700666222.h1

Seq. No. 24855

Contig ID 120269\_1.R1040 5'-most EST jex700906249.h1

Seq. No. 24856

Contig ID 120269 2.R1040 5'-most EST leu701149975.h1

Seq. No. 24857

Contig ID 120271\_1.R1040 5'-most EST sat701014517.h1

Seq. No. 24858

Contig ID 120290\_1.R1040 5'-most EST uaw700666249.h1

Method BLASTX
NCBI GI g419760
BLAST score 169
E value 3.0e-23
Match length 72
% identity 90

NCBI Description P-glycoprotein atpgp1 - Arabidopsis thaliana >gi 3849833 emb CAA43646 (X61370) P-glycoprotein

[Arabidopsis thaliana]

Seq. No. 24859

Contig ID 120300\_1.R1040 5'-most EST uC-gmronoir010g01b1

Method BLASTX
NCBI GI g4098124
BLAST score 155
E value 4.0e-10
Match length 134
% identity 31

NCBI Description (U73522) AMSH [Homo sapiens]

Seq. No. 24860

Contig ID 120300 2.R1040



5'-most EST kl1701209679.h1

Seq. No. 24861

Contig ID 120305\_1.R1040 5'-most EST uaw700666913.h1

Method BLASTX
NCBI GI g531389
BLAST score 154
E value 2.0e-10
Match length 76
% identity 46

NCBI Description (U12626) copia-like retrotransposon Hopscotch polyprotein

[Zea mays]

Seq. No. 24862

Contig ID 120313\_1.R1040 5'-most EST leu701148480.h1

Seq. No. 24863

Contig ID 120327 1.R1040 5'-most EST uaw700666288.h1

Seq. No. 24864

Contig ID 120328 1.R1040 5'-most EST uaw700666289.h1

Method BLASTX
NCBI GI g3152582
BLAST score 290
E value 2.0e-52
Match length 184
% identity 62

NCBI Description (AC002986) YUP8H12R.20 [Arabidopsis thaliana]

Seq. No. 24865

Contig ID 120343\_1.R1040 5'-most EST uaw700666310.h1

Seq. No. 24866

Contig ID 120345\_1.R1040

5'-most EST jC-gmfl02220075d10d1

Method BLASTX
NCBI GI g3426041
BLAST score 193
E value 1.0e-14
Match length 49
% identity 65

NCBI Description (AC005168) unknown protein [Arabidopsis thaliana]

Seq. No. 24867

Contig ID 120345\_2.R1040 5'-most EST uaw700666312.h1

Seq. No. 24868

Contig ID 120348\_1.R1040 5'-most EST uC-gmropic066c02b1

Seq. No. 24869



Contig ID 120360\_1.R1040 5'-most EST uaw700666328.h1

Seq. No. 24870

Contig ID 120362 1.R1040 5'-most EST zhf700962871.h1

Seq. No. 24871

Contig ID 120365\_1.R1040 5'-most EST awf700838163.h1

Method BLASTX
NCBI GI 94455287
BLAST score 441
E value 1.0e-43
Match length 118
% identity 72

NCBI Description (AL035527) putative protein [Arabidopsis thaliana]

Seq. No. 24872

Contig ID 120389\_1.R1040 5'-most EST uaw700666361.h1

Seq. No. 24873

Contig ID 120408\_1.R1040 5'-most EST awf700841025.h1

Seq. No. 24874

Contig ID 120445\_1.R1040 5'-most EST cf1700863577.h1

Method BLASTX
NCBI GI g2982434
BLAST score 514
E value 2.0e-52
Match length 142
% identity 65

NCBI Description (AL022224) putative protein [Arabidopsis thaliana]

Seq. No. 24875

Contig ID 120448 1.R1040 5'-most EST pcp700991902.h1

Seq. No. 24876

Contig ID 120454\_1.R1040 5'-most EST uaw700666445.h1

Method BLASTX
NCBI GI g3445201
BLAST score 244
E value 4.0e-21
Match length 83
% identity 61

NCBI Description (AC004786) unknown protein [Arabidopsis thaliana]

Seq. No. 24877

Contig ID 120470\_1.R1040 5'-most EST uaw700666461.h1

Seq. No. 24878



```
120474 1.R1040
Contig ID
                   uaw700666468.h1
5'-most EST
                   24879
Seq. No.
                   120477 1.R1040
Contig ID
                   jex700\overline{9}08642.h1
5'-most EST
Method
                   BLASTX
                   g4469026
NCBI GI
BLAST score
                   607
                   4.0e-63
E value
Match length
                   186
% identity
                   68
                   (AL035602) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   24880
Seq. No.
                   120488 1.R1040
Contig ID
5'-most EST
                   gsv701055745.hl
                   24881
Seq. No.
                   120489 1.R1040
Contig ID
5'-most EST
                   vzy700756733.hl
Seq. No.
                   24882
                   120489 2.R1040
Contig ID
                   uaw700666487.hl
5'-most EST
                   BLASTX
Method
                   q4490706
NCBI GI
                   182
BLAST score
                   2.0e-13
E value
Match length
                   44
                   73
% identity
                   (AL035680) putative protein [Arabidopsis thaliana]
NCBI Description
                   24883
Seq. No.
                   120506 1.R1040
Contig ID
                   uaw700666929.hl
5'-most EST
                   24884
Seq. No.
                   120508 1.R1040
Contig ID
                   uaw700666518.hl
5'-most EST
                   BLASTN
Method
                   g3510347
NCBI GI
BLAST score
                   38
                    4.0e-12
E value
                   158
Match length
                   84
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MSJ11, complete sequence [Arabidopsis thaliana]
                    24885
Seq. No.
                    120524 1.R1040
Contig ID
                   ncj700\overline{9}79142.h1
5'-most EST
                   BLASTN
Method
                    g4406790
NCBI GI
```

45

97

4.0e-16

BLAST score

Match length

E value



% identity 87
NCBI Description Arabidopsis thaliana chromosome II BAC T1016 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 24886

Contig ID 120530\_1.R1040 5'-most EST awf700836552.h1

Seq. No. 24887

Contig ID 120543\_1.R1040 5'-most EST ncj700982296.h1

Method BLASTX
NCBI GI g2688299
BLAST score 297
E value 8.0e-27
Match length 83
% identity 60

NCBI Description (AE001145) prolyl-tRNA synthetase (proS) [Borrelia

burgdorferi]

Seq. No. 24888

Contig ID 120554\_1.R1040

5'-most EST uC-gmrominsoy229f07b1

Seq. No. 24889

Contig ID 120554\_2.R1040 5'-most EST uC-gmronoir048h09b1

Seq. No. 24890

Contig ID 120562\_1.R1040 5'-most EST uC-gmronoir071e05b1

Method BLASTX
NCBI GI g799177
BLAST score 363
E value 2.0e-34
Match length 210
% identity 24

NCBI Description (U22055) 100 kDa coactivator [Homo sapiens]

Seq. No. 24891

Contig ID 120562\_2.R1040

5'-most EST uC-gmrominsoy131c02b1

Seq. No. 24892

Contig ID 120586\_1.R1040 5'-most EST sat701013691.h1

Method BLASTX
NCBI GI g4262241
BLAST score 286
E value 2.0e-25
Match length 132
% identity 55

NCBI Description (AC006200) unknown protein [Arabidopsis thaliana]

Seq. No. 24893

Contig ID 120600\_1.R1040 5'-most EST jex700903181.h1

3925



24894 Seq. No. 120617 1.R1040 Contig ID 5'-most EST uaw700666647.hl

24895 Seq. No.

120621 1.R1040 Contig ID  $crh700\overline{8}52664.h1$ 5'-most EST

BLASTX Method g1723730 NCBI GI 179 BLAST score 7.0e-13 E value 81 Match length 51 % identity

HYPOTHETICAL 78.8 KD PROTEIN IN ATF2-RNR4 INTERGENIC REGION NCBI Description

>qi 2131694 pir S64492 hypothetical protein YGR178c yeast (Saccharomyces cerevisiae) >gi\_1323315\_emb\_CAA97204\_ (Z72963) PBP1 [Saccharomyces cerevisīae] >gi\_2737884

(U46931) Mrs16p [Saccharomyces cerevisiae]

24896 Seq. No.

120645 1.R1040 Contig ID xpa700793215.h1 5'-most EST

24897 Seq. No.

120649 1.R1040 Contig ID uaw700<del>6</del>66681.h1 5'-most EST

24898 Seq. No.

120656 1.R1040 Contig ID 5'-most EST crh700851889.hl

24899 Seq. No.

120699 1.R1040 Contig ID wvk700685458.hl 5'-most EST

24900 Seq. No.

120699 2.R1040 Contig ID bth700844974.h1 5'-most EST

24901 Seq. No.

120704 1.R1040 Contig ID 5'-most EST uaw700666743.h1

24902 Seq. No.

120706 1.R1040 Contig ID 5'-most EST zhf700959484,h1

24903 Seq. No.

120721 1.R1040 Contig ID gsv701048921.hl 5'-most EST

Method BLASTX q4539335 NCBI GI BLAST score 155 E value 2.0e-10 Match length 50 50 % identity

3926



```
NCBI Description (AL035539) putative protein [Arabidopsis thaliana]
```

Seq. No. 24904

Contig ID 120722\_1.R1040 5'-most EST uaw700666763.h1

Method BLASTX
NCBI GI g3482977
BLAST score 205
E value 3.0e-16
Match length 88
% identity 55

NCBI Description (AL031369) putative protein [Arabidopsis thaliana]

Seq. No. 24905

Contig ID 120735\_1.R1040 5'-most EST ckk700605703.h2

Method BLASTN
NCBI GI g2351073
BLAST score 37
E value 2.0e-11
Match length 111
% identity 87

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MYJ24, complete sequence [Arabidopsis thaliana]

Seq. No. 24906

Contig ID 120750\_1.R1040 5'-most EST rca700998216.h1

Method BLASTX
NCBI GI g2765442
BLAST score 187
E value 8.0e-14
Match length 57
% identity 67

NCBI Description (Y15066) putative transcription factor [Arabidopsis

thaliana]

Seq. No. 24907

Contig ID 120766\_1.R1040 5'-most EST uaw700666818.h1

Method BLASTX
NCBI GI g1703029
BLAST score 253
E value 5.0e-22
Match length 87
% identity 53

NCBI Description CLATHRIN COAT ASSEMBLY PROTEIN AP47 HOMOLOG 2 (CLATHRIN COAT ASSOCIATED PROTEIN AP47 HOMOLOG 2) (GOLGI ADAPTOR AP-1

47 KD PROTEIN HOMOLOG 2) (HA1 47 KD SUBUNIT HOMOLOG 2) (CLATHRIN ASSEMBLY PROTEIN ASSEMBLY PROTEIN COMPLEX... >gi\_468382 (L07074) clathrin-associated adaptor protein

[Rattus norvegicus]

Seq. No. 24908

Contig ID 120771\_1.R1040 5'-most EST uaw700666824.h1



24909 Seq. No.

120778 1.R1040 Contig ID dpv701102694.h1 5'-most EST

BLASTX Method g2795804 NCBI GI BLAST score 261 7.0e-23 E value 90 Match length 58 % identity

(AC003674) unknown protein [Arabidopsis thaliana] NCBI Description

>gi 3355492 (AC004218) unknown protein [Arabidopsis

thaliana]

24910 Seq. No.

120780 1.R1040 Contig ID uaw700666835.hl 5'-most EST

Seq. No. 24911

120794 1.R1040 Contig ID jC-gmst02400078d01a1 5'-most EST

24912 Seq. No.

120802 1.R1040 Contig ID 5'-most EST uaw700666858.hl

BLASTX Method q3004552 NCBI GI 290 BLAST score E value 2.0e-26 Match length 99

63 % identity

(AC003673) unknown protein [Arabidopsis thaliana] NCBI Description

24913 Seq. No.

120818 1.R1040 Contig ID 5'-most EST uaw700666876.hl

24914 Seq. No.

120837 1.R1040 Contig ID

5'-most EST uC-gmrominsoy039c12b1

24915 Seq. No.

120839 1.R1040 Contig ID uxk700668665.hl 5'-most EST

Method BLASTX g3170178 NCBI GI 206 BLAST score 4.0e-16 E value Match length 66 52 % identity

(AF039689) antigen NY-CO-7 [Homo sapiens] NCBI Description

24916 Seq. No.

120852 1.R1040 Contig ID pcp700988735.h1 5'-most EST

BLASTX Method g4557062 NCBI GI BLAST score 497



E value 2.0e-55
Match length 197
% identity 60

NCBI Description (AC007045) hypothetical protein [Arabidopsis thaliana]

Seq. No. 24917

Contig ID 120853\_1.R1040 5'-most EST uaw700666926.h1

Seq. No. 24918

Contig ID 120857\_1.R1040 5'-most EST jex700903766.h1

Seq. No. 24919

Contig ID 120863\_1.R1040 5'-most EST leu701153196.h1

Method BLASTX
NCBI GI g4309734
BLAST score 242
E value 7.0e-38
Match length 123
% identity 61

NCBI Description (AC006439) putative 26S proteosome regulatory subunit 8

[Arabidopsis thaliana]

Seq. No. 24920

Contig ID 120865\_1.R1040 5'-most EST fC-gmse7000752437r1

Method BLASTX
NCBI GI g3309086
BLAST score 372
E value 1.0e-35
Match length 76
% identity 92

NCBI Description (AF076253) calcineurin B-like protein 3 [Arabidopsis

thaliana]

Seq. No. 24921

Contig ID 120867\_1.R1040 5'-most EST ncj700985414.h1

Method BLASTX
NCBI GI 94406821
BLAST score 375
E value 2.0e-36
Match length 92
% identity 75

NCBI Description (AC006201) hypothetical protein [Arabidopsis thaliana]

Seq. No. 24922

Contig ID 120884\_1.R1040 5'-most EST uaw700666960.h1

Method BLASTX
NCBI GI g3892055
BLAST score 443
E value 3.0e-47
Match length 118
% identity 79



NCBI Description (AC002330) putative transport protein [Arabidopsis thaliana]

Method BLASTX
NCBI GI 94309738
BLAST score 553
E value 1.0e-56
Match length 195
% identity 60

NCBI Description (AC006439) putative tubby protein [Arabidopsis thaliana]

Seq. No. 24924

Contig ID 120887\_1.R1040 5'-most EST uaw700666963.h1

Seq. No. 24925

Contig ID 120917\_1.R1040 5'-most EST sat701014192.h1

Seq. No. 24926

Contig ID 120929 1.R1040 5'-most EST awf700842375.h1

Seq. No. 24927

Contig ID 120931 1.R1040

5'-most EST uC-gmrominsoy165c03b1

Seq. No. 24928

Contig ID 120939\_1.R1040 5'-most EST uaw700667025.h1

Method BLASTX
NCBI GI g4558553
BLAST score 421
E value 2.0e-41
Match length 131
% identity 50

NCBI Description (AC007138) putative potassium channel [Arabidopsis

thaliana]

Seq. No. 24929

Contig ID 120965\_1.R1040 5'-most EST uC-gmropic111h08b1

Method BLASTX
NCBI GI g2623307
BLAST score 563
E value 8.0e-58
Match length 229
% identity 65

NCBI Description (AC002409) putative ubiquitin protease [Arabidopsis

thaliana]

Seq. No. 24930

Contig ID 120977\_1.R1040 5'-most EST uaw700667072.h1



Seq. No. 24931

Contig ID 120985\_1.R1040 5'-most EST uaw700667080.h1

Method BLASTX
NCBI GI g2498629
BLAST score 153
E value 2.0e-11
Match length 116
% identity 26

NCBI Description TRANSCRIPTIONAL REPRESSOR NF-X1 >gi\_2135825\_pir\_\_I38869

NFX1 - human >gi\_563217 (U15306) NFX1 [Homo sapiens] >qi 4505387 ref NP 002495.1 pNFX1 nuclear transcription

factor, X-box binding

Seq. No. 24932

Contig ID 121002\_1.R1040 5'-most EST zzp700830860.h1

Method BLASTX
NCBI GI g3831443
BLAST score 209
E value 7.0e-20
Match length 68
% identity 65

NCBI Description (AC005819) putative auxin-regulated protein [Arabidopsis

thaliana]

Seq. No. 24933

Contig ID 121006 1.R1040 5'-most EST ckk700605706.h2

Seq. No. 24934

Contig ID 121009 1.R1040

5'-most EST jC-gmro02800024e04d1

Seq. No. 24935

Contig ID 121014 1.R1040 5'-most EST sat701003048.h1

Seq. No. 24936

Contig ID 121017\_1.R1040 5'-most EST uC-gmropic107b05b1

Method BLASTX
NCBI GI g1946369
BLAST score 370
E value 3.0e-35
Match length 91
% identity 75

NCBI Description (U93215) unknown protein [Arabidopsis thaliana]

Seq. No. 24937

Contig ID 121017\_2.R1040 5'-most EST ncj700980515.h1

Method BLASTX
NCBI GI g1946369
BLAST score 150
E value 1.0e-09



Match length 66 % identity

(U93215) unknown protein [Arabidopsis thaliana] NCBI Description

24938 Seq. No.

121021 1.R1040 Contig ID 5'-most EST  $uxk700\overline{6}72623.h1$ 

24939 Seq. No.

121023 1.R1040 Contig ID

jC-gmf102220108b09a1 5'-most EST

Seq. No. 24940

121032 1.R1040 Contig ID yuv700862868.h1 5'-most EST

Seq. No. 24941

121034 1.R1040 Contig ID ckk700605736.h2 5'-most EST

24942 Seq. No.

Contig ID 121048 1.R1040 smc700747169.h1 5'-most EST

24943 Seq. No.

121051 1.R1040 Contig ID

5'-most EST q4396944

24944 Seq. No.

121051 2.R1040 Contig ID 5'-most EST ckk700605755.h2

24945 Seq. No.

121088 1.R1040 Contig ID lus701015784.hl 5'-most EST

BLASTX Method q1839188 NCBI GI BLAST score 790 5.0e-86 E value 254 Match length

63 % identity

(U86081) root hair defective 3 [Arabidopsis thaliana] NCBI Description

Seq. No. 24946

121089\_1.R1040 Contig ID

5'-most EST jC-gmro02910064c08a1

Seq. No. 24947

121111 1.R1040 Contig ID wvk700685281.h1 5'-most EST

BLASTX Method NCBI GI g3549665 238 BLAST score 8.0e-20 E value Match length 119 44 % identity

NCBI Description (AL031394) hypothetical protein [Arabidopsis thaliana]



```
24948
Seq. No.
                  121118 1.R1040
Contia ID
5'-most EST
                  uC-gmrominsoy262b06b1
Seq. No.
                  24949
                  121119 1.R1040
Contig ID
5'-most EST
                  zsq701120458.h1
                  24950
Seq. No.
Contig ID
                  121122 1.R1040
5'-most EST
                  ckk700605836.h2
                  24951
Seq. No.
                  121134 1.R1040
Contig ID
5'-most EST
                  wvk700685902.h1
                  BLASTX
Method
NCBI GI
                  q3123132
BLAST score
                  341
                  3.0e - 32
E value
Match length
                  87
                  71
% identity
NCBI Description
                  GTP-BINDING PROTEIN TYPA/BIPA HOMOLOG
                  >gi 2313589_gb_AAD07546.1_ (AE000562) GTP-binding protein,
                  fusA-homolog (yihK) [Helicobacter pylori 26695]
                  24952
Seq. No.
                  121145 1.R1040
Contig ID
                  rca701001496.hl
5'-most EST
Method
                  BLASTX
                  g3033401
NCBI GI
                  129
BLAST score
E value
                  1.0e-13
                  57
Match length
% identity
                   (AC004238) putative potassium transporter [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                   24953
                  121148 1.R1040
Contig ID
                   jC-gmst02400052d06a1
5'-most EST
                  BLASTX
Method
                  g4539437
NCBI GI
BLAST score
                   463
                  7.0e-46
E value
                  139
Match length
```

% identity 63

(AL049523) putative protein [Arabidopsis thaliana] NCBI Description

24954 Seq. No. 121187 1.R1040 Contig ID 5'-most EST  $uxk700\overline{6}67116.h1$ 24955

Seq. No. Contig ID 121194 1.R1040 5'-most EST uxk700667125.h1



```
Seq. No.
                   24956
Contig ID
                   121196 1.R1040
5'-most EST
                   ncj700988641.h1
Method
                   BLASTX
NCBI GI
                   q2660664
BLAST score
                   423
E value
                   1.0e-41
Match length
                   136
% identity
                   66
                   (AC002342) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   24957
Contig ID
                   121201 1.R1040
5'-most EST
                   uxk700667143.h1
Method
                   BLASTX
NCBI GI
                   q3776027
BLAST score
                   1127
E value
                   1.0e-123
Match length
                   339
% identity
                   67
                   (AJ010475) RNA helicase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   24958
Contig ID
                   121217 1.R1040
5'-most EST
                   uC-gmropic100b10b1
Method
                   BLASTX
NCBI GI
                   g2498995
BLAST score
                   188
E value
                   5.0e-14
Match length
                   118
% identity
                   41
                   QUEUINE TRNA-RIBOSYLTRANSFERASE (TRNA-GUANINE
NCBI Description
                   TRANSGLYCOSYLASE) (GUANINE INSERTION ENZYME)
                   >gi 1006609 dbj_BAA10764 (D64005) transfer RNA-guanine
                   transglycosylase [Synechocystis sp.]
Seq. No.
                   24959
Contig ID
                   121227 1.R1040
5'-most EST
                   uxk700\overline{6}67190.h1
Seq. No.
                   24960
Contig ID
                   121235 1.R1040
5'-most EST
                   uxk700667779.h1
Method
                   BLASTX
NCBI GI
                   g4539436
BLAST score
                   159
E value
                   2.0e-11
Match length
                   67
% identity
```

NCBI Description (AL049523) putative reverse-transcriptase-like protein

[Arabidopsis thaliana]

Seq. No. 24961

Contig ID 121268 1.R1040 5'-most EST sat701010110.h2

Seq. No. 24962



Contig ID 121274\_1.R1040 5'-most EST dpv701099171.h1

Seq. No. 24963

Contig ID 121284\_1.R1040 5'-most EST uxk700667307.h1

Method BLASTX
NCBI GI g3540219
BLAST score 304
E value 1.0e-27
Match length 118
% identity 55

NCBI Description (D87686) KIAA0017 protein [Homo sapiens]

Seq. No. 24964

Contig ID 121316\_1.R1040 5'-most EST awf700837557.h1

Seq. No. 24965

Contig ID 121339\_1.R1040 5'-most EST fde700873618.h1

Method BLASTX
NCBI GI g3335349
BLAST score 362
E value 6.0e-35
Match length 81
% identity 83

NCBI Description (AC004512) Similar to gb\_U46691 putative chromatin

structure regulator (SUPT6H) from Homo sapiens. ESTs

gb\_T42908, gb\_AA586170 and gb\_AA395125 come from this gene.

[Arabidopsis thaliana]

Seq. No. 24966

Contig ID 121343\_1.R1040 5'-most EST rry700808323.h1

Seq. No. 24967

Contig ID 121367\_1.R1040 5'-most EST crh700854990.h1

Seq. No. 24968

Contig ID 121400\_1.R1040 5'-most EST uxk700667561.h1

Seq. No. 24969

Contig ID 121401\_1.R1040

5'-most EST jC-gmle01810007e07a1

Method BLASTX
NCBI GI g2961342
BLAST score 165
E value 5.0e-11
Match length 165
% identity 28

NCBI Description (AL022140) hypothetical protein [Arabidopsis thaliana]

Seq. No. 24970

Contig ID 121402\_1.R1040



```
uxk700667567.h1
5'-most EST
                   BLASTX
Method
                   g1076382
NCBI GI
BLAST score
                   147
                   4.0e-09
E value
Match length
                   29
% identity
                   86
NCBI Description PRL2 protein - Arabidopsis thaliana (fragment)
Seq. No.
                   24971
                   121404 1.R1040
Contig ID
5'-most EST
                   uxk700667573.h1
                   24972
Seq. No.
                   121405 1.R1040
Contig ID
5'-most EST
                   uxk700\overline{6}67575.h1
                   24973
Seq. No.
                   121412 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400047a06d1
Seq. No.
                   24974
                   121414 1.R1040
Contig ID
                   ncj700984704.h1
5'-most EST
Seq. No.
                   24975
                   121435 1.R1040
Contig ID
5'-most EST
                   uxk700671721.h1
                   24976
Seq. No.
                   121439_1.R1040
Contig ID
5'-most EST
                   uxk700670139.h1
Seq. No.
                   24977
                   121447 1.R1040
Contig ID
                   zhf700\overline{9}59586.h1
5'-most EST
Method
                   BLASTN
NCBI GI
                   q2760167
BLAST score
                   34
                   2.0e-09
E value
Match length
                   74
                   86
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MCO15, complete sequence [Arabidopsis thaliana]
                   24978
Seq. No.
                   121447 2.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy061h08b1
```

Seq. No. 24979

121452 1.R1040 Contig ID 5'-most EST  $jex700\overline{9}03719.h1$ 

Seq. No. 24980

Contig ID 121466 1.R1040 5'-most EST uxk700667685.h1



```
24981
Seq. No.
                   121471 1.R1040
Contig ID
                   jC-gmf\overline{1}02220115d04a1
5'-most EST
                   {\tt BLASTX}
Method
NCBI GI
                   q4490297
BLAST score
                   401
                   6.0e-39
E value
                   154
Match length
% identity
                   53
                   (AL035678) putative protein [Arabidopsis thaliana]
NCBI Description
                   24982
Seq. No.
                   121487 1.R1040
Contig ID
5'-most EST
                   epx701105061.h1
Seq. No.
                   24983
```

121488 1.R1040 Contig ID zhf700955906.h1 5'-most EST BLASTX Method g2459441 NCBI GI

BLAST score 572 E value 5.0e-59 177 Match length % identity 61

(AC002332) putative SWI/SNF complex subunit BAF170 NCBI Description

[Arabidopsis thaliana]

24984 Seq. No. Contig ID

121489 1.R1040 fde700875949.hl 5'-most EST

BLASTX Method NCBI GI g2674203 BLAST score 267 1.0e-23 E value 61 Match length 82 % identity

NCBI Description (AF036328) CLP protease regulatory subunit CLPX

[Arabidopsis thaliana]

24985 Seq. No.

121490 1.R1040 Contig ID 5'-most EST uxk700667727.h1

Method BLASTX q3033386 NCBI GI BLAST score 215 1.0e-17 E value Match length 92 % identity 48

NCBI Description (AC004238) RING3-like protein [Arabidopsis thaliana]

24986 Seq. No.

Contig ID 121502 1.R1040 5'-most EST  $uxk700\overline{6}67749.h1$ 

Seq. No. 24987

Contiq ID 121504 1.R1040 5'-most EST uC-gmropic098e01b1



Seq. No. 24988

Contig ID 121504\_2.R1040 5'-most EST zsg701122768.h1

Seq. No. 24989

Contig ID 121505\_1.R1040 5'-most EST uxk700667767.h1

Method BLASTX
NCBI GI g4106395
BLAST score 273
E value 5.0e-24
Match length 81
% identity 62

NCBI Description (AF073744) raffinose synthase [Cucumis sativus]

Seq. No. 24990

Contig ID 121511\_1.R1040 5'-most EST uxk700667777.h1

Seq. No. 24991

Contig ID 121537\_1.R1040 5'-most EST txt700732928.h1

Seq. No. 24992

Contig ID 121544\_1.R1040 5'-most EST leu701145768.h1

Seq. No. 24993

Contig ID 121546 1.R1040

5'-most EST uC-gmrominsoy074f06b1

Method BLASTX
NCBI GI g4539291
BLAST score 328
E value 1.0e-30
Match length 83
% identity 75

NCBI Description (AL049480) putative protein [Arabidopsis thaliana]

Seq. No. 24994

Contig ID 121548 1.R1040 5'-most EST vzy700754773.h1

Method BLASTX
NCBI GI g4558564
BLAST score 451
E value 9.0e-45
Match length 151
% identity 60

NCBI Description (AC007138) predicted protein of unknown function

[Arabidopsis thaliana]

Seq. No. 24995

Contig ID 121628 1.R1040 5'-most EST zsg701125865.h1

Seq. No. 24996

Contig ID 121634 1.R1040



```
awf700841624.h1
5'-most EST
                  BLASTX
Method
                  g1769903
NCBI GI
BLAST score
                  844
                   9.0e-91
E value
Match length
                   222
% identity
                   70
                  (X95738) proline transporter 2 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  24997
                  121639 1.R1040
Contig ID
5'-most EST
                  g5677356
                   24998
Seq. No.
                   121640 1.R1040
Contig ID
5'-most EST
                   crh700849907.h1
                   24999
Seq. No.
                   121643 1.R1040
Contig ID
5'-most EST
                   zvp700764123.h1
Method
                  BLASTX
NCBI GI
                   g1001955
BLAST score
                   633
E value
                   4.0e-66
Match length
                   157
% identity
                   79
NCBI Description (U19099) unknown protein [Lycopersicon chilense ]
                   25000
Seq. No.
                   121649 1.R1040
Contig ID
5'-most EST
                   uxk700667994.hl
                  BLASTX
Method
NCBI GI
                   g3608155
BLAST score
                   492
                   9.0e-50
E value
Match length
                   136
                   71
% identity
NCBI Description
                  (ACO05314) putative RNA helicase [Arabidopsis thaliana]
                   25001
Seq. No.
                   121660 1.R1040
Contig ID
5'-most EST
                   g5666640
                   25002
Seq. No.
                   121667 1.R1040
Contig ID
                   g55090\overline{2}9
5'-most EST
Seq. No.
                   25003
                   121676 1.R1040
Contig ID
                   uxk700668040.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                   g4538929
BLAST score
                   207
                   1.0e-16
E value
Match length
                   63
```

3939

NCBI Description (AL049483) putative nucleic acid binding protein

67

% identity



## [Arabidopsis thaliana]

Seq. No. 25004

Contig ID 121690\_1.R1040 5'-most EST fua701042983.h1

Method BLASTX
NCBI GI g2894599
BLAST score 451
E value 6.0e-45
Match length 127
% identity 65

NCBI Description (AL021889) putative protein [Arabidopsis thaliana]

Seq. No. 25005

Contig ID 121693\_1.R1040
5'-most FST iC-gml=01810042d02

5'-most EST jC-gmle01810042d02a1 Method BLASTX

NCBI GI g4539324
BLAST score 152
E value 6.0e-10
Match length 113
% identity 39

NCBI Description (AL035679) kinesin like protein [Arabidopsis thaliana]

Seq. No. 25006

Contig ID 121698\_1.R1040 5'-most EST gsv701049049.h1

Seq. No. 25007

Contig ID 121701\_1.R1040 5'-most EST pxt700942611.h1

Seq. No. 25008

Contig ID 121715\_1.R1040 5'-most EST zhf700959955.h1

Method BLASTX
NCBI GI g2443870
BLAST score 175
E value 7.0e-13
Match length 96
% identity 39

NCBI Description (AC002985) R27090\_2 [Homo sapiens]

Seq. No. 25009

Contig ID 121717\_1.R1040 5'-most EST uxk700668092.h1

Method BLASTX
NCBI GI g2911073
BLAST score 324
E value 3.0e-30
Match length 108
% identity 62

NCBI Description (AL021960) putative protein [Arabidopsis thaliana]

Seq. No. 25010

Contig ID 121719 1.R1040 5'-most EST uxk700672757.h1

3940



```
25011
Seq. No.
                   121731 1.R1040
Contig ID
                   gsv701\overline{0}51648.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g542070
BLAST score
                   155
                   2.0e-10
E value
                   52
Match length
% identity
                   60
NCBI Description cytochrome P450 77A1 - eggplant
                   25012
Seq. No.
                   121735 1.R1040
Contig ID
5'-most EST
                   q5677035
Seq. No.
                   25013
                   121739 1.R1040
Contig ID
5'-most EST
                   jC-qmle01810080b05a1
                   BLASTX
Method
NCBI GI
                   q4154352
BLAST score
                   328
E value
                   6.0e-30
Match length
                   216
% identity
                   37
                   (AF110333) PrMC3 [Pinus radiata]
NCBI Description
Seq. No.
                   25014
                   121747 1.R1040
Contig ID
                   crh700851525.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q100226
BLAST score
                   346
                   2.0e-32
E value
Match length
                   185
                   42
% identity
                   hypothetical protein - tomato >gi 19275 emb CAA78112
NCBI Description
                   (Z12127) protein of unknown function [Lycopersicon
                   esculentum] >gi 445619 prf 1909366A Leu zipper protein
                   [Lycopersicon esculentum]
                   25015
Seq. No.
                   121748 1.R1040
Contig ID
5'-most EST
                   zpv700759045.h1
                   25016
Seq. No.
                   121750 1.R1040
Contig ID
5'-most EST
                   uxk700\overline{6}68139.h1
Seq. No.
                   25017
                   121754 1.R1040
Contig ID
5'-most EST
                   uxk700\overline{6}68145.h1
```

3941

BLASTN

g18634

9.0e-33

73

93

Method NCBI GI

E value

BLAST score

Match length



% identity 94

NCBI Description Soybean Gyl gene for glycinin subunit Gl

Seq. No. 25018

Contig ID 121777\_1.R1040 5'-most EST uxk700668181.h1

Method BLASTX
NCBI GI g2655098
BLAST score 438
E value 3.0e-43
Match length 110
% identity 73

NCBI Description (AF023472) peptide transporter [Hordeum vulgare]

Seq. No. 25019

Contig ID 121782 1.R1040

5'-most EST uC-gmflminsoy065h05b1

Seq. No. 25020

Contig ID 121782 2.R1040 5'-most EST smc700744391.h1

Seq. No. 25021

Contig ID 121791\_1.R1040 5'-most EST fua701041522.h1

Method BLASTX
NCBI GI g3540198
BLAST score 270
E value 1.0e-23
Match length 69
% identity 67

NCBI Description (AC004260) Unknown protein [Arabidopsis thaliana]

Seq. No. 25022

Contig ID 121794\_1.R1040 5'-most EST eep700868158.h1

Seq. No. 25023

Contig ID 121823\_1.R1040 5'-most EST kl1701206949.h1

Method BLASTX
NCBI GI g4335749
BLAST score 216
E value 1.0e-17
Match length 63
% identity 65

NCBI Description (AC006284) unknown protein [Arabidopsis thaliana]

Seq. No. 25024

Contig ID 121824\_1.R1040 5'-most EST uxk700668248.h1

Seq. No. 25025

Contig ID 121828\_1.R1040 5'-most EST zhf700951803.h1

Method BLASTX NCBI GI g2651300



BLAST score 1.0e-26 E value Match length 89

67 % identity

(AC002336) putative initiator tRNA NCBI Description

phosphoribosyl-transferase [Arabidopsis thaliana]

25026 Seq. No.

121837 1.R1040 Contig ID kl1701202466.hl 5'-most EST

25027 Seq. No.

121851 1.R1040 Contig ID 5'-most EST eep700868274.h1

BLASTX Method g2781347 NCBI GI 430 BLAST score 1.0e-42 E value 118 Match length 70 % identity

(AC003113) F2401.3 [Arabidopsis thaliana] NCBI Description

25028 Seq. No.

121852 1.R1040 Contig ID 5'-most EST uxk700668293.h1

Seq. No. 25029

121856 1.R1040 Contig ID 5'-most EST uxk700668303.h1

25030 Seq. No.

121861\_1.R1040 Contig ID 5'-most EST uxk700668310.h1

Seq. No. 25031

Contig ID 121875 1.R1040 5'-most EST  $uxk700\overline{6}68325.h1$ 

Method BLASTX NCBI GI g2244771 425 BLAST score E value 2.0e-42 Match length 92 91 % identity

NCBI Description (Z97335) kinesin homolog [Arabidopsis thaliana]

25032 Seq. No.

Contig ID 121885 1.R1040 5'-most EST  $uxk700\overline{6}68339.h1$ 

25033 Seq. No.

121895 1.R1040 Contig ID 5'-most EST wrg700789432.h2

Method BLASTX NCBI GI q2465925 BLAST score 190 E value 9.0e-15 Match length 73



% identity 52

NCBI Description (AF024649) receptor-like serine/threonine kinase

[Arabidopsis thaliana]

Seq. No. 25034

Contig ID 121895\_2.R1040 5'-most EST uxk700668352.h1

Seq. No. 25035

Contig ID 121909\_1.R1040 5'-most EST uxk700668559.h1

Method BLASTX
NCBI GI g3152576
BLAST score 278
E value 7.0e-25
Match length 108
% identity 54

NCBI Description (AC002986) Similar to liver-specific transport protein

gb L27651 from Rattus norviegicus. [Arabidopsis thaliana]

Seq. No. 25036

Contig ID 121926\_1.R1040 5'-most EST zhf700964479.h1

Seq. No. 25037

Contig ID 121927 1.R1040 5'-most EST awf700838219.h1

Method BLASTX
NCBI GI g4106395
BLAST score 956
E value 1.0e-145
Match length 318
% identity 72

NCBI Description (AF073744) raffinose synthase [Cucumis sativus]

Seq. No. 25038

Contig ID 121932 1.R1040 5'-most EST uxk700668394.h1

Method BLASTX
NCBI GI g4544409
BLAST score 562
E value 6.0e-58
Match length 156
% identity 65

NCBI Description (AC006955) putative transcription factor [Arabidopsis

thaliana]

Seq. No. 25039

Contig ID 121934\_1.R1040 5'-most EST uxk700668396.h1

Seq. No. 25040

Contig ID 121945\_1.R1040 5'-most EST kl1701206519.h1

Method BLASTX NCBI GI g121950 BLAST score 213



E value 6.0e-17
Match length 88
% identity 55

NCBI Description HISTONE H1 >gi\_22321\_emb\_CAA40362\_ (X57077) H1 histone [Zea

mays]

Seq. No. 25041

Contig ID 121946\_1.R1040 5'-most EST awf700840912.h1

Seq. No. 25042

Contig ID 121951 1.R1040

5'-most EST jC-gmro02910016d07a1

Method BLASTX
NCBI GI g2245138
BLAST score 439
E value 3.0e-59
Match length 179
% identity 64

NCBI Description (Z97344) hypothetical protein [Arabidopsis thaliana]

Seq. No. 25043

Contig ID 121961\_1.R1040 5'-most EST jC-gmle01810075f05a1

Method BLASTX
NCBI GI g2827536
BLAST score 200
E value 2.0e-15
Match length 70
% identity 51

NCBI Description (AL021633) hypothetical protein [Arabidopsis thaliana]

Seq. No. 25044

Contig ID 121982 1.R1040 5'-most EST uxk700668473.h1

Seq. No. 25045

Contig ID 121993 1.R1040 5'-most EST uxk700668486.h1

Seq. No. 25046

Contig ID 121997\_1.R1040 5'-most EST uxk700668491.h1

Method BLASTN
NCBI GI g516102
BLAST score 113
E value 8.0e-57
Match length 239
% identity 96

NCBI Description Soybean phytochrome B (phyB) gene exons 1-5, complete cds

Seq. No. 25047

Contig ID 122013\_1.R1040 5'-most EST uC-gmropic035h05b1

Seq. No. 25048

Contig ID 122036\_1.R1040

% identity



```
uC-qmronoir073b06b1
5'-most EST
                   BLASTX
Method
                   q3080426
NCBI GI
                   236
BLAST score
                   2.0e-19
E value
Match length
                   93
                   72
% identity
                  (AL022604) putative protein [Arabidopsis thaliana]
NCBI Description
                   25049
Seq. No.
                   122036 2.R1040
Contig ID
5'-most EST
                   uC-gmropic116f07b1
Method
                   BLASTX
NCBI GI
                   q3080426
BLAST score
                   235
                   1.0e-19
E value
Match length
                   56
% identity
                   77
                  (AL022604) putative protein [Arabidopsis thaliana]
NCBI Description
                   25050
Seq. No.
                   122050 1.R1040
Contig ID
5'-most EST
                   kl1701202443.h1
Method
                   BLASTX
                   q3522959
NCBI GI
                   146
BLAST score
                   2.0e-09
E value
Match length
                   68
% identity
                   41
                   (AC004411) putative pectinesterase [Arabidopsis thaliana]
NCBI Description
                   25051
Seq. No.
                   122050 2.R1040
Contig ID
                   bth700848209.h1
5'-most EST
                   25052
Seq. No.
                   122060 1.R1040
Contig ID
                   jC-gmf102220102e02a1
5'-most EST
                   25053
Seq. No.
                   122060 2.R1040
Contig ID
                   k11701\overline{2}03641.h2
5'-most EST
Seq. No.
                   25054
                   122067 1.R1040
Contig ID
                   eep700866071.h1
5'-most EST
Seq. No.
                   25055
                   122071 1.R1040
Contig ID
                   jC-qmf102220130h11d1
5'-most EST
                   BLASTX
Method
                   q2760326
NCBI GI
BLAST score
                   291
                   4.0e-26
E value
                   164
Match length
                   40
```

NCBI Description (AC002130) F1N21.11 [Arabidopsis thaliana]



```
25056
Seq. No.
                  122099 1.R1040
Contig ID
5'-most EST
                  uxk700668656.hl
Method
                  BLASTX
                  g2832661
NCBI GI
BLAST score
                  179
                  8.0e-13
E value
Match length
                  68
                  54
% identity
                  (AL021710) pherophorin - like protein [Arabidopsis
NCBI Description
                  thaliana]
                  25057
Seq. No.
                  122114 1.R1040
5'-most EST
                  uC-gmropic101f12b1
```

Contig ID

BLASTX Method NCBI GI g1001294 BLAST score 157 1.0e-10 E value Match length 62 42 % identity

(D64006) hypothetical protein [Synechocystis sp.] NCBI Description

25058 Seq. No.

122121 1.R1040 Contig ID 5'-most EST  $uxk700\overline{6}68689.h1$ 

Method BLASTX g4559327 NCBI GI BLAST score 277 E value 1.0e-26 Match length 99 % identity 58

(AC007087) hypothetical protein [Arabidopsis thaliana] NCBI Description

Seq. No. 25059

122133 1.R1040 Contig ID 5'-most EST rca700999886.h1

Method BLASTX NCBI GI g4220479 BLAST score 277 E value 1.0e-24 Match length 75 % identity 73

(AC006069) unknown protein [Arabidopsis thaliana] NCBI Description

Seq. No. 25060

Contig ID 122137 1.R1040 5'-most EST  $uxk700\overline{6}68804.h1$ 

Method BLASTX NCBI GI q4249380 BLAST score 152 E value 3.0e-10 Match length 82 % identity

NCBI Description (AC005966) ESTs gb Z37637, gb AA042498 and gb AA042269 come

from this gene. [Arabidopsis thaliana]



25062

Seq. No. 25061

Contig ID 122139\_1.R1040

5'-most EST g4290232

Seq. No.

Contig ID 122142\_1.R1040 5'-most EST bth700847938.h1

Seq. No. 25063

Contig ID 122145\_1.R1040 5'-most EST yz1700967081.h1

Seq. No. 25064

Contig ID 122150\_1.R1040

5'-most EST jC-gmro02910074b02a1

Method BLASTX
NCBI GI g2642448
BLAST score 672
E value 2.0e-70
Match length 292
% identity 49

% identity 49
NCBI Description (AC002391) hypothetical protein [Arabidopsis thaliana]

>gi 3169187 (AC004401) hypothetical protein [Arabidopsis

thaliana]

Seq. No. 25065

Contig ID 122176\_1.R1040

5'-most EST jC-gmst02400033e10d1

Seq. No. 25066

Contig ID 122176\_2.R1040 5'-most EST pxt700942715.h1

Seq. No. 25067

Contig ID 122177\_1.R1040 5'-most EST zzp700831961.h1

Method BLASTX
NCBI GI g2129575
BLAST score 594
E value 2.0e-61
Match length 123
% identity 91

NCBI Description DNA repair protein homolog XPBara - Arabidopsis thaliana

Seq. No. 25068

Contig ID 122211\_1.R1040 5'-most EST leu701150233.h1

Method BLASTX
NCBI GI g3914486
BLAST score 225
E value 1.0e-18
Match length 62
% identity 65

NCBI Description PUTATIVE PSEUDOURIDYLATE SYNTHASE (PSEUDOURIDINE SYNTHASE)

>gi 2347206 (AC002338) pseudouridine synthase isolog

[Arabidopsis thaliana]



25069 Seq. No.

122229 1.R1040 Contig ID 5'-most EST uxk700668875.h1

Seq. No. Contig ID

25070 122304 1.R1040  $dpv701\overline{0}97219.h1$ 5'-most EST

Seq. No. 25071

122305 1.R1040 Contig ID 5'-most EST uxk700668993.hl

BLASTX Method g1708934 NCBI GI BLAST score 175 8.0e-13 E value Match length 62

% identity 53

CDK-ACTIVATING KINASE ASSEMBLY FACTOR MAT1 (RING FINGER NCBI Description

PROTEIN MAT1) (MENAGE A TROIS) (CDK7/CYCLIN H ASSEMBLY FACTOR) (P36) (P35) >gi\_2137198\_pir\_A57235 CDK-activating kinase p36 - mouse >gi\_1015999 (U35249) CDK-activating

comis -

kinase assembly factor p36/MAT1 [Mus musculus]

25072 Seq. No.

122311 1.R1040 Contig ID xpa700796387.h1 5'-most EST

Method BLASTX q100225 NCBI GI BLAST score 438 1.0e-42 E value 363 Match length % identity 36

heat shock transcription factor 8 - tomato NCBI Description

>gi 19260 emb\_CAA47868\_ (X67599) heat stress transcription

factor 8 [Lycopersicon esculentum]

Seq. No. 25073

122315 1.R1040 Contig ID zhf700963620.h1 5'-most EST

Seq. No. 25074

122355 1.R1040 Contig ID 5'-most EST awf700841565.hl

Method BLASTX NCBI GI q3941322 BLAST score 675 E value 4.0e-71 164 Match length 75 % identity

(AF041340) gamma-glutamylcysteine synthetase [Medicago NCBI Description

truncatula]

25075 Seq. No.

Contig ID 122359 1.R1040 5'-most EST uxk700669087.h1



Seq. No. 25076

Contig ID 122366\_1.R1040 5'-most EST uxk700669102.h1

Method BLASTX
NCBI GI g2583128
BLAST score 251
E value 1.0e-32
Match length 185
% identity 46

NCBI Description (AC002387) hypothetical protein [Arabidopsis thaliana]

Seq. No. 25077

Contig ID 122409\_1.R1040 5'-most EST uxk700669496.h1

Method BLASTN
NCBI GI g3046856
BLAST score 51
E value 6.0e-20
Match length 143
% identity 84

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MXI22, complete sequence [Arabidopsis thaliana]

Seq. No. 25078

Contig ID 122411\_1.R1040 5'-most EST uxk700669191.h1

Seq. No. 25079

Contig ID 122430 1.R1040 5'-most EST sat701009950.h2

Seq. No. 25080

Contig ID 122442\_1.R1040 5'-most EST hyd700731210.h1

Seq. No. 25081

Contig ID 122454\_1.R1040 5'-most EST zsg701130390.h1

Method BLASTX
NCBI GI g2655098
BLAST score 695
E value 3.0e-73
Match length 230
% identity 60

NCBI Description (AF023472) peptide transporter [Hordeum vulgare]

Seq. No. 25082

Contig ID 122475\_1.R1040 5'-most EST uxk700669308.h1

Seq. No. 25083

Contig ID 122486\_1.R1040 5'-most EST uxk700669324.h1

Seq. No. 25084

Contig ID 122505\_1.R1040

5'-most EST jC-gmst02400028c09a1



Method BLASTX
NCBI GI g3434971
BLAST score 211
E value 2.0e-16
Match length 59
% identity 66

NCBI Description (AB008105) ethylene responsive element binding factor 3

[Arabidopsis thaliana]

Seq. No. 25085

Contig ID 122558\_1.R1040 5'-most EST uxk700672888.h1

Method BLASTX
NCBI GI g166949
BLAST score 502
E value 7.0e-51
Match length 157
% identity 58

NCBI Description (M32885) cytochrome P-450LXXIA1 (cyp71A1) [Persea

americana]

Seq. No. 25086

Contig ID 122564\_1.R1040 5'-most EST gsv701053059.h1

Method BLASTN
NCBI GI g2564044
BLAST score 35
E value 4.0e-10
Match length 127
% identity 86

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K19P17, complete sequence [Arabidopsis thaliana]

Seq. No. 25087

Contig ID 122597\_1.R1040 5'-most EST fC-gmse700669535a3

Seq. No. 25088

Contig ID 122612 1.R1040 5'-most EST uxk700669732.h1

Seq. No. 25089

Contig ID 122633\_1.R1040

5'-most EST g4396795
Method BLASTX
NCBI GI g4522011
BLAST score 418
E value 4.0e-41
Match length 109
% identity 68

NCBI Description (AC007069) hypothetical protein [Arabidopsis thaliana]

Seq. No. 25090

Contig ID 122638\_1.R1040 5'-most EST uxk700669605.h1

Method BLASTX NCBI GI g4468986



BLAST score 182 E value 9.0e-14 Match length 52 % identity 58

NCBI Description (AL035605) putative protein [Arabidopsis thaliana]

Seq. No. 25091

Contig ID 122651\_1.R1040 5'-most EST ncj700980989.h1

Seq. No. 25092

Contig ID 122666\_1.R1040 5'-most EST uxk700669641.h1

Seq. No. 25093

Contig ID 122670\_1.R1040 5'-most EST uxk700669647.h1

Method BLASTX
NCBI GI g2244876
BLAST score 306
E value 2.0e-28
Match length 81
% identity 72

NCBI Description (Z97338) hypothetical protein [Arabidopsis thaliana]

Seq. No. 25094

Contig ID 122682 1.R1040 5'-most EST hyd700726679.h1

Seq. No. 25095

Contig ID 122683\_1.R1040 5'-most EST uxk700669670.h1

Seq. No. 25096

Contig ID 122704\_1.R1040 5'-most EST uxk700669777.h1

Seq. No. 25097

Contig ID 122727\_1.R1040 5'-most EST hrw701058826.h1

Seq. No. 25098

Contig ID 122730\_1.R1040 5'-most EST jex700903901.h1

Seq. No. 25099

Contig ID 122756\_1.R1040 5'-most EST crh700851669.h1

Method BLASTX
NCBI GI 94115377
BLAST score 479
E value 6.0e-48
Match length 219
% identity 43

NCBI Description (AC005967) unknown protein [Arabidopsis thaliana]

Seq. No. 25100



Contig ID 122763 1.R1040

5'-most EST g5687928
Method BLASTX
NCBI GI g1703446
BLAST score 471
E value 6.0e-47
Match length 212
% identity 50

NCBI Description L-ASPARAGINASE (L-ASPARAGINE AMIDOHYDROLASE)

>gi\_1076292\_pir\_\_S53127 asparaginase - Arabidopsis thaliana >gi\_735918\_emb\_CAA84367\_ (Z34884) asparaginase [Arabidopsis

thaliana]

Seq. No. 25101

Contig ID 122767 1.R1040 5'-most EST hrw701058026.h1

Method BLASTX
NCBI GI g3023945
BLAST score 526
E value 6.0e-54
Match length 110
% identity 86

NCBI Description HISTONE DEACETYLASE (HD) >gi\_2318131 (AF014824) histone

deacetylase [Arabidopsis thaliana]

Seq. No. 25102

Contig ID 122774\_1.R1040

5'-most EST jC-gmfl02220130c04d1

Seq. No. 25103

Contig ID 122777 1.R1040 5'-most EST ncj700987061.h1

Method BLASTX
NCBI GI 94539452
BLAST score 136
E value 5.0e-16
Match length 99
% identity 54

NCBI Description (AL049500) putative phosphoribosylanthranilate transferase

[Arabidopsis thaliana]

Seq. No. 25104

Contig ID 122785\_1.R1040 5'-most EST uxk700670264.h1

Seq. No. 25105

Contig ID 122788\_1.R1040 5'-most EST uxk700669830.h1

Method BLASTX
NCBI GI g4567227
BLAST score 492
E value 7.0e-50
Match length 123
% identity 76

NCBI Description (AC007119) putative transport protein [Arabidopsis

thaliana]



Seq. No. 25106

Contig ID 122789\_1.R1040 5'-most EST xpa700792419.h1

Method BLASTX
NCBI GI g1706326
BLAST score 525
E value 1.0e-53
Match length 106
% identity 93

NCBI Description PYRUVATE DECARBOXYLASE ISOZYME 1 (PDC)

>gi\_2146786\_pir\_\_S65470 pyruvate decarboxylase (EC 4.1.1.1)

(clone PDC1) - Garden pea >gi\_1177603\_emb\_CAA91444\_ (Z66543) pyruvate decarboxylase [Pisum sativum]

Seq. No. 25107

Contig ID 122801\_1.R1040 5'-most EST ary700764320.h1

Seq. No. 25108

Contig ID 122814\_1.R1040 5'-most EST uxk700669877.h1

Seq. No. 25109

Contig ID 122815\_1.R1040 5'-most EST uxk700669878.h1

Seq. No. 25110

Contig ID 122840 1.R1040

5'-most EST jC-gmfl02220089a08d1

Seq. No. 25111

Contig ID 122842\_1.R1040 5'-most EST hrw701063202.h1

Seq. No. 25112

Contig ID 122847 1.R1040

5'-most EST jC-gmfl02220068f10a1

Method BLASTX
NCBI GI g4455259
BLAST score 378
E value 3.0e-36
Match length 169
% identity 48

NCBI Description (AL035523) putative Ser/Thr protein kinase [Arabidopsis

thaliana]

Seq. No. 25113

Contig ID 122851\_1.R1040 5'-most EST uC-gmropic058c07b1

Seq. No. 25114

Contig ID 122868\_1.R1040 5'-most EST fC-gmse700669955f2

Method BLASTN
NCBI GI g495660
BLAST score 143
E value 1.0e-74



Match length 266 % identity 89

NCBI Description Pisum sativum aspartate transcarbamoylase (pyrB2) mRNA,

complete cds

Seq. No. 25115

Contig ID 122873\_1.R1040 5'-most EST fC-gmse700669961f2

Seq. No. 25116

Contig ID 122889\_1.R1040 5'-most EST kmv700740365.h1

Seq. No. 25117

Contig ID 122890\_1.R1040 5'-most EST awf700839644.h1

Method BLASTX
NCBI GI g4106395
BLAST score 477
E value 5.0e-48
Match length 121
% identity 71

NCBI Description (AF073744) raffinose synthase [Cucumis sativus]

Seq. No. 25118

Contig ID 122895\_1.R1040 5'-most EST uxk700669992.h1

Seq. No. 25119

Contig ID 122910\_1.R1040 5'-most EST hrw701060629.h1

Method BLASTX
NCBI GI g2465923
BLAST score 170
E value 4.0e-12
Match length 90
% identity 40

NCBI Description (AF024648) receptor-like serine/threonine kinase

[Arabidopsis thaliana]

Seq. No. 25120

Contig ID 122918 1.R1040 5'-most EST uxk700670026.h1

Seq. No. 25121

Contig ID 122924\_1.R1040 5'-most EST uxk700670037.h1

Method BLASTX
NCBI GI g3047103
BLAST score 187
E value 2.0e-14
Match length 73
% identity 52

NCBI Description (AF058919) regions of weak similarity to 1-asparaginase

[Arabidopsis thaliana]

Seq. No. 25122



```
122933 1.R1040
Contig ID
                   uC-gmropic110a04b1
5'-most EST
                   BLASTX
Method
                   g4455319
NCBI GI
BLAST score
                   192
                   4.0e-14
E value
                   122
Match length
                   9
% identity
                   (AL035528) putative disease resistance protein [Arabidopsis
NCBI Description
                   thaliana]
                   25123
Seq. No.
                   122941 1.R1040
Contig ID
5'-most EST
                   uxk700\overline{6}70061.h1
Seq. No.
                   25124
```

122946 1.R1040 Contig ID zhf700963776.h1 5'-most EST

25125 Seq. No. 122946 2.R1040 Contig ID 5'-most EST txt700735620.h1

25126 Seq. No. 122966 1.R1040 Contig ID zhf700963048.h1 5'-most EST BLASTX Method g2623297 NCBI GI

BLAST score 628 3.0e-65 E value 299 Match length 48 % identity

(AC002409) unknown protein [Arabidopsis thaliana] NCBI Description >qi 3790583 (AF079180) RING-H2 finger protein RHCla

[Arabidopsis thaliana]

25127 Seq. No. 122966 2.R1040 Contig ID 5'-most EST pmv700892456.h1

25128 Seq. No. Contig ID 122976 1.R1040 5'-most EST  $uxk700\overline{6}70107.h1$ 

Seq. No. 25129 122977 1.R1040 Contig ID

5'-most EST uC-gmrominsoy227h07b1

Method BLASTN g3668068 NCBI GI 81 BLAST score 2.0e-37 E value Match length 185 % identity

Lycopersicon esculentum Pto kinase interactor 1 (Ptil) NCBI Description

mRNA, complete cds

Seq. No. 25130



```
122981 1.R1040
Contig ID
5'-most EST
                  jC-qmf102220113e03d1
                  BLASTX
Method
                  q2244996
NCBI GI
                   503
BLAST score
                   6.0e-51
E value
Match length
                  118
% identity
                   80
                  (Z97341) similarity to a membrane-associated salt-inducible
NCBI Description
                  protein [Arabidopsis thaliana]
                   25131
Seq. No.
Contig ID
                   122984 1.R1040
                   jC-gmf\overline{1}02220144c05a1
5'-most EST
                   BLASTX
Method
                   q1351819
NCBI GI
BLAST score
                   305
E value
                   1.0e-27
                   143
Match length
% identity
                   42
                  HYPOTHETICAL 81.7 KD PROTEIN IN MOL1-NAT2 INTERGENIC REGION
NCBI Description
                   >gi_2131682_pir__S60436 hypothetical protein YGR145w -
                   yeast (Saccharomyces cerevisiae) >gi_1045251_emb_CAA59803_
                   (X85807) ORF G6623 [Saccharomyces cerevisiae]
                   >gi 1323244 emb CAA97158_ (Z72930) ORF YGR145w
                   [Saccharomyces cerevisiae]
                   25132
Seq. No.
Contig ID
                   122993 1.R1040
5'-most EST
                   jex700903862.hl
                   25133
Seq. No.
                   122995 1.R1040
Contig ID
5'-most EST
                   uxk700670141.hl
Method
                   BLASTX
NCBI GI
                   q3201627
BLAST score
                   117
E value
                   4.0e-12
Match length
                   79
% identity
                   56
                  (AC004669) putative SWH1 protein [Arabidopsis thaliana]
NCBI Description
                   25134
Seq. No.
                   122996 1.R1040
Contig ID
                   uxk700670142.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g4510368
BLAST score
                   144
                   2.0e-09
E value
Match length
                   69
                   45
% identity
                   (AC007017) putative transcription factor E2F5 [Arabidopsis
NCBI Description
```

thaliana]

25135 Seq. No.

122999 1.R1040 Contig ID

5'-most EST uC-gmrominsoy115h05b1



Method BLASTX
NCBI GI g3851158
BLAST score 146
E value 6.0e-09
Match length 198
% identity 31

NCBI Description (AF092090) cp151 [Rattus norvegicus]

Seq. No. 25136

Contig ID 123002\_1.R1040 5'-most EST kl1701210739.h1

Seq. No. 25137

Contig ID 123002 2.R1040

5'-most EST jC-gmst02400020a08a1

Seq. No. 25138

Contig ID 123026\_1.R1040 5'-most EST uxk700670179.h1

Method BLASTX
NCBI GI g1770454
BLAST score 230
E value 3.0e-19
Match length 71
% identity 58

NCBI Description (X98260) M-phase phosphoprotein 11 [Homo sapiens]

Seq. No. 25139

Contig ID 123030 1.R1040

5'-most EST uC-gmflminsoy053h10b1

Method BLASTN
NCBI GI g1065907
BLAST score 510
E value 0.0e+00
Match length 855
% identity 90

NCBI Description Pisum sativum chloroplast processing enzyme mRNA, nuclear

gene encoding chloroplast protein, complete cds

Seq. No. 25140

Contig ID 123037\_1.R1040 5'-most EST uxk700670191.h1

Seq. No. 25141

Contig ID 123043\_1.R1040 5'-most EST awf700836541.h1

Seq. No. 25142

Contig ID 123044 1.R1040 5'-most EST uxk700670204.h1

Seq. No. 25143

Contig ID 123058\_1.R1040 5'-most EST uxk700670231.h1

Seq. No. 25144

Contig ID 123063\_1.R1040



```
asn701135236.h1
5'-most EST
                  25145
Seq. No.
                  123071 1.R1040
Contia ID
                  wvk700683675.hl
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2137562
BLAST score
                  207
E value
                  1.0e-16
Match length
                  61
% identity
                  61
                  mouse Dhm1 protein - mouse >gi 1060921 dbj_BAA07524_
NCBI Description
                   (D38517) Dhm1 protein [Mus musculus]
Seq. No.
                  123095 1.R1040
Contig ID
5'-most EST
                  asn701141962.hl
                  25147
Seq. No.
                  123100 1.R1040
Contig ID
5'-most EST
                  jC-gmle01810084h05d1
Seq. No.
                  25148
                  123104 1.R1040
Contig ID
5'-most EST
                  uxk700670308.hl
                  BLASTX
Method
NCBI GI
                  q2244986
BLAST score
                   231
E value
                   2.0e-19
Match length
                   97
% identity
                   34
NCBI Description (Z97340) FCA gamma [Arabidopsis thaliana]
                   25149
Seq. No.
                   123108 1.R1040
Contig ID
5'-most EST
                   vwf700679268.h1
Method
                   BLASTN
                   q1046277
NCBI GI
                   148
BLAST score
                   2.0e-77
E value
                   343
Match length
                   86
% identity
NCBI Description Phaseolus vulgaris embryo-specific acidic transcriptional
                   activator PvAlf mRNA, complete cds
                   25150
Seq. No.
Contig ID
                   123138 1.R1040
5'-most EST
                   crh700850927.h1
                   25151
Seq. No.
                   123142 1.R1040
Contig ID
5'-most EST
                   uxk700670378.h1
```

3959

25152

123145 1.R1040

uxk700670381.h1

Seq. No. Contig ID

5'-most EST



Seq. No. 25153

Contig ID 123157\_1.R1040 5'-most EST dpv701099953.h1

Method BLASTX
NCBI GI g1076264
BLAST score 220
E value 4.0e-18
Match length 102
% identity 52

NCBI Description carboxyl-terminal processing proteinase D1 precursor -

spinach >gi\_2129489\_pir\_\_S65146 photosystem II D1 protein

processing enzyme precursor - spinach

>gi 999435 dbj BAA09134 (D50585) C-terminal protease

precursor [Spinacia oleracea]

Seq. No. 25154

Contig ID 123181\_1.R1040 5'-most EST uxk700670434.h1

Seq. No. 25155

Contig ID 123219\_1.R1040 5'-most EST txt700731701.h1

Method BLASTX
NCBI GI g2497953
BLAST score 423
E value 6.0e-42
Match length 100
% identity 78

NCBI Description MOLYBDOPTERIN BIOSYNTHESIS CNX1 PROTEIN (MOLYBDENUM

COFACTOR BIOSYNTHESIS ENZYME CNX1) >gi\_1263314 (L47323) molybdenum cofactor biosynthesis enzyme [Arabidopsis thaliana] >gi\_4469123\_emb\_CAB38312\_ (AJ236870) molybdenum

cofactor biosynthesis enzyme [Arabidopsis thaliana]

Seq. No. 25156

Contig ID 123225\_1.R1040 5'-most EST awf700838914.h1

Seq. No. 25157

Contig ID 123232 1.R1040 5'-most EST uxk700670543.h1

Seq. No. 25158

Contig ID 123238\_1.R1040 5'-most EST uxk700670549.h1

Method BLASTX
NCBI GI g2689030
BLAST score 191
E value 2.0e-14
Match length 146
% identity 40

NCBI Description (AF034568) RNA guanylyltransferase [Mus musculus]

>gi\_2697127 (AF025653) mRNA capping enzyme [Mus musculus]

Seq. No. 25159

Contig ID 123241\_1.R1040 5'-most EST uxk700670553.h1



```
BLASTN
Method
                  g479059
NCBI GI
                  88
BLAST score
                  4.0e-42
E value
                  199
Match length
                  95
% identity
                  G.max (Fiskeby V) mRNA for cysteine endopeptidase
NCBI Description
                  25160
Seq. No.
                  123265 1.R1040
Contig ID
                  leu701150451.h1
5'-most EST
                  25161
Seq. No.
```

Contig ID 123302\_1.R1040
5'-most EST uxk700670677.h1
Method BLASTX
NCBI GI g3540194
RIAST score 669

BLAST score 669
E value 4.0e-70
Match length 192
% identity 69

NCBI Description (AC004260) AtVPS45p [Arabidopsis thaliana]

Seq. No. 25162

Contig ID 123302\_2.R1040 5'-most EST bth700847232.h1

Seq. No. 25163

Contig ID 123312\_1.R1040

 5'-most EST
 g5606434

 Method
 BLASTX

 NCBI GI
 g2642431

 BLAST score
 621

 E value
 1.0e-64

 Match length
 220

 % identity
 53

NCBI Description (AC002391) putative retrotransposon polyprotein

[Arabidopsis thaliana]

Seq. No. 25164

Contig ID 123338\_1.R1040 5'-most EST uxk700670741.h1

Seq. No. 25165

Contig ID 123357\_1.R1040 5'-most EST hyd700727542.h1

Seq. No. 25166

Contig ID 123360\_1.R1040 5'-most EST uxk700670807.h1

Method BLASTX
NCBI GI g1174470
BLAST score 158
E value 8.0e-11
Match length 105
% identity 35

NCBI Description OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5)



(INTEGRAL MEMBRANE PROTEIN 1) >gi\_508543 (L34260) integral membrane protein 1 [Mus musculus] >gi\_1588285\_prf\_\_2208301A integral membrane protein [Mus musculus]

25167 Seq. No. 123367 1.R1040 Contig ID jC-gmf102220052f10a1 5'-most EST BLASTX Method NCBI GI g4322107 BLAST score 242 3.0e-20 E value Match length 105 % identity 46 (AF072717) pEg7 [Xenopus laevis] NCBI Description 25168 Seq. No. 123372 1.R1040 Contig ID uxk700670833.hl 5'-most EST Method BLASTX q4539005 NCBI GI BLAST score 421 E value 4.0e-59 Match length 175 % identity 62 (AL049481) putative oxidoreductase [Arabidopsis thaliana] NCBI Description 25169 Seq. No. 123414 1.R1040 Contig ID  $uxk700\overline{6}71324.h1$ 5'-most EST 25170 Seq. No. 123425\_1.R1040 Contig ID 5'-most EST zhf700959336.h1 BLASTX Method NCBI GI g4432855 BLAST score 222 3.0e-18 E value Match length 49 % identity 90 (AC006300) unknown protein [Arabidopsis thaliana] NCBI Description 25171 Seq. No. 123425 2.R1040 Contig ID  $uxk700\overline{6}70970.h1$ 5'-most EST BLASTX Method NCBI GI g4432855 225 BLAST score 7.0e-19 E value Match length 51 86 % identity (AC006300) unknown protein [Arabidopsis thaliana] NCBI Description

Seq. No.

25172

Contig ID 5'-most EST

123463\_1.R1040 crh700851108.h1

Seq. No.



Contig ID 123479 1.R1040 5'-most EST zpv700762610.h1 Method BLASTX

NCBI GI g3695408
BLAST score 156
E value 1.0e-10
Match length 51
% identity 57

NCBI Description (AF096373) contains similarity to Solanum lycopersicum

(tomato) wound-induced protein (GB:X59882) [Arabidopsis thaliana] >gi\_4538956\_emb\_CAB39780.1\_ (AL049488) probable

wound-induced protein [Arabidopsis thaliana]

Seq. No. 25174

Contig ID 123483\_1.R1040 5'-most EST uxk700671073.h1

Method BLASTX
NCBI GI g3386617
BLAST score 164
E value 1.0e-11
Match length 36
% identity 89

NCBI Description (AC004665) putative cell division protein (ftsY)

[Arabidopsis thaliana]

Seq. No. 25175

Contig ID 123489 1.R1040 5'-most EST uxk700671085.h1

Method BLASTN
NCBI GI g862479
BLAST score 94
E value 1.0e-45
Match length 266
% identity 84

NCBI Description Glycine max valosin-containing protein mRNA, complete cds

Seq. No. 25176

Contig ID 123491\_1.R1040 5'-most EST uxk700671087.h1

Seq. No. 25177

Contig ID 123495 1.R1040 5'-most EST dpv701100357.h1

Seq. No. 25178

Contig ID 123524\_1.R1040 5'-most EST vwf700675844.h1

Method BLASTX
NCBI GI g3914832
BLAST score 342
E value 5.0e-50
Match length 124
% identity 74

NCBI Description DNA-DIRECTED RNA POLYMERASE MITOCHONDRIAL PRECURSOR >gi\_1742971 emb CAA70583 (Y09432) mitochondrial singel

subunit DNA-directed RNA polymerase [Arabidopsis thaliana]

>gi\_2330566\_emb\_CAA70210\_ (Y09006) mitochondrial



single-subunit DNA-dependent RNA polymerase [Arabidopsis
thaliana]

Seq. No. 25179

Contig ID 123526\_1.R1040 5'-most EST uxk700671476.h1

Seq. No. 25180

Contig ID 123533\_1.R1040 5'-most EST uxk700671225.h1

Method BLASTX
NCBI GI g267055
BLAST score 330
E value 3.0e-31
Match length 81
% identity 75

NCBI Description SUCROSE SYNTHASE (SUCROSE-UDP GLUCOSYLTRANSFERASE)

>gi\_66572\_pir\_\_YUMU sucrose synthase (EC 2.4.1.13) Arabidopsis thaliana >gi\_16526\_emb\_CAA43303\_ (X60987)

sucrose synthase [Arabidopsis thaliana]

Seq. No. 25181

Contig ID 123540 1.R1040

5'-most EST g5342486

Seq. No. 25182

Contig ID 123552\_1.R1040 5'-most EST fC-gmse7000764850r1

Method BLASTX
NCBI GI g4263781
BLAST score 361
E value 4.0e-34
Match length 112
% identity 60

NCBI Description (AC006068) putative membrane transport protein [Arabidopsis

thaliana]

Seq. No. 25183

Contig ID 123558\_1.R1040 5'-most EST uxk700671351.h1

Seq. No. 25184

Contig ID 123587\_1.R1040 5'-most EST vzy700753716.h1

Method BLASTX
NCBI GI g4406761
BLAST score 217
E value 7.0e-23
Match length 90
% identity 66

NCBI Description (AC006836) putative ubiquinone biosynthesis protein

[Arabidopsis thaliana]

Seq. No. 25185

Contig ID 123589\_1.R1040 5'-most EST jC-gmst02400031e01a1

Method BLASTX



```
NCBI GI
                  a927025
BLAST score
                  836
                  2.0e-89
E value
Match length
                  362
% identity
                  44
NCBI Description (L44134) SPF1-like DNA-binding protein [Cucumis sativus]
                  25186
Seq. No.
                  123594 1.R1040
Contig ID
5'-most EST
                  uxk700671437.h1
Seq. No.
                  25187
                  123600 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy028e06b1
Seq. No.
                   25188
Contig ID
                   123602 1.R1040
5'-most EST
                  jC-gmst02400017b04d1
                   25189
Seq. No.
                  123621 1.R1040
Contig ID
5'-most EST
                  ncj700983937.hl
Method
                  BLASTX
NCBI GI
                   q2828293
BLAST score
                   189
E value
                   2.0e-14
Match length
                   74
                   54
% identity
                  (AL021687) putative protein [Arabidopsis thaliana]
NCBI Description
                   25190
Seq. No.
                   123627 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810083b04d1
Method
                   BLASTX
NCBI GI
                   g4512670
BLAST score
                   176
                   9.0e-13
E value
                   63
Match length
% identity
                   48
                  (AC006931) putative cytochrome P450 [Arabidopsis thaliana]
NCBI Description
                   25191
Seq. No.
                   123635 1.R1040
Contig ID
                   jC-gmle01810045a08a1
5'-most EST
                   BLASTX
Method
                   g4519671
NCBI GI
                   347
BLAST score
                   2.0e-32
E value
                   163
Match length
                   50
% identity
                  (AB017693) transfactor [Nicotiana tabacum]
NCBI Description
```

Seq. No.

123635 2.R1040 Contig ID 5'-most EST  $jsh701\overline{0}63850.h1$ 

25192

25193 Seq. No.



Contig ID 123646\_1.R1040 5'-most EST uC-gmrominsoy309f03b1

Seq. No. 25194 Contig ID 123658\_1.R1040

5'-most EST q4296081

Seq. No. 25195

Contig ID 123659\_1.R1040 5'-most EST uxk700671630.h1

Method BLASTX
NCBI GI g3335341
BLAST score 280
E value 3.0e-25
Match length 87
% identity 64

NCBI Description (AC004512) T8F5.10 [Arabidopsis thaliana]

Seq. No. 25196

Contig ID 123667\_1.R1040 5'-most EST fde700873316.h1

Seq. No. 25197

Contig ID 123675\_1.R1040 5'-most EST uxk700671833.h1

Seq. No. 25198

Contig ID 123676\_1.R1040 5'-most EST uxk700671679.h1

Method BLASTX
NCBI GI g4512702
BLAST score 301
E value 2.0e-27
Match length 72
% identity 78

NCBI Description (AC006569) hypothetical protein [Arabidopsis thaliana]

Seq. No. 25199

Contig ID 123698\_1.R1040 5'-most EST uxk700671728.h1

Seq. No. 25200

Contig ID 123702 1.R1040 5'-most EST epx701104041.h1

Seq. No. 25201

Contig ID 123707\_1.R1040 5'-most EST uxk700671745.h1

Seq. No. 25202

Contig ID 123716\_1.R1040 5'-most EST asn701136961.h1

Method BLASTX
NCBI GI g4204304
BLAST score 227
E value 7.0e-19
Match length 105



% identity 50

NCBI Description (AC003027) lcl\_prt\_seq No definition line found

[Arabidopsis thaliana]

Seq. No. 25203

Contig ID 123735\_1.R1040 5'-most EST uxk700671813.h1

Seq. No. 25204

Contig ID 123738\_1.R1040 5'-most EST uxk700671817.h1

Seq. No. 25205

Contig ID 123777\_1.R1040

5'-most EST uC-gmflminsoy053e10b1

Method BLASTX
NCBI GI 9732233
BLAST score 151
E value 1.0e-09
Match length 91

% identity 36

NCBI Description HYPOTHETICAL PROTEIN IN XYNA 3'REGION (ORF6)

>gi\_632088\_pir\_\_S41790 hypothetical protein 6 -

thermophilic bacterium RT8.B4 (fragment) >gi\_552047

(L18965) ORF6 [thermophilic bacterium RT8.B4]

Seq. No. 25206

Contig ID 123792\_1.R1040 5'-most EST eep700865434.h1

Seq. No. 25207

Contig ID 123797\_1.R1040

5'-most EST jC-gmle01810059b12a1

Seq. No. 25208

Contig ID 123814\_1.R1040 5'-most EST uxk700671954.h1

Method BLASTX
NCBI GI g4539944
BLAST score 315
E value 2.0e-29
Match length 78
% identity 77

NCBI Description (AF133841) aldose reductase ALDRXV4 [Xerophyta viscosa]

Seq. No. 25209

Contig ID 123819\_2.R1040 5'-most EST uxk700671959.h1

Seq. No. 25210

Contig ID 123843\_1.R1040 5'-most EST kl1701208075.h1

Method BLASTX
NCBI GI g4234953
BLAST score 219
E value 2.0e-17
Match length 204



% identity 18

NCBI Description (AF098970) NBS-LRR-like protein cD7 [Phaseolus vulgaris]

Seq. No. 25211

Contig ID 123877\_1.R1040 5'-most EST uxk700672036.h1

Seq. No. 25212

Contig ID 123889 1.R1040 5'-most EST zsg701127894.h1

Seq. No. 25213

Contig ID 123925\_1.R1040 5'-most EST rca701000427.h1

Method BLASTX
NCBI GI g4544422
BLAST score 328
E value 1.0e-30
Match length 108
% identity 61

NCBI Description (AC006955) putative fimbrin [Arabidopsis thaliana]

Seq. No. 25214

Contig ID 123929 1.R1040 5'-most EST uxk700672113.h1

Method BLASTX
NCBI GI g2492504
BLAST score 301
E value 1.0e-27
Match length 69
% identity 88

NCBI Description CELL DIVISION CYCLE PROTEIN 48 HOMOLOG

>gi\_1669660\_emb\_CAA70565\_ (Y09396) protein of AAA family

[Capsicum annuum]

Seq. No. 25215

Contig ID 123930\_1.R1040 5'-most EST uxk700672431.h1

Seq. No. 25216

Contig ID 123970\_1.R1040 5'-most EST awf700837111.h1

Method BLASTX
NCBI GI g3913792
BLAST score 306
E value 2.0e-28
Match length 88
% identity 66

NCBI Description GLUTAMATE--CYSTEINE LIGASE PRECURSOR

(GAMMA-GLUTAMYLCYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS) >gi\_2243126\_emb\_CAA71801\_ (Y10848) gamma-glutamylcysteine

synthetase [Brassica juncea]

Seq. No. 25217

Contig ID 123981\_1.R1040 5'-most EST uC-gmropic031h12b1

Method BLASTX



NCBI GI g3738308 BLAST score 247 E value 3.0e-21 Match length 85 % identity 60

NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]

Seq. No. 25218

Contig ID 123987\_1.R1040 5'-most EST uxk700672205.h1

Method BLASTX
NCBI GI g3201627
BLAST score 616
E value 8.0e-76
Match length 168
% identity 83

NCBI Description (AC004669) putative SWH1 protein [Arabidopsis thaliana]

Seq. No. 25219

Contig ID 123998\_1.R1040 5'-most EST uxk700672216.h1

Seq. No. 25220

Contig ID 124011\_1.R1040 5'-most EST jC-gmro02910041066a1

Seq. No. 25221

Contig ID 124011\_2.R1040 5'-most EST wrg700786093.h2

Seq. No. 25222

Contig ID 124020\_1.R1040 5'-most EST zzp700832745.h1

Method BLASTN
NCBI GI g510545
BLAST score 187
E value 1.0e-101
Match length 299
% identity 91

NCBI Description P.sativum mRNA for starch branching enzyme I

Seq. No. 25223

Contig ID 124038\_1.R1040 5'-most EST fC-gmse700672271a3

Method BLASTX
NCBI GI g4234955
BLAST score 752
E value 1.0e-79
Match length 382
% identity 45

NCBI Description (AF098971) NBS-LRR-like protein cD8 [Phaseolus vulgaris]

Seq. No. 25224

Contig ID 124072 1.R1040 5'-most EST kl1701207792.h1

Method BLASTX NCBI GI g3004565



BLAST score 442 E value 2.0e-63 Match length 184 % identity 66

NCBI Description (AC003673) putative protein kinase [Arabidopsis thaliana]

Seq. No. 25225

Contig ID 124088\_1.R1040 5'-most EST jC-gmf102220130b02d1

Seq. No. 25226

Contig ID 124093\_1.R1040 5'-most EST uxk700672915.h1

Method BLASTX
NCBI GI g2979546
BLAST score 189
E value 1.0e-14
Match length 68
% identity 62

NCBI Description (AC003680) unknown protein [Arabidopsis thaliana]

Seq. No. 25227

Contig ID 124094\_1.R1040 5'-most EST uxk700672342.h1

Method BLASTX
NCBI GI g2642163
BLAST score 298
E value 1.0e-29
Match length 118
% identity 60

NCBI Description (AC003000) hypothetical protein [Arabidopsis thaliana]

Seq. No. 25228

Contig ID 124101\_1.R1040 5'-most EST uC-gmropic018c04b1

Seq. No. 25229

Contig ID 124126\_1.R1040 5'-most EST fC-gmse700672391f2

Method BLASTX
NCBI GI g2465923
BLAST score 262
E value 1.0e-22
Match length 156
% identity 11

NCBI Description (AF024648) receptor-like serine/threonine kinase

[Arabidopsis thaliana]

Seq. No. 25230

Contig ID 124142\_1.R1040 5'-most EST uxk700672422.h1

Seq. No. 25231

Contig ID 124146\_1.R1040 5'-most EST awf700839201.h1

Seq. No. 25232



Contig ID 124149\_1.R1040 5'-most EST jC-gmst02400063d04d1

Seq. No. 25233

Contig ID 124156\_1.R1040 5'-most EST uxk700672438.h1

Seq. No. 25234

Contig ID 124159\_1.R1040 5'-most EST uxk700672441.h1

Seq. No. 25235

Contig ID 124165\_1.R1040 5'-most EST uxk700672447.h1

Seq. No. 25236

Contig ID 124193\_1.R1040 5'-most EST rlr700900864.h1

Method BLASTX
NCBI GI g3043529
BLAST score 479
E value 5.0e-60
Match length 189
% identity 59

NCBI Description (AJ002204) polyamine oxidase [Zea mays]

Seq. No. 25237

Contig ID 124208\_1.R1040

5'-most EST jC-gmle01810033g04d1

Seq. No. 25238

Contig ID 124245\_1.R1040 5'-most EST uxk700672574.h1

Seq. No. 25239

Contig ID 124246\_1.R1040 5'-most EST bth700848988.h1

Method BLASTX
NCBI GI g4490736
BLAST score 810
E value 1.0e-86
Match length 288
% identity 33

NCBI Description (AL035708) putative protein [Arabidopsis thaliana]

Seq. No. 25240

Contig ID 124272\_1.R1040

5'-most EST jC-gmle01810011a10a1

Method BLASTX
NCBI GI g2190544
BLAST score 515
E value 1.0e-52
Match length 120
% identity 83

NCBI Description (AC001229) Similar to Saccharomyces hypothetical protein

P9642.2 (gb U40828). [Arabidopsis thaliana]



```
25241
Seq. No.
Contig ID
                  124273 1.R1040
5'-most EST
                  fC-qmse700672649a3
                  BLASTX
Method
                  q3056592
NCBI GI
                   323
BLAST score
E value
                  1.0e-29
                  150
Match length
% identity
                   45
                  (AC004255) T1F9.13 [Arabidopsis thaliana]
NCBI Description
                  25242
Seq. No.
Contig ID
                  124273 2.R1040
                  uxk700\overline{6}72617.h1
5'-most EST
Method
                  BLASTX
                  q3021265
NCBI GI
                   206
BLAST score
E value
                   3.0e-16
Match length
                  71
% identity
                   54
                   (AL022347) protein kinase - like protein [Arabidopsis
NCBI Description
                   thaliana] >gi_3292839_emb_CAA19829_ (AL031018) protein
                   kinase - like protein [Arabidopsis thaliana]
Seq. No.
                   25243
                   124281 1.R1040
Contig ID
5'-most EST
                  uxk700672627.h1
Seq. No.
                   25244
                   124302 1.R1040
Contiq ID
5'-most EST
                   uC-gmropic063e09b1
                   BLASTX
Method
NCBI GI
                   q3201541
BLAST score
                   1202
E value
                   1.0e-132
Match length
                   259
% identity
                  (AJ005077) TCTR2 protein [Lycopersicon esculentum]
NCBI Description
                   25245
Seq. No.
                   124311 1.R1040
Contig ID
5'-most EST
                   uxk700672667.h1
Seq. No.
                   25246
                   124333 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy023f04b1
Seq. No.
                   25247
                   124343 1.R1040
Contig ID
5'-most EST
                   uxk700672715.h1
                   BLASTX
Method
```

Method BLASTX
NCBI GI g3046695
BLAST score 231
E value 5.0e-19
Match length 87
% identity 55

NCBI Description (AL022224) putative protein [Arabidopsis thaliana]



```
Seq. No.
                   25248
                   124349 1.R1040
Contia ID
5'-most EST
                   uxk700672723.hl
                   BLASTX
Method
NCBI GI
                   q4557060
BLAST score
                   289
                   3.0e-26
E value
                   79
Match length
                   67
% identity
                   (AC007154) putative chromosome-associated polypeptide, 5'
NCBI Description
                   partial [Arabidopsis thaliana]
                   25249
Seq. No.
                   124356 1.R1040
Contig ID
5'-most EST
                   q4313377
Seq. No.
                   25250
                   124356 2.R1040
Contig ID
5'-most EST
                   txt700731475.h1
Seq. No.
                   25251
Contig ID
                   124383 1.R1040
5'-most EST
                   vzy700755280.h1
                   BLASTX
Method
                   a3286691
NCBI GI
                   237
BLAST score
                   3.0e-20
E value
Match length
                   67
                   67
% identity
                   (AJ007450) auxilin-like protein [Arabidopsis thaliana]
NCBI Description
                   25252
Seq. No.
                   124385 1.R1040
Contig ID
5'-most EST
                   uxk700\overline{6}72761.h1
Method
                   BLASTX
NCBI GI
                   q4417267
BLAST score
                   173
E value
                   1.0e-12
Match length
                   62
% identity
                   (AC007019) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   25253
                   124396 1.R1040
Contig ID
                   uxk700\overline{6}72774.h1
5'-most EST
                   25254
Seq. No.
                   124398 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810091c01a1
```

Seq. No. 25255

Contig ID 124412\_1.R1040 5'-most EST zhf700952207.h1

Seq. No. 25256

Contig ID 124413\_1.R1040



```
jC-gmro02800033a07d1
5'-most EST
                  25257
Sea. No.
                  124414 1.R1040
Contig ID
                  uxk700672796.h1
5'-most EST
                  25258
Seq. No.
                  124430 1.R1040
Contig ID
                  awf700843104.hl
5'-most EST
Seq. No.
                  25259
                  124434 1.R1040
Contig ID
                  qsv701050727.h1
5'-most EST
                  BLASTX
Method
                  q2982458
NCBI GI
                  765
BLAST score
                  2.0e-81
E value
Match length
                  221
                  70
% identity
                  (AL022223) putative protein [Arabidopsis thaliana]
NCBI Description
                  25260
Seq. No.
                  124442 1.R1040
Contig ID
5'-most EST
                  uxk700672843.h1
                  25261
Seq. No.
                  124449 1.R1040
Contig ID
                  uxk700673492.hl
5'-most EST
Method
                  BLASTX
                   q3702342
NCBI GI
                   172
BLAST score
                   1.0e-12
E value
Match length
                   80
% identity
                   47
NCBI Description (AC005397) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   25262
                   124455 1.R1040
Contig ID
5'-most EST
                   uxk700672862.hl
                   25263
Seq. No.
                   124457 1.R1040
Contig ID
5'-most EST
                   g4299814
                   25264
Seq. No.
                   124458 1.R1040
Contig ID
                   fua701042227.h1
5'-most EST
                   BLASTX
Method
                   q3176710
NCBI GI
                   197
BLAST score
                   2.0e-15
E value
                   65
Match length
                   58
% identity
NCBI Description (AC002392) unknown protein [Arabidopsis thaliana]
```

Contig ID 124461\_1.R1040

Seq. No.



```
5'-most EST
                   ncj700980209.hl
Method
                   BLASTN
                   q3510347
NCBI GI
BLAST score
                   39
E value
                   2.0e-12
Match length
                   201
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MSJ11, complete sequence [Arabidopsis thaliana]
Seq. No.
                   25266
                   124501 1.R1040
Contig ID
                   uxk700\overline{6}73191.h1
5'-most EST
                   25267
Seq. No.
                   124508 1.R1040
Contig ID
5'-most EST
                   uC-gmronoir028e08b1
```

Seq. No. 25268 124508 2.R1040 Contig ID 5'-most EST leu701153756.h1

25269 Seq. No. Contig ID 124541 1.R1040 5'-most EST crh700851681.h1

25270 Seq. No. 124543 1.R1040 Contig ID

5'-most EST pmv700891704.hl BLASTX Method g4220480 NCBI GI BLAST score 201 2.0e-15 E value

Match length 128 % identity

(AC006069) unknown protein [Arabidopsis thaliana] NCBI Description

25271 Seq. No.

124555 1.R1040 Contig ID uxk700673026.h1 5'-most EST

25272 Seq. No.

124571 1.R1040 Contig ID hrw701056931.hl 5'-most EST

BLASTN Method g218250 NCBI GI BLAST score 58 5.0e-24 E value Match length 86 92 % identity

Rice mRNA for low molecular weight heat shock protein, NCBI Description

complete cds

25273 Seq. No.

124583 1.R1040 Contig ID fC-gmro700870403f3 5'-most EST Method BLASTX



```
NCBI GI
                   q3953601
BLAST score
                   234
                   1.0e-19
E value
Match length
                   65
% identity
                   71
                   (AB008489) response regulator 6 [Arabidopsis thaliana]
NCBI Description
                   25274
Seq. No.
                   124586 1.R1040
Contig ID
5'-most EST
                   hrw701061851.hl
Seq. No.
                   25275
                   124604 1.R1040
Contig ID
5'-most EST
                   uxk700673110.h1
Seq. No.
                   25276
                   124627 1.R1040
Contig ID
5'-most EST
                   jC-qmst02400028b03a1
                   BLASTX
Method
                   g2132182
NCBI GI
                   648
BLAST score
                   5.0e-68
E value
Match length
                   152
% identity
                   76
                   hypothetical protein YPL086c - yeast (Saccharomyces
NCBI Description
                   cerevisiae) >gi_1151240 (U43281) Lpg22p [Saccharomyces
                   cerevisiae]
                   25277
Seq. No.
                   124629 1.R1040
Contig ID
5'-most EST
                   zhf700954545.h1
                   BLASTN
Method
                   g2618600
NCBI GI
BLAST score
                   41
                   2.0e-13
E value
Match length
                   49
% identity
                   96
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MDC12, complete sequence [Arabidopsis thaliana]
                   25278
Seq. No.
                   124636 1.R1040
Contig ID
                   uxk700\overline{6}73146.h1
5'-most EST
```

Method BLASTX g2979563 NCBI GI 207 BLAST score

E value 2.0e-16 Match length 112 % identity

(AC003680) unknown protein [Arabidopsis thaliana] NCBI Description

25279 Seq. No.

124637 1.R1040 Contig ID fC-gmse700673147f2 5'-most EST

Method BLASTX q3402694 NCBI GI Ĭ067 BLAST score



E value 1.0e-117
Match length 289
% identity 71

NCBI Description (AC004697) putative Mlo-hi protein [Arabidopsis thaliana]

Seq. No. 25280

Contig ID 124644\_1.R1040 5'-most EST uxk700673154.h1

Seq. No. 25281

Contig ID 124663 1.R1040 5'-most EST asn701140409.h1

Seq. No. 25282

Contig ID 124668 1.R1040

5'-most EST uC-gmflminsoy054c04b1

Method BLASTX
NCBI GI g2244833
BLAST score 256
E value 7.0e-22
Match length 192
% identity 33

NCBI Description (Z97337) centromere protein homolog [Arabidopsis thaliana]

Seq. No. 25283

Contig ID 124678\_1.R1040 5'-most EST rry700808476.h1

Seq. No. 25284

Contig ID 124686 1.R1040

5'-most EST uC-gmrominsoy192h06b1

Seq. No. 25285

Contig ID 124741\_1.R1040 5'-most EST uxk700673281.h1

Method BLASTX
NCBI GI g4455367
BLAST score 296
E value 7.0e-27
Match length 122
% identity 34

NCBI Description (AL035524) putative protein [Arabidopsis thaliana]

Seq. No. 25286

Contig ID 124742 1.R1040

5'-most EST uC-gmflminsoy066e12b1

Seq. No. 25287

Contig ID 124754\_1.R1040 5'-most EST uxk700673304.h1

Method BLASTX
NCBI GI g3461849
BLAST score 490
E value 1.0e-49
Match length 113
% identity 77

NCBI Description (AC005315) putative cytochrome P450 [Arabidopsis thaliana]



Seq. No. 25288

Contig ID 124789\_1.R1040 5'-most EST uxk700673353.h1

Method BLASTX
NCBI GI g3695379
BLAST score 313
E value 7.0e-29
Match length 94
% identity 67

NCBI Description (AF096370) contains similarity to a C. elegans hypothetical

protein F44G4.1 (GB:Z49910) and several yeast hypothetical proteins such as 35.1 KD protein in NAM8-GAR1 intergenic

region (SP:P38805) [Arabidopsis thaliana]

Seq. No. 25289

Contig ID 124790\_1.R1040 5'-most EST uxk700673356.h1

Seq. No. 25290

Contig ID 124806\_1.R1040 5'-most EST fde700874719.h1

Seq. No. 25291

Contig ID 124824\_1.R1040 5'-most EST gsv701045829.h1

Seq. No. 25292

Contig ID 124825\_1.R1040 5'-most EST uC-gmropic043h02b1

Method BLASTX
NCBI GI g1688072
BLAST score 214
E value 4.0e-17
Match length 116
% identity 45

NCBI Description (U41369) biotin holocarboxylase synthetase [Arabidopsis

thaliana]

Seq. No. 25293

Contig ID 124846\_1.R1040 5'-most EST asn701141953.h1

Method BLASTX
NCBI GI g3023932
BLAST score 552
E value 5.0e-62
Match length 160
% identity 66

NCBI Description HISTONE DEACETYLASE 3 (HD3) >gi\_2791688 (AF039753) histone

deacetylase-3; HD-3 [Gallus gallus]

Seq. No. 25294

Contig ID 124888\_1.R1040 5'-most EST kmv700738665.h1

Seq. No. 25295

Contig ID 124926\_1.R1040



```
djj700606031.h2
5'-most EST
                   25296
Seq. No.
                   124955 1.R1040
Contig ID
                   djj700606069.h2
5'-most EST
                   25297
Seq. No.
                   124959_1.R1040
Contig ID
                   zzp700833893.h1
5'-most EST
                   25298
Seq. No.
                   125025 1.R1040
Contig ID
                   jC-qmfl02220070g07d1
5'-most EST
                   25299
Seq. No.
                   125038 1.R1040
Contig ID
                   sat701\overline{0}14116.h1
5'-most EST
                   BLASTX
Method
                   g322641
NCBI GI
BLAST score
                   702
E value
                   7.0e-74
Match length
                   238
% identity
                   beta-1,3-glucanase homolog (clone A6) - rape (fragment)
NCBI Description
                   >gi 17738 emb CAA49513 (X69887) beta-1,3-glucanase
                   homologue [Brassica napus]
                   25300
Seq. No.
                   125071 1.R1040
Contig ID
                   vwf700\overline{6}75127.h1
5'-most EST
                   25301
Seq. No.
                   125094 1.R1040
Contig ID
5'-most EST
                   g5058427
                   25302
Seq. No.
                   125105 1.R1040
Contig ID
                   vwf700673738.h1
5'-most EST
                   25303
Seq. No.
                   125132 1.R1040
Contig ID
                   fC-gmf1700906093a1
5'-most EST
```

BLASTX Method NCBI GI g4335745 BLAST score 636 5.0e-66 E value Match length 306 % identity 43

(AC006284) putative hydrolase (contains an NCBI Description

esterase/lipase/thioesterase active site serine domain

(prosite: PS50187) [Arabidopsis thaliana]

25304 Seq. No.

125167 1.R1040 Contig ID vwf700673852.h1 5'-most EST

BLASTX Method g1169200 NCBI GI



BLAST score 204
E value 9.0e-16
Match length 103
% identity 47

NCBI Description DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT111 PRECURSOR

>gi\_421829\_pir\_\_S33706 DNA-damage resistance protein Arabidopsis thaliana >gi\_166694 (M98455) [Arabidopsis
thaliana recombination and DNA-damage resistance protein
(DRT111) mRNA, complete cds.], gene product [Arabidopsis

thaliana]

Seq. No. 25305

Contig ID 125192\_1.R1040 5'-most EST vwf700673893.h1

Method BLASTX
NCBI GI g2842424
BLAST score 144
E value 1.0e-08
Match length 91
% identity 40

NCBI Description (AJ223948) RNA helicase [Homo sapiens]

Seq. No. 25306

Contig ID 125203\_1.R1040 5'-most EST vwf700678932.h1

Method BLASTX
NCBI GI 94220514
BLAST score 387
E value 7.0e-38
Match length 81
% identity 81

NCBI Description (AL035356) putative protein [Arabidopsis thaliana]

Seq. No. 25307

Contig ID 125210\_1.R1040 5'-most EST vwf700678945.h1

Method BLASTX
NCBI GI g1174862
BLAST score 148
E value 9.0e-10
Match length 82
% identity 37

NCBI Description PUTATIVE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE C13A11.04C

(UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING

PROTEASE) (DEUBIQUITINATING ENZYME)

>gi 984225 emb\_CAA90805\_ (Z54096) unknown

[Schizosaccharomyces pombe]

Seq. No. 25308

Contig ID 125218\_1.R1040 5'-most EST vwf700673942.h1

Method BLASTX
NCBI GI g3337361
BLAST score 277
E value 9.0e-25
Match length 98
% identity 53



709

174

34

5.0e-75

BLAST score

Match length % identity

NCBI Description

E value

```
NCBI Description (AC004481) ankyrin-like protein [Arabidopsis thaliana]
                  25309
Seq. No.
                  125219 1.R1040
Contig ID
5'-most EST
                  uC-gmflminsoy071c01b2
                  BLASTX
Method
                  g3152938
NCBI GI
BLAST score
                  166
                  2.0e-11
E value
                  137
Match length
                  35
% identity
                  (AF065482) sorting nexin 2 [Homo sapiens]
NCBI Description
                  >gi 4507141_ref_NP_003091.1_pSNX2_ sorting nexin
                  25310
Seq. No.
                  125226 1.R1040
Contig ID
                  vwf700673956.h1
5'-most EST
                  BLASTX
Method
                  g4115388
NCBI GI
                  367
BLAST score
                  7.0e-35
E value
                  126
Match length
                  57
% identity
                  (AC005967) putative prolylcarboxypeptidase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  25311
                  125231 1.R1040
Contig ID
5'-most EST
                  vwf700673964.hl
                  25312
Seq. No.
                  125235 1.R1040
Contig ID
                  vwf700674103.h1
5'-most EST
Method
                  BLASTN
                  q3869071
NCBI GI
BLAST score
                   47
E value
                   2.0e-17
                   107
Match length
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MIL23, complete sequence [Arabidopsis thaliana]
                   25313
Seq. No.
                   125280 1.R1040
Contig ID
5'-most EST
                   vwf700674055.hl
                   25314
Seq. No.
                   125310 1.R1040
Contig ID
                   gsv701049601.h1
5'-most EST
Method
                   BLASTX
                   q2950210
NCBI GI
```

3981

(Y14615) Importin alpha-like protein [Arabidopsis thaliana]



Seq. No. 25315 125313 1.R1040 Contig ID vwf700674117.h1 5'-most EST BLASTX Method g3789799 NCBI GI 192 BLAST score 6.0e-14 E value Match length 182 14 % identity (AF060219) RCC1-like G exchanging factor RLG [Homo sapiens] NCBI Description >gi\_4557445\_ref\_NP\_001259.1\_pCHC1L\_ RCC1-like G exchanging factor RLG 25316 Seq. No. 125358 1.R1040 Contig ID vwf700674203.h1 5'-most EST 25317 Seq. No. 125360 1.R1040 Contig ID fC-gmse700674206f2 5'-most EST BLASTX Method g3540207 NCBI GI 656 BLAST score 2.0e-68 E value Match length 193 70 % identity (AC004260) Putative protein kinase [Arabidopsis thaliana] NCBI Description 25318 Seq. No. 125363 1.R1040 Contig ID vwf700674213.h1 5'-most EST 25319 Seq. No. 125365\_1.R1040 Contig ID jC-gmst02400072f12a1 5'-most EST 25320 Seq. No. Contig ID 125371 1.R1040 hrw701060624.hl 5'-most EST Method BLASTX a2501555 NCBI GI 461 BLAST score 4.0e - 46E value 133 Match length % identity 64 POSSIBLE APOSPORY-ASSOCIATED PROTEIN C >gi 549984 (U13148) NCBI Description possible apospory-associated protein [Pennisetum ciliare] Seq. No. 25321 Contig ID 125403 1.R1040 5'-most EST fC-qmse700674289f2

Method BLASTX
NCBI GI g3617742
BLAST score 242
E value 4.0e-20
Match length 64
% identity 69



NCBI Description (AC005687) RAP2.6 [Arabidopsis thaliana]

Seq. No. 25322

Contig ID 125415\_1.R1040 5'-most EST vwf700674314.h1

Method BLASTN
NCBI GI g3510336
BLAST score 40
E value 2.0e-13

Match length 80 % identity 88

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K18J17, complete sequence [Arabidopsis thaliana]

Seq. No. 25323

Contig ID 125427\_1.R1040 5'-most EST vwf700674327.h1

Seq. No. 25324

Contig ID 125430\_1.R1040 5'-most EST vwf700674330.h1

Seq. No. 25325

Contig ID 125435\_1.R1040 5'-most EST vwf700674373.h1

Method BLASTX
NCBI GI g2342683
BLAST score 545
E value 7.0e-56
Match length 109
% identity 89

NCBI Description (AC000106) Contains similarity to Bos beta-mannosidase

(gb\_U46067). [Arabidopsis thaliana]

Seq. No. 25326

Contig ID 125501\_1.R1040 5'-most EST vwf700674453.h1

Seq. No. 25327

Contig ID 125528 1.R1040 5'-most EST zpv700763665.h1

Method BLASTN
NCBI GI g169928
BLAST score 218
E value 1.0e-119
Match length 258
% identity 86

NCBI Description Glycine max alpha'-type beta conglycinin storage protein

gene, complete cds, clone ch4A

Seq. No. 25328

Contig ID 125532 1.R1040 5'-most EST kl1701204351.h2

Method BLASTX NCBI GI g1657619 BLAST score 264 E value 7.0e-23



Match length 139 % identity 42

NCBI Description (U72504) G5p [Arabidopsis thaliana] >gi\_3068710 (AF049236) putative transmembrane protein G5p [Arabidopsis thaliana]

Seq. No. 25329

Contig ID 125534\_1.R1040 5'-most EST vwf700678746.h1

Seq. No. 25330

Contig ID 125549\_1.R1040 5'-most EST sat701013124.h1

Seq. No. 25331

Contig ID 125558\_1.R1040 5'-most EST fC-gmse700674558f2

Method BLASTN
NCBI GI g2286199
BLAST score 224
E value 1.0e-122
Match length 664
% identity 87

NCBI Description Pisum sativum polynucleotide phosphorylase (pnp) mRNA,

complete cds

Seq. No. 25332

Contig ID 125558\_2.R1040

5'-most EST jC-gmst02400052c10a1

Method BLASTN
NCBI GI g2286199
BLAST score 145
E value 1.0e-75
Match length 261
% identity 89

NCBI Description Pisum sativum polynucleotide phosphorylase (pnp) mRNA,

complete cds

Seq. No. 25333

Contig ID 125562\_1.R1040 5'-most EST uC-gmropic031g09b1

Method BLASTX
NCBI GI g1871192
BLAST score 432
E value 2.0e-42
Match length 185
% identity 56

NCBI Description (U90439) Cys3His zinc finger protein isolog [Arabidopsis

thaliana]

Seq. No. 25334

Contig ID 125582\_1.R1040 5'-most EST 94395901

Seq. No. 25335

Contig ID 125610\_1.R1040 5'-most EST sat701006239.h2

Method BLASTX



NCBI GI q548585 BLAST score 143 E value 1.0e-08 Match length 129 22 % identity POLY [ADP-RIBOSE] POLYMERASE (PARP) (ADPRT) (NAD(+) NCBI Description ADP-RIBOSYLTRANSFERASE) (POLY[ADP-RIBOSE] SYNTHETASE) >gi 476993 pir A47474 NAD+ ADP-ribosyltransferase (EC 2.4.2.30) - fruit fly (Drosophila melanogaster) >gi 303546 dbj BAA02964 (D13806) poly(ADP-ribose) polymerase [Drosophila melanogaster] >gi 3044062 (AF051548) poly(ADP-ribose) polymerase [Drosophila melanogaster] 25336 Seq. No. 125620 1.R1040 Contig ID 5'-most EST epx701110107.hl Seq. No. 25337 Contig ID 125635 1.R1040 vwf700675064.h1 5'-most EST Method BLASTN q167227 NCBI GI BLAST score 178 1.0e-95 E value 349 Match length % identity 88 NCBI Description Canavalia ensiformis urease (ure) mRNA, complete cds Seq. No. 25338 125643 1.R1040 Contig ID 5'-most EST epx701108171.h1 25339 Seq. No. Contig ID 125686 1.R1040 5'-most EST jC-gmf102220106h12a1 Seq. No. 25340 125694 1.R1040 Contig ID 5'-most EST bth700847010.h1 Method BLASTX q2829894 NCBI GI BLAST score 200 2.0e-15 E value Match length 89 % identity 46 (AC002311) Unknown protein [Arabidopsis thaliana] NCBI Description Seq. No. 25341 125699 1.R1040 Contig ID kmv700743686.hl 5'-most EST BLASTN Method q4220643 NCBI GI

NCBI GI g422064:
BLAST score 87
E value 5.0e-41
Match length 375
% identity 81

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:



## MWD22, complete sequence [Arabidopsis thaliana]

25342 Seq. No. 125705 1.R1040 Contig ID 5'-most EST vwf700674833.h1 Seq. No. 25343 125709 1.R1040 Contig ID 5'-most EST cks700764885.h1 Method BLASTX NCBI GI q3894190 BLAST score 196 E value 4.0e-15 Match length 67 52 % identity NCBI Description (AC005662) putative RNA polymerase [Arabidopsis thaliana] Seq. No. 25344 125711 1.R1040 Contig ID 5'-most EST vwf700674842.h1 Seq. No. 25345 Contig ID 125720 1.R1040 5'-most EST uC-gmflminsoy080a11b1 Method BLASTX NCBI GI q3892057 BLAST score 774 E value 1.0e-82 Match length 177 % identity 43 NCBI Description (AC002330) hypothetical protein [Arabidopsis thaliana] Seq. No. 25346 125742 1.R1040 Contig ID 5'-most EST vwf700674908.h1 25347 Seq. No. 125777 1.R1040 Contig ID 5'-most EST vwf700674975.h1 Method BLASTX NCBI GI g3122914 BLAST score 786 E value 8.0e-84 Match length 173 % identity 81 NCBI Description VALYL-TRNA SYNTHETASE (VALINE--TRNA LIGASE) (VALRS) >gi 1890130 (U89986) valyl tRNA synthetase [Arabidopsis thaliana] Seq. No. 25348 125798 1.R1040 Contig ID 5'-most EST vwf700675015.h1 Method BLASTX

NCBI GI g1483177 BLAST score 139 E value 1.0e-08 Match length 93

3986

**,** -



% identity 37

NCBI Description (D86598) antifreeze-like protein (af70) [Picea abies]

Seq. No. 25349

Contig ID 125824\_1.R1040 5'-most EST kl1701207005.h1

Seq. No. 25350

Contig ID 125841\_1.R1040 5'-most EST vwf700675114.h1

Seq. No. 25351

Contig ID 125872 1.R1040 5'-most EST vwf700675171.h1

Seq. No. 25352

Contig ID 125876 1.R1040 5'-most EST kl1701211832.h1

Seq. No. 25353

Contig ID 125876 2.R1040 5'-most EST asn701131910.h1

Seq. No. 25354

Contig ID 125890\_1.R1040 5'-most EST vwf700675204.h1

Seq. No. 25355

Contig ID 125940 1.R1040 5'-most EST vwf700675280.h1

Seq. No. 25356

Contig ID 125942 1.R1040 5'-most EST hrw701061557.h1

Method BLASTX
NCBI GI g4468984
BLAST score 217
E value 1.0e-17
Match length 118
% identity 39

NCBI Description (AL035605) putative protein [Arabidopsis thaliana]

Seq. No. 25357

Contig ID 125943\_1.R1040 5'-most EST fC-gmf1700907258a1

Method BLASTX
NCBI GI g3367516
BLAST score 543
E value 3.0e-55
Match length 243
% identity 43

NCBI Description (AC004392) Similar to beta-glucosidase BGQ60 precursor

gb\_L41869 from Hordeum vulgare. [Arabidopsis thaliana]

Seq. No. 25358

Contig ID 125943 2.R1040 5'-most EST vwf700675285.h1



 Seq. No.
 25359

 Contig ID
 125955\_1.R1040

 5'-most EST
 jC-gmst0240004

jC-gmst02400040b04a1 BLASTX

Method BLASTX
NCBI GI 94006876
BLAST score 178
E value 6.0e-13
Match length 88
% identity 53

NCBI Description (Z99707) hypothetical protein [Arabidopsis thaliana]

Seq. No. 25360

Contig ID 125986\_1.R1040 5'-most EST vwf700675367.h1

Method BLASTX
NCBI GI 94580455
BLAST score 582
E value 2.0e-60
Match length 138
% identity 86

NCBI Description (AC006081) unknown protein [Arabidopsis thaliana]

Seq. No. 25361

Contig ID 126019 1.R1040 5'-most EST kl1701208986.h1

Seq. No. 25362

Contig ID 126026\_1.R1040 5'-most EST jC-gmle01810073g03a1

Seq. No. 25363

Contig ID 126027\_1.R1040

5'-most EST jC-gmst02400057e07d1

Seq. No. 25364

Contig ID 126028 1.R1040

5'-most EST uC-gmflminsoy032f03b1

Seq. No. 25365

Contig ID 126053\_1.R1040 5'-most EST vwf700675492.h1

Seq. No. 25366

Contig ID 126062 1.R1040 5'-most EST eep700868534.h1

Seq. No. 25367

Contig ID 126071 1.R1040 5'-most EST crh700851883.h1

Seq. No. 25368

Contig ID 126113\_1.R1040 5'-most EST awf700841684.h1

Seq. No. 25369

Contig ID 126124 1.R1040



5'-most EST dpv701097948.h1 Seq. No. 25370 126154 1.R1040 Contig ID 5'-most EST vwf700675670.h1 Seq. No. 126199 1.R1040 Contig ID 5'-most EST vwf700675738.hl Seq. No. 25372 Contig ID 126225 1.R1040 5'-most EST hyd700726391.h1 Seq. No. 25373 126235 1.R1040 Contig ID 5'-most EST vzy700754350.h1 Seq. No. 25374 Contig ID 126274 1.R1040 5'-most EST vwf700675866.h1 Seq. No. 25375 Contig ID 126277 1.R1040 5'-most EST  $jsh701\overline{0}69279.h1$ Seq. No. 25376 Contig ID 126288 1.R1040 5'-most EST vwf700675886.h1 Seq. No. 25377 126308 1.R1040 Contig ID 5'-most EST vwf700675919.hl Method BLASTX NCBI GI q4539384 BLAST score 250 1.0e-21 E value Match length 90 % identity 54 NCBI Description (AL035526) putative protein [Arabidopsis thaliana] Seq. No. 25378 Contig ID 126338 1.R1040 5'-most EST jC-gmf102220144e08a1 Seq. No. 25379 Contig ID 126343 1.R1040 5'-most EST g4290835

Seq. No. 25380

Contig ID 126389\_1.R1040 5'-most EST fC-gmse700676040f2

Method BLASTX
NCBI GI g3256035
BLAST score 855
E value 4.0e-92
Match length 204



% identity (Y14274) putative serine/threonine protein kinase [Sorghum NCBI Description bicolor] 25381 Seq. No. Contig ID 126391 1.R1040 5'-most EST vwf700676046.h1 Seq. No. 25382 126405 1.R1040 Contig ID 5'-most EST vwf700676066.h1 Seq. No. 25383 Contig ID 126417 1.R1040  $vwf700\overline{6}76286.h1$ 5'-most EST Method BLASTX q2213626 NCBI GI BLAST score 186 E value 3.0e-14Match length 67 52 % identity NCBI Description (AC000103) F21J9.18 [Arabidopsis thaliana] Seq. No. 25384 Contig ID 126422 1.R1040 5'-most EST vwf700679640.h1 Method BLASTX q4539346 NCBI GI BLAST score 654 E value 2.0e-68 Match length 214 69 % identity NCBI Description (AL035539) putative protein [Arabidopsis thaliana] Seq. No. 25385 Contig ID 126429 1.R1040 5'-most EST awf700836564.h1 Method BLASTX NCBI GI q3046696 BLAST score 633 E value 3.0e-66 Match length 157 % identity 75 NCBI Description (AL022224) CTP synthase like protein [Arabidopsis thaliana] 25386 Seq. No. Contig ID 126430 1.R1040 5'-most EST leu701145212.h1 Seq. No. 25387

Contig ID 126435\_1.R1040 5'-most EST vwf700676313.h1

Method BLASTX
NCBI GI g2347208
BLAST score 192
E value 6.0e-15
Match length 80



% identity 41
NCBI Description (AC002338) APG protein isolog [Arabidopsis thaliana]

Seq. No. 25388

Contig ID 126442 1.R1040 5'-most EST kl1701214183.h1

Method BLASTX
NCBI GI g1076802
BLAST score 227
E value 2.0e-18
Match length 150
% identity 2

NCBI Description extensin-like protein - maize >gi\_600118\_emb\_CAA84230\_

(Z34465) extensin-like protein [Zea mays]

>gi 1096557 prf\_\_2111476A extensin-like domain [Zea mays]

Seq. No. 25389

Contig ID 126442\_2.R1040

5'-most EST g5753657

Seq. No. 25390

Contig ID 126451\_1.R1040 5'-most EST vwf700679635.h1

Seq. No. 25391

Contig ID 126464\_1.R1040 5'-most EST vwf700676159.h1

Seq. No. 25392

Contig ID 126469\_1.R1040 5'-most EST zhf700960289.h1

Method BLASTX
NCBI GI g4262167
BLAST score 265
E value 1.0e-45
Match length 131
% identity 73

NCBI Description (AC005275) putative LRR receptor-linked protein kinase

[Arabidopsis thaliana]

Seq. No. 25393

Contig ID 126472 1.R1040

5'-most EST g5126841
Method BLASTX
NCBI GI g688423
BLAST score 147
E value 2.0e-09
Match length 97
% identity 42

NCBI Description (D26453) tumor-related protein [Nicotiana glauca X

Nicotiana langsdorffii]

Seq. No. 25394

Contig ID 126482 1.R1040 5'-most EST vwf700676280.h1

Seq. No. 25395



Contig ID 126519\_1.R1040 5'-most EST vwf700678648.h1

Method BLASTX
NCBI GI g3292829
BLAST score 332
E value 2.0e-31
Match length 90
% identity 66

NCBI Description (AL031018) putative protein [Arabidopsis thaliana]

Seq. No. 25396

Contig ID 126536\_1.R1040 5'-most EST fua701038758.h1

Method BLASTX
NCBI GI g3023961
BLAST score 928
E value 1.0e-100
Match length 206
% identity 87

NCBI Description HOMEOBOX PROTEIN KNOTTED-1-LIKE >gi\_1946222\_emb\_CAA96512\_ (Z71980) knotted1-like homeobox protein [Malus domestica]

Seq. No. 25397

Contig ID 126538 1.R1040

5'-most EST uC-gmflminsoy075e02b1

Seq. No. 25398

Contig ID 126544\_1.R1040 5'-most EST rca700996206.h1

Seq. No. 25399

Contig ID 126553\_1.R1040 5'-most EST euj700698052.h1

Seq. No. 25400

Contig ID 126571\_1.R1040 5'-most EST hyd700729047.h1

Method BLASTX
NCBI GI g2196878
BLAST score 376
E value 2.0e-36
Match length 76
% identity 93

NCBI Description (Y08292) NADH glutamate dehydrogenase [Nicotiana

plumbaginifolia]

Seq. No. 25401

Contig ID 126592\_1.R1040 5'-most EST vwf700676377.h1

Seq. No. 25402

Contig ID 126608\_1.R1040 5'-most EST vwf700676422.h1

Seq. No. 25403

Contig ID 126617\_1.R1040 5'-most EST vwf700676438.h1



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25404
Seq. No.
                   126624 1.R1040
Contig ID
                   vwf700676449.h1
5'-most EST
                   BLASTX
Method
                   g2088650
NCBI GI
BLAST score
                   207
                   4.0e-16
E value
                   53
Match length
                   77
% identity
                   (AF002109) peroxisomal ATP/ADP carrier protein isolog
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   25405
                   126629 1.R1040
Contig ID
5'-most EST
                   vwf700676456.h1
                   25406
Seq. No.
                   126643 1.R1040
Contig ID
5'-most EST
                   vwf700\overline{6}76475.h1
                   25407
Seq. No.
                   126651 1.R1040
Contig ID
5'-most EST
                   vwf700676494.h1
Method
                   BLASTX
                   g4510395
NCBI GI
BLAST score
                   476
                   5.0e-48
E value
Match length
                   101
% identity
                   82
                   (AC006587) putative beta-galactosidase precursor
NCBI Description
                   [Arabidopsis thaliana]
                   25408
Seq. No.
Contig ID
                   126652 1.R1040
5'-most EST
                   vwf700676496.h1
                   25409
Seq. No.
                   126680 1.R1040
Contig ID
5'-most EST
                   vwf700676656.h1
Seq. No.
                   25410
                   126708 1.R1040
Contig ID
                   ncj700\overline{9}86649.h1
5'-most EST
Method
                   BLASTN
                   g4567193
NCBI GI
BLAST score
                   66
E value
                   2.0e-28
Match length
                   308
                   83
% identity
```

NCBI Description Arabidopsis thaliana chromosome II BAC T26C19 genomic sequence, complete sequence

Seq. No. 25411

Contig ID 126735\_1.R1040 5'-most EST cks700764716.h1

Method BLASTX



```
NCBI GI
                  q3859534
BLAST score
                  906
E value
                   4.0e-98
                  185
Match length
% identity
                  (AF095452) asparagine synthetase [Arabidopsis thaliana]
NCBI Description
                  25412
Seq. No.
Contig ID
                  126778 1.R1040
                   jC-gmro02910071c08a1
5'-most EST
Method
                  BLASTX
NCBI GI
                   q4006894
BLAST score
                   302
                   3.0e-27
E value
Match length
                   96
                   61
% identity
NCBI Description (Z99708) homeodomain protein [Arabidopsis thaliana]
Seq. No.
                   25413
Contig ID
                   126809 1.R1040
                   vwf700676849.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3292811
BLAST score
                   236
E value
                   4.0e-20
Match length
                   86
% identity
                   53
NCBI Description (AL031018) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   25414
                   126810 1.R1040
Contig ID
                   vwf700676762.h1
5'-most EST
Seq. No.
                   25415
                   126820 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy010b07b1
                   25416
Seq. No.
Contig ID
                   126829 1.R1040
5'-most EST
                   vwf700676785.h1
                   25417
Seq. No.
                   126830 1.R1040
Contig ID
5'-most EST
                   vwf700676786.h1
Method
                   BLASTX
NCBI GI
                   q2347198
BLAST score
                   322
E value
                   4.0e-30
Match length
                   63
% identity
                   90
                   (AC002338) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   25418
Seq. No.
                   126831 1.R1040
Contig ID
                   vwf700\overline{6}79213.h1
5'-most EST
```

Seq. No. 25419



Contig ID 126834\_1.R1040 5'-most EST leu701146111.h1

Seq. No. 25420

Contig ID 126840\_1.R1040 5'-most EST zpv700760882.h1

Seq. No. 25421

Contig ID 126850\_1.R1040 5'-most EST fC-gmro700846408a1

Method BLASTX
NCBI GI g4191775
BLAST score 1175
E value 1.0e-129
Match length 295
% identity 74

NCBI Description (AC005917) putative acyl-CoA cholesterol acyltransferase

[Arabidopsis thaliana]

Seq. No. 25422

Contig ID 126869\_1.R1040 5'-most EST vwf700676850.h1

Seq. No. 25423

Contig ID 126885\_1.R1040 5'-most EST vwf700679471.h1

Seq. No. 25424

Contig ID 126935 1.R1040

5'-most EST jC-gmfl02220085a10a1

Method BLASTX
NCBI GI g1345132
BLAST score 978
E value 1.0e-106
Match length 275
% identity 17

NCBI Description (U47029) ERECTA [Arabidopsis thaliana]

>gi\_1389566\_dbj\_BAA11869\_ (D83257) receptor protein kinase

[Arabidopsis thaliana] >gi\_3075386 (AC004484) receptor

protein kinase, ERECTA [Arabidopsis thaliana]

Seq. No. 25425

Contig ID 126937\_1.R1040

5'-most EST g5753028

Seq. No. 25426

Contig ID 126957\_1.R1040 5'-most EST wvk700683311.h1

Seq. No. 25427

Contig ID 126959\_1.R1040 5'-most EST vwf700676995.h1

Seq. No. 25428

Contig ID 126965\_1.R1040 5'-most EST zsg701118332.h1



Seq. No. 25429

Contig ID 126979\_1.R1040

5'-most EST uC-gmrominsoy241d04b1

Seq. No. 25430

Contig ID 126983\_1.R1040 5'-most EST vwf700679120.h1

Seq. No. 25431

Contig ID 126996\_1.R1040 5'-most EST pmv700895158.h1

Method BLASTX
NCBI GI g2651309
BLAST score 390
E value 5.0e-38
Match length 87
% identity 90

NCBI Description (AC002336) unknown protein [Arabidopsis thaliana]

Seq. No. 25432

Contig ID 127027\_1.R1040 5'-most EST zpv700759319.h1

Seq. No. 25433

Contig ID 127028\_1.R1040 5'-most EST vwf700677110.h1

Seq. No. 25434

Contig ID 127037\_1.R1040 5'-most EST txt700735495.h1

Seq. No. 25435

Contig ID 127076\_1.R1040 5'-most EST sat701010592.h1

Method BLASTX
NCBI GI g2492782
BLAST score 284
E value 4.0e-37
Match length 101
% identity 75

NCBI Description ALPHA-GALACTOSIDASE PRECURSOR (MELIBIASE)

(ALPHA-D-GALACTOSIDE GALACTOHYDROLASE) >gi\_504489 (L27992)

alpha-galactosidase [Coffea arabica]

Seq. No. 25436

Contig ID 127132\_1.R1040 5'-most EST vwf700677801.h1

Seq. No. 25437

Contig ID 127162 1.R1040 5'-most EST vwf700677457.h1

Method BLASTX
NCBI GI g3249095
BLAST score 247
E value 7.0e-35
Match length 86
% identity 83